

251	ATCAGATACC	TCCAAGCTGC	CGGCAATCAG	TGGTGGTGAT	GACCGTGCGG
301	ACCGTGACA	TGACCGTGTG	CGATTTCCTC	ATCGGATGCA	TCGCGCACAC
351	TTTCAACCGT	AGCCTTTAAAG	CGGATTTTCA	TGCGTGCCAA	AGGATGGTTG
401	CGGTCCACCA	CCGCTTTACC	TCGGGCAACA	TCGGTTACAC	GATAGACGAC
451	AACATCGCCG	GTTTCAGGAT	CGTCGGCTTC	AAACATCATG	CCGACTTCGA
501	CTTCAACAGG	GAACACGCCC	GCATCTTCAA	TACGGACCAA	CTCCGGATCC
551	TGCTCGCCGA	ACGCATCGTC	GGCGCAAAAG	GCCACATCGA	CCGSTATCGCC
601	GGCATCTCTA	CCTGCAACG	CCTCTTCCAC	CAAAGGGAAA	ATGCCGTCGT
651	AACCGCCGTG	CAGATACGCA	ATCGGTTCTT	CGGTTTTGTC	CAAAAGCTGA
701	TTGTGGGCAT	CATACATCTC	ATAATGCAGC	GAACCACGG	AATTCTTCAC
751	GATAGCCATA	TTTGTCTTTT	CAGGAACAGC	AGATTAAATA	CAGGCGCATT
801	CTAA				

```
a241.pep
1  MPTRPTRAAK HPTPPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVVMTVR
101 TVDMTVCDFL IGCIAHTFNR SLKADFHAQC RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDFNR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTQQLRFH QRENAVVTAV QIRNRFFGFV QKLIVGIHL IMORNHGILH
251 DSHICPFNRN RLITGAF*
```

```

                                10          20          30
m241.pep                      RQSVVVM TVRAVDMTVCDFLIGCIAHAFNC
                               |||||:|||||:|||||:|||||:|
a241      QPTYLLHPSNKM PSEMEQT LFRRHQIP PSQRQSVVVM TVRTVDM TVCDFLIG CIAHTFN R
              70          80          90         100        110        120

              40          50          60          70          80          90
m241.pep    SLKADFACQRM VAVHHRLAVGNIGYTID DNIAGFRI VGFKHHAD FDNREHARIFD TDQ
              |||||:|||||:|||||:|||||:|||||:|||||:|
a241      SLKADFACQRM VAVHHRLTVGNIGYTID DNIAGFRI VGFKHHAD FDNREHARIFNTD Q
              130        140        150        160        170        180

              100        110        120        130        140        150
m241.pep    LRILLAERIVGR QRHRIDRIAGILTVQ RLFLHQREN AVVTAVQIR NRFFGFVQKLIVGI IHL
              |||||:|||||:|||||:|||||:|||||:|||||:|
a241      LRILLAERIVGR KRHRIDRIAGILTVQ RLFLHQREN AVVTAVQIR NRFFGFVQKLIVGI IHL
              190        200        210        220        230        240

              160        170
m241.pep    IMQRNHGIFHD SHICPFNRNSRLITGA FX
              |||||:|||||:|||||:|||||:|
a241      IMQRNHGILHD SHICPFNRNSRLITGA FX
              250        260

```

g241-1.seq

1	ATGATAGAAG	TCATACATTT	CTTCGGCACC	GAAACGCGCA	GACAGTTTGC
51	TTGTGCCGAC	TTGTGACGAT	TTCTGTCATGA	TGCCGCGCAC	ATCCAAGAAG
101	GGGTAAACAT	GGGTATCGCG	CACGGGAGAC	GGTCCGATTT	TATAAGGCTG
151	CGTATTACG	CGTTCGTTC	AATCGGTTT	GCCCGCATCC	AATGCGCTTG
201	CAATACAAA	CGGTTTGATT	GCCGAACCGG	GTCGATCAT	ATCGGTTACG
251	GCACGGTTGC	GCCGCTGTTT	GCTGTCTGCC	CGGCCGGGCC	TGTTGGGATC
301	GTAGCGGGCG	GTTATGGCCA	AGGCCAGGAT	TTCCCCGGTG	CGGGCATCCA
351	ATACCCACC	CGATTCGGCT	TTTGGCTGAT	GGTATTCCAG	CGCCTTGTTG
401	AACCTTTCAT	AGGCCAAGGT	CTGAATCCTC	TGATCAGAGG	AAAGGATGAT
451	GTCTTTGGCG	TTTTTTCGGG	CTTTAKTGCG	CGGGGAGTCC	AAGCTGTCCA
501	CAATATTGCC	CTCGCGGTCC	CGCAAAAAGCA	CTTCGCGGCC	GTCTTCGCCA
551	TGCAAGCTGT	CTTCAAGCGA	AAGTTCCAAA	CCTTCCTGAC	CTTTGCCGTC
601	AATATCGGTA	AATCCGATGA	CGTGTGCAAA	CAGGTTGCCC	ATCGGGTAAT
651	GGCGTTTTAA				

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

555

```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTC AACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCGGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1  MPTRPTRA AK HPTPTWLQT AYCPRPYP RP SVQTHPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPS RQSVVMTVR
101 TVDMTVCD FL IGCIAHTFNR SLKADFACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDNR EHARIFNTDQ LRILLAERIV GRKRHDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTWLQTAYCPRPYP RP SVQTRTPREPASSTCAAKSANRRENSHNA					
a241	MPTRPTRA AKHPTPTWLQTAYCPRPYP RP SVQTHPHEPASSTCAAKSANRRENFHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSN KMPSETEQTLFRRHQIPPS RQSVVMTVR AVDMTVCD FLIGCIAHAFNC					
a241	QPTYLLHPSN KMPSEMEQTLFRRHQIPPS RQSVVMTVR TVDMTVCD FLIGCIAHTFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFACQ RMVAVHRLAVGNIGYTIDD NIAGFRIVGF KHHADFDNR EHARIFD TDQ					
a241	SLKADFACQ RMVAVHRLTVGNIGYTIDD NIAGFRIVGF KHHADFDNR EHARIF NT DQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIV GRORHDRIA GILTVQRLFHQRENAVVTAV QIRNRFFGFV QKLIVGIIHL					
a241	LRILLAERIV GRKRHDRIA GILTVQRLFHQRENAVVTAV QIRNRFFGFV QKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFH DSHICPFRNS RLITGAF X					
a241	IMQRNHGILH DSHICPFRNS RLITGAF X					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1  atgatcggcg aacttggtgt ttgttcgtg atcgagcact tcaagcaacg
51  cgctggcggg atcgccccga aagtcgctgc ccaatttgtc gatttcgtcg
101 agcaggaaca acgggtttct tacgcctgct ttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccg cggatttcgc
201 ttctgctcgc cacgcgcccc aaggccatac ggacatat ttcgccccgtt
251 gctttggcga tggattcgcc caaagaggtt ttgccacgc ccggagggcc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt ttttggacgg
351 cgaggtatcc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcattccagca ccagtcgggc ttggcgatg tctttgctga cgcgggattt
451 tttcttccac ggcagtcgca gcagggtgct gatgtagttg cgtacgacgg

```

557

	130	140	150	160	170	180
m242 . pep	QNPFDFDFQAVVVGIIQHSGFGDVFADAGFFLPRQLEQSVDDVAYDGGFRRHRWHHFELF					
g242	QNPFDFDFQAVVVGIIQHSGFGDVFADAGFFLPRQSEQGVDDVAYDGGFGRHRHHFEFF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m242 . pep	QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS					
g242	QFGQAFFFRFFGHTRLFDACLGIIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS					
	190	200	210	220	230	240
	250	260	270	280	290	
m242 . pep	AYAFFGLHNVFEGFQLCQQEFHFPADFQNLNLLALRQFQLQMRCDRIGX					
g242	AYAFFGLHNVFEGFQLCQQEFHFPADFQNLNLLALRQFQLQMRCDRIGX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 921>:

```

a242 . seq
1  ATGATCGGCG  AACTTGTGTG  TTTGCTCGGG  ATCAAGCACT  TCGAGCAACG
51  CGCTGGCGGG  ATCGCCCCGG  AAGTCGCTAN  CCAATTGTGC  GATTTCGTGC
101 AGCAGGAACA  ATGGGTTTTT  TACGCCGGCT  TTTGCCATAT  TCTGCAAAAT
151 CTTACCGGGC  ATGGAGCCGA  TATAGGTGCG  GCGGTGTCCC  CGGATTCGC
201 TTTCGTCGCG  CACGCCGCC  AAAGCCATGC  GGACATATTT  CCGCCCCGTT
251 GCTTTGGCGA  TGGATTCGCC  CAAAGAGGTT  TTGCCACAGC  CTGGAGGGCC
301 GACCAGGCAC  AGAATCGGGC  CTTTGAGTTT  GTCCATACGT  TTTTGACGG
351 CGAGGTATTC  CAAAATCCGT  TCTTTGACTT  TTTCCAGGCC  GTAGTGGTCG
401 GTATCCAGCA  CCAATCCGGC  TTTGGCGATG  TCTTTGCTGA  CGCGGGATTT
451 TTTCTTCAC  GGCAGTTCGA  GCAGGTGTC  GATGTAGTTG  CGTACGACGG
501 TGGATTCGGC  AGACATCGGC  GGCATCATTT  TGAGCTTTTT  CAGTTCGGAC
551 AGGCATTTTT  CTTCCGCTTC  TTTGGTCATA  CCCGCCTTTT  TGATATCTGC
601 TTCCAAGGCA  TCCAGTTCGC  CGTTTTCGTC  TTCTTCGCCC  AGTTCTTTGT
651 GTATCGCTTT  AATCTGTTCG  TTCAGATAAT  ATTCGCGCTG  GGATTTTCC
701 ATTTGGCGTT  TGACGCGTCC  GCGTATGCGT  TTTTCGGCCT  GCATAATGTC
751 GAGTTCGGAT  TCCAGCTGTG  CCAGCAGGAA  TTCCATCCGT  TTGCCGATTT
801 CGGGAATTTC  CAAAATCTGT  TGGCGTTGCG  CCAGTTTCAA  CTGCAATGCG
851 GCTGCGACCG  TATCGGTTAG

```

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

```

a242 . pep
1  MIGELVVLGG  IKHFEQRAGG  IAEVAXQFV  DFVEQEQWVF  YAGFCHILQN
51  LTGHGADIGA  AVSPDFAFVA  HAAQSHADIF  PPRCFDGF  QRGFAHAWRA
101 DQAQNRAFEF  VHTFLDGEVF  QNPFDFDFQA  VVVGIIQHSG  FGDVFADAGF
151 FLPRQFEQGV  DVVAYDGGFG  RHRHHHFELF  QFGQAFFFRF  FGHTRLFDIC
201 FQGIQFAVFV  FFAQFFVYRF  NLFVQIIFAL  GFFHLAFDAS  AYAFFGLHNV
251 EFGFQLCQOE  FHPADFQNF  QNLLALRQFQ  LQMRCDRIG*

```

m242/a242 95.2% identity in 289 aa overlap

	10	20	30	40	50	60
m242 . pep	MIGKLVVLFIEHFEQRAGGIASEVVTQFVDFVEQEQGVFHAGFCHILQNLTGHRADIGA					
a242	MIGELVVLGGIKHFEQRAGGIAEVAXQFVDFVEQEQWVFYAGFCHILQNLTGHGADIGA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242 . pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGFQARGFAHARRADQAQNRAFEFVHTFLDGEVF					
a242	AVSPDFAFVAHAAQSHADIFPPRCFGDGFQARGFAHAWRADQAQNRAFEFVHTFLDGEVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m242 . pep	QNPFDFDFQAVVVGIIQHSGFGDVFADAGFFLPRQLEQSVDDVAYDGGFRRHRWHHFELF					

559

70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCAGGCCAC
151 ATCCAGCGGT TTTGACGGA ATCCAAGACG GGGCGAATA AGTCTTCCTC
201 TTCTTGCAAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCTGCA ACGGTCACCC TGCCGATGAG CTTTTTGTTC
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSTFLF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX					
	:					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSTVTLPMSTFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1  atgccgcctg aagcccgcc ggccgggttc gacggcattg ccgctttact
51  tcgatacggt tacaacgaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcatacgctg atggatattc
251 ggatcgagct tatcgccgcg tttaggattg atttccttga ttgctggtgc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcatacga attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acattttcac ggcaaaactc tgcctggcga acttgtgcgt
451 atcggcaatt tcctgctggt ggccggcgcg cagggtttgc tcgtttgcca
501 aagcgcgcag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggtcggcg gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacgggttc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgctgtgtct gttcgctcat atcgatatcc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgcccgc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1  MPPEARPAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LPCHRNHSRA
51  QHTVQGQITL LHHTNHGIGF LLTGHRHLRL MDIRIELIAR FRIDFLDLRG
101 IKRLLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRQLILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRF TVLLCLFAH IVSLKTNWKS KSGYYPKSKIR
251 TFSRNFKQRQ EISHPPNTL PQPKYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

```
m244.seq
```


561

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1  ATGCCGTCTG AAGCCCGACA GCGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCTT CTTTCATCAG CCCACCACGG
201 TATTGGGTTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCTTGA TTTGCGTAGC
301 ATCAATGCTT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAATTC TGTCGGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GGCGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTCG TGCTGTGTCT GTTCGTCAT ATCGTATCCC
701 TTAAACAAAA TTGGAATCA AAATCCAGTT ATTACCGCG CAAGATAAGG
751 ACATTTTCAA GAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1  MPSEARQAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAO LLVFQLRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHVGQRITL					
a244	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLCHRNHSRAQHVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244.pep	IAALIQRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSA-LLVFQLRFQL					
a244	IAALIQRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	230
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
a244	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	240	250	260	270		
m244.pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKKXYRRX					
a244	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKXYRRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1  atgcccgcctg aagccccggc ggcgggttca gacggcattg cgcctttact
```

563

	130	140	150	160	170	180
m244-1.pep	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSAALLVFQRLRFQL					
g244-1	ITALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSAQLFVFQRLRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
g244-1	GNPRLQILISRLGGSLFLYTVRISYCLDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKX					
g244-1	KSGYYPSKIRTFSRNFKQRQEISHPPNPTLPQKPKYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

```

1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTC ACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACACGG TATAACCCCT CTTTCATCAG CCCACCACGG
201 TATTGGGTTC CTGTTCGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGCGGCGC CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATT CTCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTCG TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTAACAACAA TTGGAAATCA AAATCCAGTT ATTACCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCTCA CCGAAAAAT NA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

```

1  MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTSPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQRLRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNREF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQORQ RISNSFSNPL PKK*

```

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTSPSGFLLRHRNHSRAQHAVGQRITL					
a244-1	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTSPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244-1.pep	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSA-LLVFQRLRFQL					
a244-1	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSAQLLVFQRLRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	239
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
a244-1	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
	180	190	200	210	220	240

565

	70	80	90	100	110	120
m246.pep	130	140	150			
	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
g246	130	140	150	160		
	HGFAFDHQLAVFGCDDVVDNLAGFGRGFRPVYFHAQLSQVFFQLLQQRGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246.seq (partial)

```

1  ATGCACGGGC  GGAACGGTGG  TACTCAAGCG  ACCGTTGCCT  TCGTTTCCCA
51  CCAGACACAG  CGTACCTGTT  TCAGCAACGG  CGAAGTTCAC  GCCACTCAAA
101 CCGACATCGG  CAGTGCTGTA  AATATCGGTC  AGTGCTTTAC  GGGCGAAGCC
151 GGTCACTTGG  TCTACGTCGT  CCGTTAACGG  TGTGCCGAGG  TTTTGGTGGA
201 ACAGTTCGCT  AACCTGTTCT  TTGGTTTAT  GGATTGCGGG  CATCACGATA
251 TGGGTCGGTT  TTTACCTGCT  CATTGGACG  ATGAAGTCGC  CCAAGTCGCT
301 TTCCACCGCT  TTAATGCCTT  TTGCTTCAAG  ATAATGGTTC  AGCTCGATTT
351 CCTCGCTGAC  CATCGATTG  CCTTTGACCA  TCAGCTTGCC  GTTTTGGCT
401 GTGATGATGT  CGTGGATGAT  TTCGCAGGCT  TCGGCCGGTG  TTCCGCCCA
451 GTGTACTTTT  ACGCCCAACT  TGGTCAGGTT  TTCTCCAGC  TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246.pep (partial)

```

1  MHGRNNGGTQA  TVAFFVHQQT  RTCFSNGEVH  ATQTDIGSAV  NIAQCFTGEA
51  GQLVYVVR*R  CAEVLVEQFA  NLFFGFMDCG  HHDMGRFFTC  HLDDELAQVA
101 FHRFNAFCFK  IMVQLDFLAD  HRFAFDHQLA  VFGCDDVDD  FAGFGRCFRP
151 VYFYAQLGQV  FFQLLQQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQQTQRTCF	SNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR				
a246	MHGRNNGGTQATVAFVFHQQTQRTCF	SNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR				
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDDELAQVAFYR	FNACFKIMXQLDFLAD				
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFTC	HLDELAQVAFHRFNAFCFKIMVQLDFLAD				
	70	80	90	100	110	120
m246.pep	130	140	150			
	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
a246	130	140	150	160		
	HRFAFDHQLAVFGCDDVDDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247.seq

```

1  atgaaacgta  aaatgctaaa  cgtaccaaag  ggcggttatg  atggatatgaa
51  ggggtttacc  attgttgaat  ttctggttgc  gggcctgctc  agtataattg
101 tcctgatagc  ggtcgtatcg  agttacttta  catcccggaa  attaaatgat
151 gtggcaaacg  agcgtcttgc  cattcaacag  gattttcgga  atgcggcaac
201 attaatgtgc  cgcgatgcaa  gaatggcggg  gagcttcggt  tgtttcaata
251 tgtccgagca  tactaaaagac  gatattggtg  attcaagtaa  tcaaaactcaa
301 tctaaccttg  caaaacccgg  tgccaaacaa  gaaaatcccc  ttttttcctt
351 aaaaaggagc  ggcattggata  aacaactgat  tcccgttgct  gaatccatag
401 atattaaata  tccgggtttt  atccagcgcc  ttaacgcatt  ggttttccaa
451 tacggtatcg  atgatcttga  tgcgagtgtc  gagactgttg  tagtcagcag
501 ctggttccaa  atagcaaaac  cgggtaagaa  aatatctacc  ttgcaagaag
551 caaagagtgc  attacagatt  actaatgatg  ataaacaaaa  tggaaatatc

```

```

g247      GMDKQLIPVAESIDIKYPGFIQRLNALVFQYGIDDLDAETAETVVSSCSKIAPGKKIST
           130         140         150         160         170         180

m247.pep  170         180         190         200         210         220
          LEDAKKELKIPDQDKEQNGNIARQRHVVNAYAVGRIAD-EESLFRFQLDDKGKWGNPQL
          |::|||::|::| ||||::|::|||||||::|:: ||||| ||||| ||||| |||||
g247      LQEAKSALQITNDDK-QNGNITRQKHVVNAYAVGRFGNNEESLFRFQLDDKGKWGNPQLL
           190         200         210         220         230

g247      VKKVVRMDEVRYIYVSGCPEDEDAGKEEFRTYNKFDSKNNAVTPAGVEVLLDLSGLNAKIA
           240         250         260         270         280         290

```

```
a247.seq
1   ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCATGCTC  AGTATGATTG
101 TCTGTAGTGGC  GGTCTGAGTC  AGTTATCTCA  CATCCCGGAA  ATTAATGAT
151 GCGGCAAACG  AGCGTCTTTC  CGCGCAACAG  GATTTCGGGA  ATGCGGCAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGCTTCGGT  TGTTCCAATA
251 TGTCCGAGCA  TCTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAAC
301 CAACATGTCC  TACTAAAAAC  CGGTGCCAAA  CAAGAAAATC  CCGTTTTTTC
351 TTTAGAGTGG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAAATTGA
401 TTCTATTGTC  TGAATCCACA  GATATTAAAT  ATCCGGGTTT  TGCCGAGCTC
451 CGTCCGGCAT  TGATTTTTCA  ACTCGGCATC  GATGATCTTG  ATGCGAGTGC
501 TGAGATGTTT  GTAGTCAGCA  GCTGTTCCAA  AATAGCAAAA  CGGGTAAGA
551 AAATATCTAC  CTTGCAAGAA  GCAAAGAGTG  CATTACAGAT  TACTAATGAT
601 GATAACAAA  ATGGAAATAT  CACCCGTCAA  AGGCATGTGG  TCAATGCCTA
651 TGCGGTTCGG  AGGATTGCCG  GTGAGGAAGG  TTTGTTCCCG  TTCCAATTGG
701 ATGATAAGGG  CAAGTGGGGT  AATCCTCAGT  TGCTCTGTA  AAGATTAGA
751 CATATGAAAG  TCGGTATAT  CTATGTTTCC  GACTGTCTGT  AAGATGACGA
801 TGCCGGCAAA  GAGGAAAAAT  TCAAATATAC  GGGTACATT  GACAGCTCCA
851 CAAATGCTGT  TACGCCCGCG  GGGGTGGAGG  TTTTATTGAG  TANCGGTACT
901 GATACCAAGA  TTGCCGCTTC  TTCAGACAT  CATATTATG  CTTACCGTAT
951 CGATCGGACA  ATACGCGGGG  GAAATGTATG  CGAAACAGA  CACTTTGA
```

a247.pap

1	MRRKMLNVPK	<u>GNYDGMKGFT</u>	<u>II</u> EFLVAGML	SMIVLMAVGS	SYFTRSKLND
51	AANERLSAQQ	DLRNAATLIV	RDARMAGGFG	CFNMSEHTKN	DIIVDSPKQT
101	QHPVPKPGAK	QENPLFSLEW	ANTNNTNNTT	AKLIPIAEST	DIKYPGGAQA
151	RPALIFQYGI	DDLDAEAETV	VVSSCSKIAK	PGKKISTLQE	AKSALQITND
201	DKQNGNITRQ	RHVVNAYAVG	RIAGEEGLFR	FQLDDKKGKW	NPQLLVKKIR
251	HMKVRYIYVS	DCPEDDDAGK	EEKFKYTGTF	DSSTNAVPTA	GVEVLLSXGT
301	DTKIAASSDN	HYYAYRIDAT	IRGGNVCANR	TL*	

```

              10          20          30          40          50          60
m247.pep      XRRKMLNVXXGSYDGMKGFTTIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAAANERLAAQQ
              |||||  |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a247          MRRKMLNVPKGNYDGMKGFTTIEFLVAGMLSMIVLMAVGSSYFTSRKLNDAAANERLSAQQ
              10          20          30          40          50          60

              70          80          90          100
m247.pep      DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNSPFSCLK-
              |||||  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a247          DLRNAATLIVRDARMAGGFGCFNMSEHTKNDIIVDPSKQTOHPVPKPGAKQENPLFSLEW
              70          80          90          100          110          120

              110         120         130         140         150         160
m247.pep      -----RNGIDKLIPIAESSNINYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISK
              |:  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a247          ANTNNNTNNNTAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLDASETVVVSSCSKIAK
              130         140         150         160         170         180

```

m247-1 / g247-1 72.1% identity in 222 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

1	AATAATACAG	CTAATTGGAT	TCCTATTGCT	GAATCCACAG	ATATTAAATA
51	TCGGGGTTTT	GCCCAGGCTG	GTCGCGCATT	GATTTTCCAA	TCGGGCATCG
101	ATGATCTTGA	GCCAGGTGCT	GAGACTGTGT	TAGTTCACAG	CATGTTCCAAA
151	ATAGCAAAAC	CGGGTAAGAA	AATATCTACC	TTGCAAGAAG	CAAAGAGTGC
201	ATTACAGATT	ACTAATGATG	ATAACACAAA	TGGAAATATC	ACCCGTCAAA
251	GGCATGTGGT	CAGTCCTAT	GCGGTGCGCA	GGATTGCCGG	TGAGGAAGGT
301	TTGTTCCGCT	TCCAATTGGA	TGATAAGGGC	AAGTGGGGTA	ATCCTCAGTT
351	GCTCGTGAAA	AAGATTATAG	TATGAAAGT	CGGGTATATC	TATGTTCCCG
401	ACTGTCTCGA	GATGACCATG	GCCGGCAAAG	AGGAAAAATC	CAAAATATAC
451	GGTACATTCG	ACAGCTCCAC	AAATGCTGTT	ACGCCGCCCG	GGGTGGAGGT
501	TTTATTGGAT	AGCGGCTATG	ATACCAAGAT	TGCCGCTTCT	TCAGACAATC
551	ATATTTATGC	TTACGTATCG	GATGCGACAA	TACCGGGGGG	AAATGTATGC
601	GC AAAACGAA	CAC TT TGA			

1	NNTAKLIPIA	ESTDIKYPGF	AQARPALIFQ	YGIDDLDA	ETVVVSSCSK
51	IAKPGKIST	LQEAKSALQI	TNDKQNGNI	TRQRHVUNAY	AVGRIAGEEG
101	LFRFQLDDKG	KWGNPQLLVK	KIRHMKVRYI	YVSDCPEDDD	AGKEEFKYTY
151	GTFDSSSTNAV	TPAGVEVLLS	SGTDTKIAAS	SDNHIYAYRI	DATIRGGNVC
201	ANRTL*				

m247-1 / a247-1 80.6% identity in 206 aa overlap

[illegible]

571

```

g248      MRKQNTLTGIP TSDGQRGSALFIVLMVMI VVAF LVVTA AQS YNTEQRISANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYD TDSKVTFS ENCGKGLXAAV NVRTNND-NEEAFDNI VVQGKP
           |||  |||||:|||||: ||||||||| ||| :||| |||||: :||| |||||||
g248      LAEAAALREGEFQVLDLEYAADSKVTFS ENCKGLCTAV NVRTNNNGSEEA FGNIVVQGKP
           70      80      90      100      110      120

           110      120      130      140      150
m248.pep  TVEAVKRSCPA-----NSTDL CIDKKGKEYKKGTRS VTKMPRIYIEYLG VNXNGENVYRVTA
           :||||||| |||||||:| |||:|: :|: ||||||||| |||: |||||||
g248      AVEAVKRSCPAKSGKNSTDL CIDNKGMEY NKGAAGVSKMPRIYIEYLG VKNQGNVYRVTA
           130      140      150      160      170      180

           160      170      180
m248.pep  KAWGKNANTVVVLQSYVSN NDEX
           ||||||||| |||||: |||
g248      KAWGKNANTVVVLQSYVGNDE QX
           190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```
a248.seq
1  ATGCGCAAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA TGTGTTATCG TGCTGATGGT GATGATCGTG GTGGCTTTTT
101 TGGTTGTGAC TGCGCGCGAG TCCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAAACGTG GGAAAAGGTC TGTGTACCCG AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGCTTTT GACAATATCG TGGTGCAGAG
351 CAAGCCACG CTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAAAG
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA
```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

a248.pep

1	MRKQNTLTGI	PTSDGQRGFA	<u>LFIVLMVMIV</u>	<u>VAFVLVTTAAQ</u>	SYNTEQRISA
51	NESDRKLALS	LAAEALREGE	LQVLDDLEYDT	DSKVTFSENC	GKGLCTAGVN
101	RTNNDNEEAF	DNIVVQCKPT	VEAVKRCSA	KSTGLCIDNK	GMEYKKGTSV
151	VSKMPRYIIE	YLGVKNGENV	YRVATAKAWGK	NANTVVVLQS	YVSNND*

m248/a248 89.4% identity in 180 aa overlap

```

m248.pep      10          20          30          40
               GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
               |||:||||| |||| | ||||| ||||| ||||| ||||| |||||
a248          MRKQNTLTGIIPTSDGQRGFALFIVLMMIVVAVFLVVTAQSYNTEQRISANESDRKLALS
              10          20          30          40          50          60

              50          60          70          80          90          100
m248.pep      LAEXXXREGELQVLDDLEYDTSKVTFSENCCKGLXAAVNVRTNNDNEEAFDNIVVQGKPT
              ||| ||||| ||||| ||||| ||||| ||||| : ||||| ||||| ||||| |||||
a248          LAEAALREGELQVLDDLEYDTSKVTFSENCCKGLCTAVNVRTNNDNEEAFDNIVVQGKPT
              70          80          90          100          110          120

              110         120         130         140         150         160
m248.pep      VEAVKRSCPANSTDLCIDKKGXKEYKKGTGRSVTKMPRYIIIEYLGVMNGENVYRVTAWGWK
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248          VEAVKRSCSTAKSTGLCIDNKGMYYKKGTQSFSKMMPRYIIIEYLVKNGENVYRVTAWGWK
              130         140         150         160         170         180

              170         180
m248.pep      NANTVVVLQSYVSNNDEX

```

573

```

                190
m248-1.pep  NANTVVVLQSYVSNNDEX
            |||||
a248        NANTVVVLQSYVSNNDEX
                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

```

g249.seq
1  atgaagaata atgattgctt ggcctgaaa aatccccagt ccggtatggc
51  gttgatagaa gtcttggtcg ctatgctcgt tctgaccatc ggtatcttgg
101 cattgctgtc cgtacagttg cggacagtcg ctcccgtag ggaggcggaa
151 acgcaaacca tcg*cagcca aatcacgcaa aacctgatgg aaggaatggt
201 gatgaatccg accatcgatt tggacagcaa caagaaaaac tatagctctt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgcttgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tgccggatgc ggtagctatt cattacgccg
401 tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcggtagt
451 tttcttcaa attgcgacaa taaggcaaac ggggataact tgattaaagt
501 attgtgggta aatgattcgg caggggatcc ggatatttcc cgtacgaatc
551 ttgaagtgag cggcgacaat atcgtatata cctatcaggc aagggtcggg
601 ggtcgtgaat ga

```

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

```

g249.pep
1  MKNNDCLRLK NPQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDLDSNKK YSLYMGKQTL SAVDGEFMLD
101 AEKSKAQLAE EQLKRFSHEL KNALPDAVAI HYAVCKDSSG DAPTLSDSGA
151 FSSNCDNKAN GDTLIKVLWV NDSAGSDIS RTNLEVSGDN IVYTYQARVG
201 GRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

```

m249.seq
1  ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CGGACAGTCN NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATTT TGCGATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTTAG
351 TTATGAGCTG AAAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAACGGG GATACTTAA TTAAAGTATT
501 GTGGGTAAAT GATTCGGCAG GGGATTCGGA TATTTCCCGT ACGAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTGCGAGGT
601 CGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

```

m249.pep
1  MKNNDCFRLK DSQSGMALIE VLVAMLVLT I GILALLSVQL RTVXXXXXXXX
51  XXXXXXXXXXX XLMGMLMNP TIDSDSNKK YNLYMGNHTL SAVDGDFAID
101 AMKTKGQLAE AQLKRFSYEL KNALPDAAAI HYAVCKDSSG NAPTLSGNAF
151 SSNCDNKANG DTLIKVLWVN DSAGSDISR TNLEVSGDNI VYTYQARVG
201 RE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

```

m249/g249
                10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXX
            |||||:||||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

```

              10      20      30      40      50      59
m250.pep      MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLLMTSMNFAGGSEF
              |||:::|||||||||||||||||||||||:|||||:|||||
g250          MHTHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKGMGRLEMLLMTGMNPFAGGSEF
              10      20      30      40      50      60

              60      70      80      90      100     110
m250.pep      ATVNLWAEPLPILLIATVTFMINSRHI LMGGGACAPAPERNTAEKSRARTVFYVX
              |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g250          ATVNLWAEPLPILLIATITFMINSRHI LMGGGACHAHERNTAEKSRARAVFYV
              70      80      90      100     110

```

1	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
51	AAGTTCGCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGTA
101	TGCAGGGTGG	ACAAAAAGGC	ATGAGCTGGC	TGGAAATGTT	GTTGATGACC
151	GGTATGAACT	TCGCCGGCGG	CTCCGAGTTT	GCCACGGCTA	ACCTGTGGGC
201	GGAACCTCTG	CCGATACTGC	TTATCGCCAC	CGTAACCTTA	ATGATTAATT
251	CTCCGCATAT	CTGATGGGG	G.CGGCACTT	GCCCCGACC	TGAAAGAAAT
301	ACCGCTGAAA	AAAGCCGTGC	CCGCACTGTT	TTTTATGTGT	GA

```

1  MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMOGGQKG MSWLEMLLMT
51  GMNFAGGSEF ATVNWLAEPL PILLIATVTF MINSRHILMG XGTCPAPERN
101 TAEKSARTV FYV*

```

```

                    10          20          30          40          50
59
m250.pep
MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLLMTSMNFAGGSEF
      |
||::|||||
a250
MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLLMTGMNFAGGSEF
                    10          20          30          40          50
60

m250.pep        60          70          80          90         100         110
ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRTVFYVX
|||||
a250            ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCPAPERNTAEKSRTVFYVX
                  70          80          90         100         110

```

```

1  atgcctgacc caatagggat tcttttcgct gccgtcgggg ttgatttttt
51  tgccgttggt ttgagggggc gttttcaacg aataggcgcg gttggcatgt
101 tgataataat aatcctgatg gcggaggctg gaacccaaac ggtcgtaacc

```

579

	100	110	120	130	140	150
m251.pep	MLIIIIILMAEIRAKAVKPEIHAQVVADFGGIEGFFECRLQEPVAFPNHAIQFVIGKRLV					
g251	MLIIIIILMAEVGKTKTVVTEVDAQVVADFGGIEGFFECRLQEPVAFPNHAIQFVIGKRLV					
	40	50	60	70	80	90
	160	170	180	190	200	210
m251.pep	GTRAAIFVRTVGRVRLKMIQTALPVRVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV					
g251	GTRAAIFVRTVGGTVRLKMIQTDALPVRVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV					
	100	110	120	130	140	150
	220	230	240	250	260	270
m251.pep	VKHARTVFRAHQRTVFAVGKQSAVFVVARVFAVTGQRTLFFICIKNRLGQECRNRIAR					
g251	VKHARTVFRAHLRTVFTVGNQPAVFAAARVFAVASYRS-VFFIFIKNRLGQECRNRIAR					
	160	170	180	190	200	210
	280	290	300			
m251.pep	VESLLRVFEYAADVPLILKTKTRAEQPRPAFVX					
g251	VESLLRAFEYAADVVPFVKTKTRAEQPRPAFVX					
	220	230	240			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 985>:

a251.seq	
1	ATGCGTGCTG CGGTAGTCGT AGCGCAACCC CGCGCCGACA TCCGCCCACC
51	TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTGCCGTTG
101	ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151	TTGCCCCGTA ACCACATTTC CCCTGCCTAT GCTGACCCAA TAGGGTTGGT
201	CCTTGCCGCC GTTGGGGTTG GCGGTTTGTAG GGGGCGTTTT CGACGAATAG
251	GCGCGGTTGG CATGTTGATA ATAATAATCC TGATGGCGGA GATTAGAGTC
301	AAAGCGGTCA AAACCCAGAT TCACGCTCAG GTTGTGGCGG ATTTTGGCGG
351	TATCGAAGGA TTTTTGAAT GCCGCCTGCA AGAGCCTGTG GCTTTCCTCG
401	TAAATCACGC GGTGCGATTT GTAGTAGGAA AACGGCTTGT CGGCACTCGG
451	GCGGCAATAT TTGTCCGAAC CGTCGGCAGA ACAGTGCCTC TGCTGAAAAT
501	GATTGTCCAA ACCGATGCCC TGCCGGTCGT AAGAGAGGCG GGCATAATCC
551	ACCCAAGTGT CTTTATCGGC ATTGGTATAG ACATATTCCA AACCGTAGCG
601	GCTTTTGGTG TGCGTCTCGT CGTAAACAC GCCCGTACCG TATTCCGCGC
651	CCACCAGCGC ACCGTTTTCG CCGTTGGTAA ACAGACCGCC GTATTTGTGG
701	TCGCCCGCGT ATTTGCCGTT GCCTCTTATC GGTCCTGATT TTCTATTTTC
751	ATCAAAAACC GCCTTGGTCA GGAATGCCGG AACCGTCATA TCGCGCGTGT
801	CGAAAGTTTG TTGCGTGTGT TCGAGTATGC CGCCGATGTA GTGCCGTTTG
851	TTTTCAAAAC GAAAACCCGG GCGGAACAGC CACGATCGGC TTTCGTATGA

This corresponds to the amino acid sequence <SEQ ID 986; ORF 251.a>:

a251.pep	
1	MRAAVVVAQP RADIRPPAQT DIVPNCRVIA FAVDAARRAV RISIVAQAAD
51	LPRNHISPAY ADPIGLVLAA VGVGGFRGRF RRIGAVGMLI <u>IIILMAEIRV</u>
101	KAVKTEIHAQ VVADFGGIEG FFECLRLQEPV AAFPVNHAVGF VVGKRLVGTR
151	AAIFVRTVGR TVRLKMIQV TDALPVRVREA GIIHPSVFIG <u>IGIDIFQTVA</u>
201	AFGVRLVVKH ARTVFRAHQRT TVFAVGKQTA VFVVARVFAV ASYRSVFSTF
251	<u>IKNRLGQECR</u> NRHIARVESL LRVFEYAADV VPFVFKTKTR AEQPRSAFV*

m251/a251 88.5% identity in 304 aa overlap

	10	20	30	40	50	60
m251.pep	MRAAVVVAQARADIRPPAQTDIVPNCRVIAFTVDAARRAVRISIVAQAADLPRNDISPAY					
a251	MRAAVVVAQPRADIRPPAQTDIVPNCRVIAFAVDAARRAVRISIVAQAADLPRNHISPAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m251.pep	GDPIGAGFTAVGADFFAVVLRGRVRRIGAVGMLIIIIILMAEIRAKAVKPEIHAQVVADFG					
	:	:				

m253.seq

This corresponds to the amino acid sequence <SEQ ID 990; ORF 253>:

m253.pcp

1	MIDRNRMLRE	TLERVAGSF	WLWVVAATFA	FFTGFSVTYL	LMDNQGNLFF
51	<u>LVLAGVLGMN</u>	<u>TLMLAVWLAM</u>	<u>LFLRVKVGRF</u>	<u>FSSPATWFRG</u>	<u>KDPYVQAVLR</u>
101	<u>LYADEAWRQS</u>	<u>VRWKIGATSH</u>	<u>SLWLCTLLGM</u>	<u>LVSULLLLLV</u>	<u>RQVTNFWNEST</u>
151	<u>LLNSAAPSVA</u>	<u>VEMLAWLPSK</u>	<u>LGFPVPDARA</u>	<u>VIENRNGNI</u>	<u>ADARAWSGLL</u>
201	<u>VGSIACYGIL</u>	<u>PRLLAWVVCK</u>	<u>ILLKTSENGL</u>	<u>DLEKPPYQAV</u>	<u>IRRWQNKITD</u>
251	<u>ADTRRETVSA</u>	<u>VSPKILKND</u>	<u>PKWAVMLETE</u>	<u>WDQGEWFEGR</u>	<u>LAQEWLDKGV</u>
301	<u>ATNREQVAAL</u>	<u>ETPKIKCPAQ</u>	<u>LLIGVRAQT</u>	<u>PDRGVLRIQV</u>	<u>RLSEAAQQGA</u>
351	<u>VVQLLAEQGL</u>	<u>SDDLSEKLEH</u>	<u>WRNALAECGA</u>	<u>AWLEPDRAAQ</u>	<u>EGRLKDQ*</u>

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

m253/g253

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
	: : : : :					
g253	MIDDRDRLRDTLERVRAGSFWLWVVVASMMFTAGFSGTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	: :					
g253	TLMLAVWLATLFLRVKVGRRFFSSPATWFRGKGPVNQAVLRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGLMVSLLLLLVQRQYTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
g253	SLWLCTLLGLMVSLLLLLVQRQYTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
	130	140	150	160	170	180

583

m253/a253 97.2% identity in 395 aa overlap

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLEVRAGSFWLVVAATFAFFTGFVSVTYLLMDNQGLNFFLVLAGVLGMN					
a253	MIDRNRMLRETLEVRAGSFWLVVAATFAFFTGFVSVTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
m253.pep	TLMLAVWLAMFLRVKVGRRFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMFLRVKVGRRFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMFLRVKVGRRFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMFLRVKVGRRFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
m253.pep	SLWLCTLLGMLVSVLLLLVRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLVRQYTFNWESTLLGDSSSVRLVEMLAWLPAKLGFPVPDARA					
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLVRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLVRQYTFNWESTLLGDSSSVRLVEMLAWLPAKLGFPVPDARA					
	130	140	150	160	170	180
m253.pep	VIEGRINGNIADARAWSGLLVGSIACYGILPRLAWVVKILLKTSENGLDLEKPYQAV					
a253	VIEGRINGNIADARAWSGLLVGSIACYGILPRLAWVVKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
m253.pep	VIEGRINGNIADARAWSGLLVGSIACYGILPRLAWVVKILLKTSENGLDLEKPYQAV					
a253	VIEGRINGNIADARAWSGLLVGSIACYGILPRLAWVVKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
m253.pep	IRRWQNKITDADTRRETSAVSPKIIINDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253	IRRWQNKITDADTRRETSAVSPKIVINDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
m253.pep	IRRWQNKITDADTRRETSAVSPKIIINDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253	IRRWQNKITDADTRRETSAVSPKIVINDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
m253.pep	ATNREQVAALETELKQKPAQLLIGVRAQTVPRGVLRQIVRLSEAAQGGAUVVQLLAEQGL					
a253	AANREQVAALETELKQKPAQLLIGVRAQTVPRGVLRQIVRLSEAAQGGAUVVQLLAEQGL					
	310	320	330	340	350	360
m253.pep	ATNREQVAALETELKQKPAQLLIGVRAQTVPRGVLRQIVRLSEAAQGGAUVVQLLAEQGL					
a253	AANREQVAALETELKQKPAQLLIGVRAQTVPRGVLRQIVRLSEAAQGGAUVVQLLAEQGL					
	310	320	330	340	350	360
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRLKDQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRLKTNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

```

g254.seq
1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcagggttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg ttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gactggttt ctttgagaaa cgggcccggc
301 tggacggtat ttctactgtc ctggctgctg gcggctgcag gaatcgaca
351 agaactcacc atcggaacgga aaagcgaaaa acgtctgctg tcatattgca
401 tttatatcgt aatgggctgg atggtcttgg cgtaaatgaa atccctgaca
451 gcctcactcc cggcggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtatttg gcggcagcat aaccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

```

g254.pep
1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDCRIF SVSVYGISLL

```

585

```

301 TGGACGGTAT TTCTACTGTC CTGGCTGCTG GCGGCTGCAG GAATCGCACA
351 AGAACTCACC ATTGGACGGA AAAGCGAAAA ACGACTGCTG TCTATTGCGA
401 TTTATATCGT AATGGGCTGG ATGGTCTTGG CCGTAATGAA ATCCCTGACA
451 GCCTCACTCC CGCCGGCAGG ACTGGCTTGG CTGGCGGCAG GCGGTATGCT
501 GTACAGCGTC GGCATTTACT GGTTTGTAAG CGATGAAAAA ATCCGACACG
551 GGCACGGAAT CTGGCATCTG TTCGTATTGG GCGGCAGCAT CACCCAATTT
601 GTCAGCGTGT ACGGTTACGT AATCTGA

```

This corresponds to the amino acid sequence <SEQ ID 998; ORF 254.a>:

a254 .pep

```

1 MYTGERFNTY SHLSGLILAA AGLALMLLKT IGHGDGYRIF SVSVYGISLL
51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMY VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLS SIAIYIVMGW MVLAVMKSIL
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

m254/a254 97.6% identity in 167 aa overlap

```

                                     10                               20
30
m254 .pep
VSVYGISLLLLLYLSSWLYHGIAAGKLKSIL
                                     |||||||||||||
|||||||||||||
a254
HLSGLILAAAGLALMLLKTIGHGDGYRIFSVSVYGISLLLLLYLSSSLYHGIAAGKLKSIL
                                     20       30       40       50
70
                                     40       50       60       70
90
m254 .pep
KKTDHCMYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLS
|||||||||||||||||||||||||||||||||||||||||||||||||||||
a254
KKTDHCMYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLS
                                     80       90      100      110
130
                                     100      110      120      130
150
m254 .pep
IVIYVVMGWMVLAVMKSILTASLPSAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF
      ||:|||||||||||||||||
|||||||||||||||||||||||||||||
a254
IAIYIVMGWMVLAVMKSILTASLPPAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF
                                     140      150      160      170
190
                                     160
m254 .pep      VLGGSITQFVSVYGYVIX
               |||||||||||
a254          VLGGSITQFVSVYGYVIX
               200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

130 140 150 160 170 180

	189
m255.pep	AALVGIADX
	:
g255	AALVGVADX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```
a255.seq
1   GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCGG TGTTTCGCTGC
51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCCAC GCCTTTGACG
101 GCGTTGATGC CCATCATGGC GTAGCGGATT TCGCATACGA GCGGGTCGAA
151 TACGGGTTTCG CCCAGCCGA CGGGGACGTT GCGGCTTCA ATATGCAGCT
201 TCGCGCGCGAC GGAATCCAAG GATTTCGCGA CGCTGTCCAT ATAGTTTTCC
251 AGCTCGGCCAA TTTGGCTATG GTTGGCGGCA AAAAAGGAT TTTGGGAAAT
301 GTGTTGCGAC CTTCAAAACC GGATTTCTTT TTCGCGGACT TGGTGAACGT
351 AGGCGGTGAT TTCCGTGCCG AATTTTTCTT TCAACCATTT TTTGGCAACG
401 GCTCCGCGCG CAACGCGGGC GCGGTTTCG CGGCGGAAC TCCTGCGGCC
451 GCCCCGGTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGGCGT
501 GCGCGGGGCG GAAGCGGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551 TCGGTATTGC GGATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

a255.pep

1	VVGQ	EALRGE	FVAV	FAAALR	YAVK	TCADFH	AFDG	VDAHHG	VGDF	GIEAVE
51	YGA	FQADGDV	GGFN	MQLRAD	GIQ	GFAHAVH	IVF	QLGNLH	AM	VGGKKRILGN
101	VFA	AFKPDF	FADL	GNVGGD	FRAE	FFFPF	FGN	GSGGNAG	GG	FAGGTCAA
151	APV	VARAVF	PIGI	VGVA	GA	GGDVAVVF	AAL	VG	IA	D*

m255/a255 93.1% identity in 188 aa overlap

		10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVVGDFGIEAVKNRFAQADRD	I					
a255	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVVGDFGIEAVYGFQAQADGDV	I					
		10	20	30	40	50	60
		70	80	90	100	110	120
m255.pep	GCDFMQLRADGIQGF	FAHAVHIVFQLGNL	LAMVGGKKRILGNVFAAFKPDFF	FADLGNVGGD			
a255	GGFNMQLRADGIQGF	FAHAVHIVFQLGNL	LAMVGGKKRILGNVFAAFKPDFF	FADLGNVGGD			
		70	80	90	100	110	120
		130	140	150	160	170	180
m255.pep	FRAEFFFQPF	FGNGSGSNAGGGFTGGAPAAA	AVVARAVFVPIGIVGVAGAEAGGDVAVVF				
a255	FRAEFFFQPF	FGNGSGGNAGGGFAGGTPAAA	PVVARAVFVPIGIVGVAGAEAGGDVAVVF				
		130	140	150	160	170	180
		189					
m255.pep	AALVGIAD	X					
a255	AALVGIAD	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```
g256.seq
1   atgctcgcgg  tacgcaatcg  ggggtggcac  ggcgcagtcg  tccattttccg
51  cagctgcggc  ggcgtagcga  acacgcgccc  ggtgttctac  cactttgggtg
101 atctgcgcga  aatcgctctt  gcttggaca  cgctcacccg  gcgttacctg
151 gaaatatacg  ccgtcggcgt  atcgctgggc  ggcaacgcgc  cggcaaaaata
201 ttggggcgaa  caggcgaaaa  aggcattgcc  gcacgcctcg  gccgcgcgat
251 ccgcccccg  tgatgcagag  gcggcaggca  gcgcgtctcg  cagcgccgat
301 acgcggctgc  tctacacgcq  ctacttcctc  cgcacactga  tccccaacag
```

589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

```
a256.seq
1  ATGCTCGCGG TACGCGATCG GGGTTGGAAC GCGGTAGTCG TCCATTTCCG
51  CAGTGCAGGC GCGGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACCGCCGA AATTGCCTTT ACTTTGGACA CGCTCGCCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCGAAA ACGCGCTGCC GCAAGCCGCC GCCGTTCATCT
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCGCGCA GACGAAGTGT CCGAAGCGCT TACCTGTTT
601 CAGCCGACAC ACGGTGGTCA TGTCGGCTTT GTCGGCAGCA CCGGCGCAG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

```
a256.pep
1  MLAVRDRGWN GVVVHFRSCG GVANTAPVFY HLGDTAEIAF TLDTLAARYR
51  EYAVGVSLG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVG FVSTGGRLHL QWLPQTVLSY FDSFRTNRR*
```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVVHFRSCGGIANTAPVFYXLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : :					
a256	MLAVRDRGWNQVVHFRSCGGVANTAPVFYHLGDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGGKALPQAAVISAPVDAEAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	: : : : :					
a256	GNALAKYLGEQGENALPQAAVISAPVDAEAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCPKLLKHVAKPLLLLNAVNDP					
	: : : : :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCPKLLKHVAKPLLLLNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

```
g256-1.seq
1  ATGATTTTGA CACCGCCGGA CAGGCCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACA CCGCGCACC GCATACCGCC
```

591

```

g256-1      |||||
             L V V L F H G L E G S S R S H Y A V E L M L A V R N R G W H G A V V H F R S C G G V A N T A P V F Y H L G D T A E I A F
             70      80      90      100      110      120

m256-1.pep  120      130      140      150      160      170      179
             T L D T F A A R Y R E I Y A V G V S L G G N A L A K Y L G E Q G K K A L P Q A A A V I S A P V D A E A A G R R F D S G I
             :|||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1      130      140      150      160      170      180
             A L D T L T A R Y R E I Y A V G V S L G G N A P A K Y L G E Q G K K A L P H A S A A V S A P V D A E A A G S R F D S G I

m256-1.pep  180      190      200      210      220      230      239
             T R L L Y T R Y F L R T L I P K A K S L Q G F O T A F A A G C K T L G E F D D R F T A P L H G F A D R H D Y Y R Q T S C
             |||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1      190      200      210      220      230      240
             T R L L Y T R Y F L R T L I P K A R S L Q G F O T A F A A G C K T L G E F D D R F T A P L H G F A D R H D Y Y R Q T S C

m256-1.pep  240      250      260      270      280      290      299
             K P L L K H V A K P L L L N A V N D P F L P P E A L P R A D E V S E A V T L F Q P A Y G G H V G F V S S T G G R L H L
             |||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1      250      260      270      280      290      300
             K P L L K H V A K P L L L N A A N D P F L P P E A L P R A D E A S E A V T L F Q P A H G G H A G F V S S T G G R L H L

m256-1.pep  300      310      319
             Q W L P Q T V L S Y F D S F R T N R R X
             |||||
g256-1      310      320
             Q W L P Q T V L S Y F D S F R T N R R X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

a256-1.seq

```

1   ATGATTTTGA CACCGCCGGA CACACCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAT TCCTGCAACG CTCGCACCT GCATACCGCC
101 GCGAGCTGCT TCCCGACAGC ACGGGTAAAA CAAAACCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TCGCCGCTG GTCTGTGTG TTCACGTTT
201 GGAGGGCGGC AGTGGCAGCC ATTACGCGGT CGAACTGATG CTCGGGTGAC
251 GCGATCGGGG TTGGAACGGC GTAGTCGTCC ATTTCCGCAG CTGCGGCGGC
301 GTAGCGAACA CCGCCCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 TGCCTTTACT TTGGACACGC TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGCGGTATC GCTGGGCGGC AACGCGCTGG CAAAATATTT GGGCGAACAG
451 GGGCAAAACG CGCTGCCGCA AGCCGCCGCC GTCATCTCCG CACCCGTCGA
501 TGCAGAGGCG GCAGGCAACC GCTTCGACAG CGGCATCACA CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGCA ACACGTATAC CCAAAGCACG GTCGCTCCAA
601 GGTTTTCAGA CGGCATTTCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGTTTC ACCGCACCGC TGCACGGCTT TGCCGATCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGTCTA ATGCCGTCAG CGACCCCTTC CTGCCGCCCG AAGCGCTGCC
801 CCGCGCAGAC GAAGTGTCAG AAGCCGTTAC CCTGTTCCAG CCGACACACG
851 GTGGTCATGT CGGCTTTGTC GGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGTTGCCGC AGACCGTCTT GTCCTATTTT GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

a256-1.pep

```

1   MILTPPDTPF FLRNGNADTI AAKFLQRSAP AYRRELLPDS TGKTKTAYDF
51  SDGISPDAPL VVLFHGLEGG SGSHYAVELM LAVDRGWNG VVVFHFRSCGG
101 VANTAPVFYH LGDTAEIAFT LDTLAARYRE IYAVGVSLGG NALAKYLGEQ
151 GENALPQAAA VISAPVDAEA AGNRFDSGIT RLLYTRYFLR TLIPKARSLQ
201 GFQTAFAGC KTLGEFDDRF TAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PTHGGHVGFV GSTGGRLLHQL
301 WLPQTVLSYF DSFRNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

a256-1.pep  10      20      30      40      50      60
             M I L T P P D T P F F L R N G N A D T I A A K F L Q R S A P A Y R R E L L P D S T G K T K T A Y D F S D G I S P D A P L
             |||||
m256-1      10      20      30      40      50      60
             M I L T P P D T P F F L R N G N A D T I A A K F L Q R P A P A Y R R E L L P D S T G K T K V A Y D F S D G I S P D A P L

a256-1.pep  70      80      90      100      110      120
             V V L F H G L E G G S G S H Y A V E L M L A V R D R G W N G V V V H F R S C G G V A N T A P V F Y H L G D T A E I A F T
             |||||
m256-1      70      80      90      100      110      120
             V V L F H G L E G S S R S H Y A V E L M L A V R D R G W H G V V V H F R S C G G I A N T A P V F Y H L G D T A E I A F T

```


593

```

m257.pep  MGRHFGQRFLTVAAVAAGTAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAD
          |||||:||||:||||: |||||:||||| |||||:||||:|||||:|||||:
g257      MGRHFGRRRFLTAAAVAVAGAASFLPNPFAAGGEKRNMDKKRDENVFFWKGVGALGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRAADLVNKKVLAEEVARLEKLFSLYREDSLSRLNRDGYLTSPSADFLLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257      LRLFGVDDRQAADLVNKKVLAEEVARLEKMFSLYREDSLSRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTXX
          |||||
g257      AAIFTRX
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC  ATTCGGGCG  CAGGCGTTTT  TTGACAGTTG  CCGCCGTTGC
51  GCGGCGGGC  GCGGCGGTTT  CTTTCCTGCC  GAATCCTTTT  GCCGCCGATG
101 ATGAAAAACG  CAATAAAGAT  GAAAAACGCA  ATGAAAATGT  GTTTTCTGG
151 AAAGGTGTCG  CACTGGGTTC  CGGTGCGGAG  CTCCGTCTGT  TCGGTGTGGA
201 CGACAGGCGT  GCGGCGGATT  TGGTCAACAA  GGTTTTGGCG  GAAGTGGCGC
251 GTTTGGAAAA  AATGTTCAGC  CTTTACCGTG  AAGACAGCCT  GATCAGCCGT
301 CTGAACCGTG  ACGGTTATTT  GACTTCGCCG  CCGGCGGATT  TTTTGGAACT
351 GTTGAGCCTG  GCCGTGATAT  TCACGCGCTG  A
  
```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF  LTVAAVAAAG  AAVSFLPNPF  AADDEKRNKD  EKRNENVFFW
51  KGVGALGSGAE  LRLFGVDDRR  AADLVNKKVLA  EVARLEKMF  LYREDSLSSE
101 LNRDGYLTSP  PADFLELLSL  AVIFTR*
  
```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGXQRFLTVAAVAAGXAASFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAX
          |||||      :|||||: |||||:|||||:|||||:
a257      MGRHFGRRRFLTVAAVAAGAASFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAE
          10      20      30      40      50
60

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRAADLVNKKVLAEEVARLEKLFSLYREDSLSRLNRDGYLTSPSADFLLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
a257      LRLFGVDDRRAADLVNKKVLAEEVARLEKMFSLYREDSLSRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110
120

m257.pep  AAIFTXX
          |||||
a257      AVIFTRX
  
```

m258 . pep

1	<u>MRRFLPIAAI</u>	<u>CAVVLLYGLT</u>	<u>AATGSTSSLA</u>	<u>DYFWWIVAFS</u>	<u>AMLLLVL SAV</u>
51	<u>LARYVILLLLK</u>	<u>DRRDGVFGSQ</u>	<u>IAKRLSGMFT</u>	<u>LVAVLPGVFL</u>	<u>FGVSAQFING</u>
101	<u>TINSWFGNDT</u>	<u>HEALERSLNL</u>	<u>SKSALNLAAD</u>	<u>NALGNAPVPQ</u>	<u>IDLIGAASLP</u>
151	<u>QDMGRVLEHY</u>	<u>AGSGFAQAL</u>	<u>YNSASGKIEK</u>	<u>SINPHKLDQP</u>	<u>FPKGARWEKI</u>
201	<u>QRGGSVRDLE</u>	<u>SIGGVLYAQG</u>	<u>WLAAGTHNGR</u>	<u>DYALFFRPQV</u>	<u>PKGVAEDAVL</u>
251	<u>IEKARAKYAE</u>	<u>LSYSKGLQOT</u>	<u>FFLATLNLIAS</u>	<u>LLSLFLALVM</u>	<u>ALYFARFVE</u>
301	<u>PVLSLAEGAK</u>	<u>AVAQGDFSQT</u>	<u>RPVLRNDEFG</u>	<u>RLTKLFNHMT</u>	<u>EQLSIAKEAD</u>
351	<u>ERNRRREEAA</u>	<u>RHYLECVLEG</u>	<u>LTTGVVVFDE</u>	<u>QGCLKTFNKA</u>	<u>AEQILGMPLT</u>
401	<u>PLWGSSRHGW</u>	<u>HGVSAQQSLL</u>	<u>AEVFAAIGAA</u>	<u>AGTDKPVHVK</u>	<u>YAAPDDAKIL</u>
451	<u>LGKATVLPED</u>	<u>NGNGVVMVID</u>	<u>DITVLIHAQD</u>	<u>EAAQGEVAKR</u>	<u>LAHEIRNPLT</u>
501	<u>PIQLSAERXA</u>	<u>XLGGLKDEQ</u>	<u>DAIYLTHSTK</u>	<u>TIVKQVAALK</u>	<u>EMVEAFRNVA</u>
551	<u>RSPSLKLENO</u>	<u>DLNALIGDVL</u>	<u>ALYEAGPCRF</u>	<u>AADLPANR*</u>	

homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

m258/q258

		10	20	30	40	50	60
m258 . pep		MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAMPLLLVLSAVLARYVILLLK					
g258		MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVSFSAMPLLLVLSAVLARYVILLLK					
		10	20	30	40	50	60
		70	80	90	100	110	120
m258 . pep		DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSINL					
		:					
g258		DRRDGVFGSQIAKRLSGMFTLVAVLPGFLFGISAQFINGTINSWFGNDTHEALERSINL					
		70	80	90	100	110	120
		130	140	150	160	170	180
m258 . pep		SKSALNLAADNALGNAPVPQIDLIGAASLPGDMGRVLEHYAGSGFAQLALYNAASGKIEK					
		: :					
g258		SKSALDLAADNAVSNAPVPQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK					
		130	140	150	160	170	180
		190	200	210	220	230	240
m258 . pep		SINPHKLDQPPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV					
		: : :					
g258		SINPHQFDQPLPDKEHWEKIQQTGSVRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI					
		190	200	210	220	230	240

597

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```

a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQQ WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAGGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLEDEQ DAQILTRSTD TI IKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIFKNAA EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIIEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*

```

m258/a258 99.0% identity in 584 aa overlap

	10	20	30	40	50	60
m258.pep	MRRFLPIAAICAVVLLYGLTAATGSTSSLA	DYFWWIVAFS	AMLLLVLSAV	LARYVILLLK		
a258	MRRFLPIAAICAVVLLYGLTAATGSTSSLA	DYFWWIVAFS	AMLLLVLSAV	LARYVILLLK		
	10	20	30	40	50	60
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFING	TINSWFGNDTHEALERSLNL				
a258	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFING	TINSWFGNDTHEALERSLNL				
	70	80	90	100	110	120
m258.pep	SKSALNLAADNALGNAPVQIDLIGAASLP	GDMGRVLEHYAGSGFAQLAL	YNAASGKIEK			
a258	SKSALNLAADNALGNAPVQIDLIGAASLP	GDMGRVLEHYAGSGFAQLAL	YNAASGKIEK			
	130	140	150	160	170	180
m258.pep	SINPHKLDQPFPGKARWEKI	QAGSVRDLESIGGVLYAQQ	WLSAGTHNGRDYALFFRQPV			
a258	SINPHKLDQPFPGKARWEKI	QAGSVRDLESIGGVLYAQQ	WLSAGTHNGRDYALFFRQPV			
	190	200	210	220	230	240
m258.pep	PKGVAEDAVLIEKARAKYAE	LSYSKKGLQTFFLATLLIAS	LLSIFLALVM	ALYFARRFVE		
a258	PKGVAEDAVLIEKARAKYAE	LSYSKKGLQTFFLATLLIAS	LLSIFLALVM	ALYFARRFVE		
	250	260	270	280	290	300
m258.pep	PVLSLAEGAKAVAQGDFSQ	TRPVLRNDEFGRLTKLFNHMT	EQLSIAKEAD	ERNRRREEAA		
a258	PVLSLAEGAKAVAQGDFSQ	TRPVLRNDEFGRLTKLFNHMT	EQLSIAKEAD	ERNRRREEAA		
	310	320	330	340	350	360
m258.pep	RHYLECVLEGLTTGVVVFDE	QGCLKTFNKA	AEQILGMPLT	PLWGSSRHGW	HGVSAQQSLL	
a258	RHYLECVLEGLTTGVVVFDE	QGCLKTFNKA	AEQILGMPLT	PLWGSSRHGW	HGVSAQQSLL	
	370	380	390	400	410	420
m258.pep	AEVFAAIGAAAGTDKPVHV	KYAAPDDAKILLG	KATVLPED	NGNGVVMVID	DITVLIHAQK	
a258	AEVFAAIGAAAGTDKPVHV	KYAAPDDAKILLG	KATVLPED	NGNGVVMVID	DITVLIHAQK	

599

151 GETYGRVFAD IFELSALEG RAFKGLKLT AEYKXHLRRC LPFGNGVG
 201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.p	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.p	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.p	VLPDDEDARTIAAELAKMDMFALGTD AVASGETI GRVFADIFELSALEGRAF KGLKLT					
g259	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALERRAFKGLKLT					
	130	140	150	160	170	180
	190	200	210			
m259.p	AEYKXHLRRC LPFGNGVGGR TQSGVAGDFKNIR					
g259	AEYKXHLRRC LPFGNGVGFGR AQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

```

1 ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51 TTTGATTTTC TTTGCCGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGCTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCTAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCGC
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTGCGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAA.CATCT TCGGCGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCGCTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCG GAAAAGTCCA
651 A
  
```

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.p (partial)

```

1 MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51 ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTD AVAS
151 GETYGRVFAD IFELSALEG RAFKGLKLT AEYKXHLRRC LPFGNGVG
201 RAQSGVAGDF KNIGKVQ
  
```

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.p	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYT L L PPLLSALSAVALVWLAWAFV					

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHKGMAEQVRFKAE			
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHKGMAEQVRFKAE			
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDMFALGTD	AVASGETYGRVFADIFELSAALE				
m259-1	VLPDDEDARTIAAELAKMDMFALGTD	AVASGETYGRVFADIFELSAALEGRAFKGMLKLT				
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1   ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTGCGCGGTT TTTTGACCGC GCAAACTCTG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CTTCCGCTTC TGTCCGCATT GTCCGCGGTC
151 GCGCTGGTGT GGCTGGCGTG GCGCTTCGTG TCGGCGCGTT CAAAGGCTAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCGG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTGCGCTCG
451 GCGGAAACCT ATGGACGCGT GTTCGCGCAT ATTTTCGAGT TGTGCGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCCG AAACGGCGTT GGAGTTGGGC
601 GCGCTCAATC AGGCGTTGCA GGAGATTTC AAAAAATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1   MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQALQEIS KTSEKSKRIF Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHKGMAEQVRFKAE			
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHKGMAEQVRFKAE			
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDMFALGTD	AVASGETYGRVFADIFELSAALEGRAFKGMLKLT				
m259-1	VLPDDEDARTIAAELAKMDMFALGTD	AVASGETYGRVFADIFELSAALEGRAFKGMLKLT				
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALELGALNQALQEISK	TSEKSKRIFYX				
m259-1	AEYKNIFGDACRSETALELGALNQALQEISK	TSEKSKRIFYX				
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

603

g260 GICPKYPTGCRPV
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

```
a260.seq
1  ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCAGCATG
101 CCGCTGAATG CCACTTCCTG CCGGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGGCGC GGCAGCGGTT TCTTTCGCGG AAACGATTTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATTCATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTCT CCGTCAACCT GCGGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGGTCCCA CAGGCGGCC CCATTGCCAC GGGCTGTACA GGTATTGCGC
551 CGAAATGCCC CACAGGTGT CGCCCTGTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

```
a260.pep
1  MGAGMVVFVF RPFSSLFRAL FEDRVGIVEG AHDAAECDL PEEFTRIRIG
51  DVFIDSVGVQ AARLFQAFGV NPGAQVQGP AFRAREQARR GSGFFAGNDL
101 RVPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*
```

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFPSSLFRALFEDRVGIVEGAHDAAECDLPEEFTRIRIGDVFIDSVGVQV					
a260	MGAGMVVFVFRPFPSSLFRALFEDRVGIVEGAHDAAECDLPEEFTRIRIGDVFIDSVGVQV					
	10	20	30	40	50	60
m260.pep	AARLFQAFGVNPGAQVQGPAPFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
a260	AARLFQAFGVNPGAQVQGPAPFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAQVQGPAPFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
a260	AARLFQAFGVNPGAQVQGPAPFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVPQ					
a260	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVPQAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

```
g261.seq
1  atggagcttg ggcataatcg attccttctg ctttgcgcgc gttcagacgg
51  cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctcgggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctggttcgcg atgtagtcca acacgcccac ttcgtccgcc aacgcccacg
201 tttgcgcctt ggtcaggtac atcagcggcg tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcatt gatttgacga acacgccgcg
301 gcagtcggga tagcccga aaatcggttc gcacacgccc gcgatgatgt
351 gccgatacc ctgccctttg gcaaaaatgg cggcgtaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattgca acgccgttgt cggcggtttc
451 gatggcggcg gtttcgatgg cggcggtttc gtccatcagg gcgttgtgcg
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tctgcgcga tccactctgc gcgttcacgc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggcct ggacgttttc gcgccgtag gtttggattg
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1   ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTCGCGCT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCAAG
201 TTTGCGCCTT GGTCAATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCGGAGA AGTCGGTTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTT CCGCAGTTTC
451 GATGCGGCGG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGT TGTTCGACG CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGGACG TTTTCGCGCC CGTAGGTTT GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1   MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPRLRL QQIHQRRVDL KIIVHRQIKG NVHGFQKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA	AVGIAGEVGF	AHARDDVPYP			
a261	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHGFQKHVT	AVGIAGEVGF	AHARDDVPYP			
	130	140	150	160	170	180
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV	EYGLFDAQIL				
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV	EYGLFDAQIL				
	190	200	210	220	230	
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAVGLDCLNQAGGRILTARKDDQGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAVGLDCLNQAGGRILTARKDDQGLLVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1   atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgcaa
51  accgcgcgta gaggccgtac ccaaaaacaa cggctttatc cccaacctca
101 tcggcggtatt ggcaaacgcc ccgaagctt tggcggttta ccaagaagtc
151 ggcaagctca acgccgcaaa cagcctgacc gccggcgaaag tcgaagtgat
201 ccggatcatc gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acaccaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgccccgc ctttggcggc aggtaaatct gacgatgcca aactcgcgcc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

607

m263/a263 97.4% identity in 77 aa overlap

					10	20	30
m263.pep					AAGEFDDAKLGALAAFTQAVMAKKGAVSDE		
a263	QCGFCVAGHTKLATLKKLLSEQSVKAARALAAGEFDDAKLGALAAFTQAVMAKKGAVSDE						
	80	90	100	110	120	130	
		40	50	60	70		
m263.pep	ELKAFFDAGYNQQQAVEVVMGXLLATLCNYVNNLGQTEINPELQAYAX						
a263	ELKAFFDAGYNQQQAVEVVMGVALATLCNYVNNLGQTEINPELQAYAX						
	140	150	160	170	180		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

g264.seq

```

1   ttgactttaa cccgaaaaac ccttttcctc ctcaccgccc cggtccggcac
51  acactccctt cagacggcat ccgcccagcg agtgrtcaag ccggaaaaaac
101 tgcacgcctc cgccaaccgc agctacaaag tcgcccgaatt cacgcaaac
151 ggcaacgcct cgtggtagcg cggcagggtt cacgggcccga aaacttccgg
201 cggagaccgc tacgatatga acgcctttac cgcgcgccac aaaacctgc
251 ccatccccag ccatgtgcgc gtaaccaaca ccaaaaacgg caaaagcgtc
301 atcgtccgcg tcaacgaccg cggccccctc cacggcaacc gcatcatcga
351 cgtatccaaa gccgcgcgcg aaaaattggg ctttgtcagc caagggacgg
401 cacacgtcaa aatcgaacaa atcgtcccg gccaatccgc accggttgc
451 gaaaacaaag acatctttat cgacttgaaa tctttcggta cggaaacaga
501 agcacaagcc tatctgaacc aagccgccc aaatttcgcc gttcgtcat
551 caagcccga cctctcgggt gaaaaacgcc gttacgaata cgttgtcaaa
601 atgggcccgt ttgcctcgca ggaacgcgcc gccgaagccg aagcgcaggc
651 acgcggtatg gttcgggcgg tactgacctc cggttga

```

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

g264.pep

```

1   LTLTRKTLFL LTAAFGTHSL QTASADAVVK PEKLHASANR SYKVAEFTQT
51  GNASWYGGRF HGRKTSGGDR YDMNAFTA AH KTLPIPSHVR VTNTKNGKSV
101 IVRVNDRGPF HGNRIIDVSK AAAQKLGFVS QGTAHV KIEQ IVPQGSAPVA
151 ENKDIFIDLK SFGTEHEAQA YLNQAAQNFA ASSSSPNLSV EKRRYEYVVK
201 MGPFASQERA AEAEQAQARG VRAVLTSG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

m264.seq

```

1   TTGACTTTAA CCCGAAAAAC CCTTTTCCTT CTCACGCCG CATTCCGGCAC
51  ACACCTCCCTT CAGACGGCAT CCGCCGACGC AGTGGTCAAG GCAGAAAAAC
101 TGCACGCCTC CGCCAACCGC AGCTACAAAG TCGCCGGAAC ACGCTACACG
151 CCGAAAAAACC AAGTCGCCGA ATTCACGCAA ACCGCAACG CCTCGTGGTA
201 CGGCGGCAGG TTTCACGGGC GCAAACTTC CGGCGGAGAA CGATACGATA
251 TGAACGCCTT TACCGCCGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAAATT GGGCTTTGTC AACCAAGGGA CGGCACACGT CAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACCGGTT GCCGAAAACA AAGACATCTT
501 TATCGACTTG AAATCTTTCG GTACGGAACA CGAAGCACA GCCTATCTGA
551 ACCAAGCCGC CCAAACTTC GCCGTTTCGT CATCGGGTAC GAACCTCTCG
601 GTTGAAAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTTACCTC
651 GCAGGAACGC GCGCCGAAG CCGAAGCTCA GCGCGCGGT ATGGTTCGGG
701 CGGTATTGAC CCGCGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264.pep

```

1   LTLTRKTLFL LTAAFGTHSL QTASADAVVK AEKLHASANR SYKVFQKRYT
51  PKNQVAEFTQ TGNASWYGGF FHGRKTS GGE RYDMNAFTA HKTLPIPSYV
101 RVTNTKNGKS VIVRVNDRGP FHGNRIIDVS KAAAQKLGFV NQTAHV KIE
151 QIVPGQSAPV AENKDIFIDL KSFGEHEAQ AYLNQAAQNF AVSSSGTNLS
201 VEKRRYEYVV KMGPFTSQER AAEEAQARG MVRAVLTAG*

```


609

	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSF GTEHEAQ					
a264	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSF GTEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAE AQRGMVRAVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAE AQRGMVRAVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```
m265 . seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GCGCGGGCTG ATGATTTTGT CTTGTTTGTG GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGGCGGAA
151 ATGCTCAGCA GTGCGGTTGC GCGGAGGTC AAGAGAAGGT GTTTGATGTT
201 CATAT .TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGGCGGTCA ATACCGCCCG AACCATACCG
301 CGCGCTGAG CTTCGGCTTC GCGGCGCGGT TCCTGCGAGG TAAACGGTCC
351 CATTTGACG ACGTATTCGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```
m265 . pep
1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFI XFVNRGLENV DINKVSNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265 . pep	MSVILPPTRANAAFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGAE MPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFVNRGLENVDINKVSNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
g265	KRRCLMFI - FALVNQGLKNGDINKVSNRQPEVSTARTIPRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

611

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

```
m266/g266

      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g266      MQFRRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
          10      20      30      40      50

      70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g266      LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          60      70      80      90      100     110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTTG CTGCTTGCCT
101  TGATTTTTCG CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAAACATT CCGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTGCGCTG ACCGCCGTTT TGCCTACAT CCTCGAATCC CGTGCGGGAG
251  CGGTACAUGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301  CTGATTTTTC CGTTCCCTG TTTCGTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

```
      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a266      MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTLKFGIVPLKRKHFGHH
          10      20      30      40      50      60

      70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a266      LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          70      80      90      100     110     120

m266.pep  X
          |
a266      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

```
g267.seq
```

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGOVDVV TLGAARAVFA
51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGOVDVV	TLGAARTVFTFFRFDVNRHC			
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGOVDVV	TLGAARAVFAFFRFDVDRHC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPFAVRIP	PFLRVQTAETHGLRRFLFGE	INCVFAGEKVFERAHTFYQF			
	:::	:::				
a267	GANGFTQFTRDAAFLAVWIT	ALRVQTAETHGLRRFLFGK	INRVFAGKKVFERAHTFYQF			
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaat
101 cctgcggaag cgaagagact aaagagattt tgggtcaaact ggcccgcgac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201 ccaagcattt gccgatatcg gcataatcgca tatccgcaga atggtcgaac
251 gtttggcat aaccgtcgat gaagtcgaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccgacga
351 tgttgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451 tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaagcaa
501 aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctggtgtc tatggcactg attaaagagc cgttggacaa agcgaacaa
601 aggaacgaaa aacttgaaagc ggcagaagcc accgcgcagg aagcgaaggga
651 ggcagaagaa gcggcggcgc aggaggcatt gggtcgggag caggaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801 ctgcagaaaa acatggaaaa gcggtatgga caagatctgt gccacaatg
851 cgaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901 tgtaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLGIGNPFSG KEISCGSEET KEILVKLVRD
51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTEKTD
101 SSKLKCEAAL KLDVDDVDV YAVAAQSIG NSHKKTPDFF EPYYRKEGAY
151 YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201 RNEKLEAAEA TAQEAREAE AAAQEALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKLOASQK TWKSGMDKIC ANNAKAEGET PNGIKVSELA
301 CKTAETEARL EELHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAAGAGCC GTTGGACAAA GTGAAACAAA GGAACGAAGA
```

		10	20	30	40	50	60
		70	80	90	100	110	120
m268.pep		PQT	VQNK	LQPS	QKTW	KS	GMDK
a268		PQT	VQNK	LQAS	QKTW	KS	GMDK
		70	80	90	100	110	120
		130	140				
m268.pep		KAL	IDEM	XREAD	XKEL	SKRL	X
a268		KAL	IDEM	XREAD	XKEL	PKRL	X
		130	140				

m268-1.seq

1	GTGCAATCCC	GATATGATGG	TTTGATAAAA	TTTAAACATA	TATGTTCGCG
51	AGCTATGGCA	CTGATTAAAG	AGCCGTATTGGA	CAAAGTGAAA	CAAGAAGGAAC
101	AAAGAATTGA	AGCGGCAGAA	GAAGCGCGCG	CGCAGGAGGC	ATTGGGTCCG
151	GACGAGGAAG	CCGCGCCGCT	ATCGCAATGG	GAAAGAACGC	ACAGCTGTCT
201	CGCGAGCGAG	TTTGACGACGT	TCTGGAAAGG	ATTGCCTCAA	ACCGTACAGAA
251	ATAAGCTGCA	AGCCTACAGC	AAAACTGGA	AAAGCGGGAT	GGATAATCTC
301	TGTGCCAACA	ATGCGAAAGC	TGAAGGTAAA	AGCCGCAACG	GCATAATCTC
351	CAGCGAACTG	GCATGCAAAA	CGGCGAAAAC	CGAAGCACGC	TTGGAAAGGC
401	TGCAACAACG	TAAAAAAGCG	CTTATCGACG	AAATGGCCAG	GGGAAGCGGAC
451	AAGAAGAAGAC	TGTCTAAGCG	GCTCTGGA		

m268-1.pgp

```

1  VQSRDYDLGHK FKHICSAAMA LIKEPLDKVK QRNEELEAAE EAAAQEALGR
51 EQEAAARVSEW EERYKLSRSE FEQFWKGLPO TVQNKLOASQ KTWKSGMDK1
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKLSSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

					10		20		30
m268-1.pep					VQSR	YDGLHFKFKHCSAAMALI	KEPLDKVKQRNE		
					:	:	:	:	:
g268					KEGAYVVKTI	SYSVQPTDDKSKIFAELSQA	HDIIHPLSELVS--MALI	KEPLDKAKQRNE	
	150	160	170	180	190	200			
		40		50		60		70	
m268-1.pep		ELEAAE-----	-----EAAAQ	EALGREQEAARVSEWEERY	KLRSRSEFEQFWKGLP	QTVQN			
		:	:	:	:	:	:	:	:
g268		KLEAAEATAQEAREAE	EAQAQALGREQEAARVSEWEERY	KLRSRSEFEQFWKGLP	QTVQN				
	210	220	230	240	250	260			
		90	100	110	120	130	140		
m268-1.pep		KLQASQKTWKS	GMDKICANNAKAEGKTP	NGIKFSELACKTAKTEAR	LEELHNRRKKALIDE				
		:	:	:	:	:	:	:	:
g268		KLQASQKTWKS	GMDKICANNAKAEGKTP	NGIKVSELACKTAETEAR	LEELHNRRKKALIDE				
	270	280	290	300	310	320			
	150	159							
m268-1.pep		MAREADKKELSKRLX							
		:	:	:	:	:	:	:	:
g268		MVREEDKKELPKRLX							
	330								

a268-1.seq

1	GTGCAATCCC	GATATGATGG	TTTGATAAAA	TTTAAACATA	TATGT1TCCCG
51	AGCTATGGCA	CTGATTAAAG	AGCCCTTTGA	CAAGCGGAAA	CAAAAGGAGCT
101	AGAACTTGTG	AGCGGCAGAA	GAAAGCGCGG	CCAGGAGAGC	ATTGGGTCCGG
151	GACGAGGAA	TGCAAGCCGCT	ATCCGAATGG	GAAAGAAGCT	ACRAGCTGTCT
201	GCGCAGCGAG	TTGAGGACAG	TTCTGAAAGG	ATTGCTCTAA	ACCGTACAGAA
251	ATAAGCTGCA	AGCCTCACAG	AAAACATTTGA	AAGCGGGGAT	GGATAAAATC
301	TGTGCGCAAC	ATCGGAAAGC	TGAAGGTTGA	ACGCCAAACG	CGTAAATTTT
351	CAGCGCAACT	GATATGCAAAA	GCGGCGAAAC	CGAAGCAGCG	TTGGAAGAGCG

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng)

from *N. gonorrhoeae*:

```

m269.pep      MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQT  59
               |||
g269          MVWRVNCAATAALIFSSSPWIWAAVWVWSRFAFSCKPCASLDASSAPALAVSPWDFIRNT  60
               |||

m269.pep      ASPKVSAAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSPKFSSVQVDTSAALLCLSLRS 119
               |||
g269          ASPKVSAAALMHSFKTRALGRFSAPPVAILLSNRGVKKPLSPKSPSVQVDTSAALLCLSLRS 120
               |||

m269.pep      SX 121
               ||
g269          SX 122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269.seq
1  ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCGCGT CCAGCGCGCC GCGTTGACG
151 GTTTCGCCGT GGGACTTTAT CCAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTAA AAACCAGGGC TTTGGGGCGG TTTTCGTCGC
251 CGCCTGTGCG CATTGTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTTGTCG
301 TTTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269.pep
1  MVWRVNCAAT AVLIFSSSPW IWAADVWVAR SALSWRFCAS VPASSAPALT
51 VSPWDFIQT ASPKVSAAAL HSFKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

               10      20      30      40      50      59
m269.pep      MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQT
               |||
a269          MVWRVNCAATAVLIFSSSPWIWAAVWVWSRFAFSCKPCASLDASSAPALAVSPWDFIRNT
               |||
               10      20      30      40      50      60

               60      70      80      90      100     110     119
m269.pep      ASPKVSAAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSPKFSSVQVDTSAALLCLSLRS
               |||
a269          ASPKVSAAALMHSFKTRALGRFSAPPVAILLSNRGVKKPLSPKSPSVQVDTSAALLCLSLWS
               |||
               70      80      90      100     110     120

m269.pep      SX
               ||
a269          SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270.seq
1  atgaataaaa accgcaaatt actgcttgcc gcactgctgc tgactgcctt
51 tgccgccttc aagctcggtt tggtgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg aggggtgcac gctgccggac
151 ggaagccgtg tccgcgccgc cgcctgttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgcccc cgggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcata cgcctgcccc tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacgcgatt taccgccgaa taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALL	LIAFAAV	KLVLLOW	QAXQPQ	AVAAQC
a270	MNKNRKL	LLAALL	LIAFAAV	KLVLLOW	QAXQPQ	AVAAQC
	70	80	90	100	110	120
m270.pep	TKKPFDI	YIEHAP	AGTEQV	SISFSM	KNMDMG	FNRYMF
a270	TKKPFDI	YIEHAP	AGTEQV	SISFSM	KNMDMG	FNRYMF
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADIT	IGSRTF	QTAFTA	EX		
a270	DFTADIT	IGSRTF	QTAFTA	EX		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

```

1   atgttcagtt cgcggatggc gaggatttgg gcgacggggg taacgttgtg
51  tatggtcagt ccgtgtccgg cgttgacgac caagcccaaa tcgccggcga
101 aatgcgcgcc gttttggatg cgctcgaaact gcctgatttg ttcggcggtg
151 ctttgtgcgt cggcatatgc gccggtgtgc agctcgacaa cgggcgcgcc
201 gacatcacgg gcggccttga ttgcctgtc gtcggcatcg ataaacaagg
251 acacgcgtat gcccgcgctc gtcaggattt tggcgaattc ggcgattttt
301 tcctgttgcg ccaatacgtc caaaccgcct tcggtcgtga ttctctgcgc
351 tttttcaggc acgatgcaca cgtcttccgg catcacttta agcgcgtttt
401 cgagcatttc ttccgtcaac gccatttcaa ggttcaggcg cgtgcggatg
451 gcgtttttga cggcaaatac atccgcgtct ttgatgtggc ggcggcttct
501 gcgcagggtg atggtaatca ggtctgcacc gtgcgtttcg gcaaccagtg
551 ccgcctccac ggggctggga taa

```

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

```

1   MFSSRMARIW ATGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51  LCASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILANSAIF
101 SCCANTSKPP SVVISCRFSG TMHTSSGITL SAFSSISSVN AISRFRRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRSAPCVS ATSAASTGLG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

```

1   AwGTTcAGTT CGCGGATGGC GAGGATTtGG GCGATGGGGG TAACGTTtGTG
51  TATGGTCAGT CCGTGtCCGG CGTTGACGAC CAAGCCCAAA TCgCCGGCgGA
101 AATGCGCGCC GTTTTGGATG CGCTCGAACT GCCTGATTtG TtCGGCGGTGG
151 CTGCGCGCGT CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201 GACATCACGG GCGGCTTtGA TTTGCCTGTC GTCGGCATCG ATAAACAAG
251 ACACGCGTAT GCCTGCGTCG GTCAGGATTt TGGTGAACCC GGCGATTtTT
301 TCCTGTtGCG CCAATACGTC CAAACCGCCT TCGGTCGTGA TtTCCTGACG
351 TTTTTCAGGC ACGATGCACA CGTCTCCGG CATCACTtTC AAAGCGTtTT
401 CCAACATTTC TTCCGTCAAC GCCATTtCAA GGTTCAGGCG CGTGCGGATG
451 GCGTtTTTGA CGGCAAAAC ACCTCCGCTT TTGATGTGGC GGCGGTCTTC
501 GCGCAGGTGC ATGGTAATCA AATCCGCACC GTGCGTTTCG GCAACCAAGT
551 CCGCTCCAC GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

```

1   XFSSRMARIW AMGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51  LRSAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNPAIF
101 SCCANTSKPP SVVISXRFSG TMHTSSGITL KAFNLISSVN AISRFRRVRM
151 AFLTANTSAS LMWRRSSRRC MVIKSAPCVS ATSAASTGLG *

```

Computer analysis of this amino acid sequence gave the following results:

621

	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRKAPCVS					
a271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRKAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1   atgactgcaa aggaagaact gtctgcatgg ctgcgccata tgaacaaaaa
51  caaagggtcc gacctgtttg tgacgaccca tttcccgccc gctatgaagc
101 tggacggcaa aatcaccgcg atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cgaagaattt
201 ttcctcgacc aacgagtgcg atttcgccat cagcctgccg gacaccagcc
251 gcttcgcggt caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggccttgaag gatgttgcgc tgaaaaaacg cgggctggtt atttttgcg
401 gcggcaccgg ctccgggcaa tcgacttcgc tcgcctcgct tategactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaag atccgatcga
501 gttgtgccac gaacacaaaa actgcatcat taccagcgcg gaggtcggcg
551 tggacacgga aaactggatg gcggcggtga aaaatacgct gcgtcaggcg
601 ccggatgtga tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc tttgccgaaa cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctgcaccgca tcatcaactt cttccccgag
751 gagcggcgcg aacaattgct gacggatttg tcgctcaacc ttcaggcggt
801 tatctcgcaa cgcctcgctc cgcgagacgg cggcaagggc aggggtggcg
851 cagtcgaggt gctgctcaat tcgcccctga tttcggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgcgt
1051 ttggcggtac agttgcgcag ccgcagggca caaagttccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1   MTAKEELFAW LRHMNKNKGS DLFVTTTHFPF AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNM IQRGATALVF
101 RAITSGIKPF ESLNLPALK DVALKKRGLV IFVGGTGSGK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDLELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1   ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCC GACCTGTTTC TGACAACCCA TTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACC CGC ATCACGGACG AACCCTGAC GCGGAAAAA
151 TGTATGAAA TCgccttttc GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAaaaaaac CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG

```

623

```

          370
m272.pep  QXSXSPDLXLLX
          || :||| |||
g272      QSSDPDLELLX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272.seq
1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTTCG TGACGACCCA TTCCCGCCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GCGGAAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGTCG
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTTCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTGTGCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTGCGCG
551 TGGATACGGA AAAGTGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGCAG
751 GAGCGGCGCG AACCAATTGCT GACGGATTG TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCCGGAGT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGCA GGATGCCTTG AAAAATGCCG ATTCCGCACA CGATTTCGCT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTTCCG GTCCCGATTT
1101 GGAAGTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272.pep
1  MTAKEELFAW LRHMNKNKGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNM IQRGATALVF
101 RAITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

          10      20      30      40      50      60
m272.pep  MTAKEELFAWLRHMNQXKNGSDLFVTTHFPPAMKLDGKITRITDEPLTAEKMEIAFSIMS
          ||||| :|||||
a272      MTAKEELFAWLRHMNKNKGSDFVTTHFPPAMKLDGKITRITDEPLTAEKMEIAFSIMS
          10      20      30      40      50      60

          70      80      90      100     110     120
m272.pep  AKQAEFSSTNECNFAISLPDTSRFRVNMIIQRGATALVFRTITSKIPKFESLNLPPVVK
          ||||| :|||||
a272      AKQAEFSSTNECNFAISLPDTSRFRVNMIIQRGATALVFRAITSKIPKFESLNLPPVVK
          70      80      90      100     110     120

          130     140     150     160     170     180
m272.pep  DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR
          ||||| :|||||
a272      DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR
          130     140     150     160     170     180

```


m273/q273

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

```

1  MSLQAVFVYP  PSRTAQYNEN  QENGKKAHKQ  GQSGKHADRR  QDIGVFQTGT
51  PFTVFLPLFV  AFEIKDDAGK  QRGSRARH*H  NVHCCSLTVK  NPPVRATVEK
101 RR*ITKEVGG  RALLQSGREF  GHDALPRVPD  IICRSPAKLP  RTRFAGFPHC
151 PLVSYGVCLL  FVFOAVFSYA  *

```

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNNQENGGKAHKQGGSGKHADRCQDIGVFKAGTPFPVFLPLLV					
a273	MSLQAVFVYPPSRTAQYNNQENGGKAHKQGGSGKHADRRQDIGVFTGTPTFTVFLPLFV					
	10	20	30	40	50	60
m273.pep	AFEIKDDAGKQGRSRAHXXHCVHCCSLMLKNPPVRATVL-RRQIAKFVCGRVPKSGRFE					
a273	AFEIKDDAGKQGRSRAHXXHNVHCCSLTVKNPPVRATVFKRRXITFKVGGRRALLQSGRFK					
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRAHXXHCVHCCSLMLKNPPVRATVL-RRQIAKFVCGRVPKSGRFE					
a273	AFEIKDDAGKQGRSRAHXXHNVHCCSLTVKNPPVRATVFKRRXITFKVGGRRALLQSGRFK					
	70	80	90	100	110	120
m273.pep	GCSRRAALCAGVICRSPAKSPTRTFAEFPHCLPLVSYGVVLFPVXQAVFSYAX					
a273	GHDALPRV-PDIIICRSPAKLPRTRFAGFPHCLPLVSYGVCLLFVQAVFSYAX					
	120	130	140	150	160	170
m273.pep	GCSRRAALCAGVICRSPAKSPTRTFAEFPHCLPLVSYGVVLFPVXQAVFSYAX					
a273	GHDALPRV-PDIIICRSPAKLPRTRFAGFPHCLPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

627

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1  ATGGCGGGGC  CGATTTTGT  CGTCATCGCC  AGCGTCGCTA  TGTTTTTGT
51  CGCGCAGCAG  CACGCGACAG  ATTTGGTTAC  GGACGATTAT  TATAAAGACG
101 GCAAGCATAT  CGACATCCAG  CTTTCATCGG  ATGAAGAAGC  CGTCAGACGG
151 CATATCGGGG  TGCAGGTTCT  CATTTCCCCC  GATATGAATG  CGGCAAAAGT
201 GTTTGTCGGC  GCGGAGTTTG  ACGGCAAACA  GCCTTTGAAC  CTGCTGCTGA
251 TGCACCCGAC  CCGCAAGGCG  GACGATCAA  CCGTCGCCCT  CAAGCCCGTC
301 GGCAGCGCGC  AGAACGGCAG  GGCGGAATAT  GAGGCGGTGT  TCAAAACCCG
351 TTCGCCGACC  AACCCTGGT  ATGTGCGCGT  GAGGACGCG  GCAGGCGTGT
401 GGCGCGTCGA  GAACAAATGG  ATTACCAGCC  AAGGCAATGC  GGTTCGATTG
451 ACCCCGATGG  ACAAACTTT  CAATAATACT  GAAAGCAAAT  AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1  MAGPIFVVIA  SVAMFFVAQQ  HATDLVTDDY  YKDGKHIDIQ  LHRDEEAVRR
51  HIGVQVLISP  DMNAAKVFG  GEFDGKQPLN  LLLMHPTRKA  DDQTVALKPV
101 GSAQNGRAEY  EAVFKTLSPT  NHWYVRVEDA  AGVWRVENKW  ITSQNAVDL
151 TPMDKLFNNT  ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
a274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m274.pep	DMNAAKVFGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
a274	DMNAAKVFGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
m274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1  atgattttgc  cgccatccat  gacgatgatg  cggtcggcgg  attcgacggt
51  ggtcaggcgg  tgggcgacga  tgatgccggt  gcggttttcc  atcaggcggt
101 cgagcgcttg  ttggacgagg  cggttcggtt  cggtgtccaa  tgcgctggtg
151 gcttcgtcca  ataataatat  cggcgcgtct  ttcaaatgg  cgcgggcgat
201 ggcgacgcgt  tgccgctgtc  cgccggataa  gttgctgccg  ttcgatccga
251 tgggctggtg  cagtcgagc  ggggatgcgt  cgatcaggct  ttgcagggtg
301 gcggtcttga  gggcggacag  gacttcggct  tcgccgcgt  cgggacggct
351 gtatcggacg  ttttcaaaca  ggggtgtcgt  aaacaggaat  acgtcttggg
401 agacgagggc  gaattgggcg  cgcaggcagt  cgagtttgat  gtcggcgatg
451 tcgataccgt  ctatgcagat  gttgcggca  gacggttcga  caaagcgggg
501 cagaagggtg  acgacggtg  atttgccgct  gccggaacgt  ccgaccaggg
551 cgacgcgttc  gccttgcttg  atgtcgaggt  tgaagtgtc  gagggctttg
601 atgccgtctg  aacggtattc  gacatcgacg  ttgcggaagc  tgatgcgccc
651 ttgcacacgc  tgcggcgcg  gcgtgccttt  gtcctgttcg  ggcggggtgt
701 cgagaaatgc  acatacgccg  tcggcgcgca  ggaacatcgt  ctgcataggg
751 atgctgatgt  tggcaaggct  tttgatggg  gcgtacattt  gcagcatcgc
801 gacgatgaat  gccataaatt  cgccgatggt  ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

629

	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

```
a276.seq
1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTCAAGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGGTGTCGTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC AAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGGGTGCGA GCGTGCCTTT GTCCTGTTCC GGCGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATTG GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

```
a276.pep
1  MILPSSITMM RSAPSMVVRW WATMMPVRF SIRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKGRSRL TTVDLPLPER PTRATRSPCL MSRLKPSRAL
201 MPSERYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*
```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRF SIRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVVRWATMMPVRF SIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKGRSRLTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKGRSRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSERYSTSLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
a276	PTRATRSPCLMSRLKPSRALMPSERYSTSLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

631

```

                                     :|||||: |:||:|||||:||||:||||
m277      GLRFVVVELAQQPVGI AVFEVVGGLLDFVLVHVAVG DGVAVERFCPNEVVDV FYTLQVH
           30      40      50      60      70      80

           40      50      60      70      80      90
g277.pep   RQAFDAVGNFAEYGRAIDTADLLEIGKLG YFHAVEPDFPAQTPRTEGGVFPV VFDKADV
           |||||:|||||:||||:||||:||||:||||:||||:||||:||||:||||
m277      RQAFDAVG DFAEYGRAVDAADLLEIGKLG YFHAVEPDFPAQTPRAEGGVFPV VFDKADV
           90      100     110     120     130     140

           100     110     120     130     140     150
g277.pep   DFGIDAQFAQGV EIEVLDIGGGGFEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGK PRL
           |||||:|||||:||||:||||:||||:||||:||||:||||:||||
m277      DFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGK PRL
           150     160     170     180     190     200

           160     170     180     190     200
g277.pep   GAERAQAGGGMGCAGTDFHVEGLDDGA AFVCP EQLQFEDDLLEGKHGLL
           ||| |||||:|||||:||||:||||:||||:||||:||||
m277      GAECAQAGGGMGCAGTDFHVEGLDDGA AFVCP ECLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAC TGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTG TTC
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT GAACTGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTCGACAAA GCGGATGTCG TGCACTTTGG GGTGCGATGCC
451 CAATTCGCGC AGGGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGCGGCG
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGT GGATGACGGT GCAGCCTTTG
701 TCTGCCCAGA ATGTTGCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DFVLVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VG DFAEYGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GG VFPV VFDK ADVVHFGVDA
151 QFAQGV EIEV LDIGGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPR LGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCP ECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

           10      20      30      40      50      60
m277.pep   MPRFEDKLVGRQEGGVFFGKQAFGLRFVVVELAQQPVGI AVFEVVGGLLDFVLVHVAV
           |||||:|||||:||||:||||:||||:||||:||||:||||:||||
a277      MPRFEDKLVGRQEGGVFFGKQAFGLRFVVVELAQQPIGI AVFEVVGGLDFVLVHVAV
           10      20      30      40      50      60

           70      80      90      100     110     120
m277.pep   GDGVAVERFCPNEVVDV FYTLQVHRQAFDAVG DFAEYGRAVDAADLLEIGKLG YFHAVEP
           : |||:|||||:||||:||||:||||:||||:||||:||||:||||
a277      SYCITVQRFCPNEVIDVFHALQVHRQAFDAVG DFAEYGGAVDAADLLEIGELGYFHTVEP
           70      80      90      100     110     120

           130     140     150     160     170     180

```

633

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

```

g278/m278

      10      20      30      40      50      60
g278.pep  LRAITPGAIFSTGAVKVVLIIGPLPSIGRPNASTTRPTNSRPTGTSKIRPVQVTVSPSLIC
          |||||
m278      LRAITPGAIFSIGAVKVVLIIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC
          10      20      30      40      50      60

      70      80      90     100     110     120
g278.pep  SYSPNTTAPTESRSRFFIAKPKVLPGNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT
          |||||
m278      SYSPNTTAPTESRSRFFIAKPKVLPGNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT
          70      80      90     100     110     120

      130     140     150     160     170
g278.pep  DRFSILALIRSLISAGLSCMKTLIRHSRVQSTQFALYRQIQNLITHFNF
          |||||
m278      DRFSILALIKSLISAGLSCMKTLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF
          130     140     150     160     170     180

m278      DRDFQLAVETLIQHLHLQADLFVGQRIGTVNDGRFDMVE*
          190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

```

a278.seq
1  TTGCGCGCAA TCACGCCCGG TGCGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG TCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTCAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCAATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTGAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

```

a278.pep
1  LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLIC SCSPTTAPT ESRSRFFIAK KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLRQLAD
201 LFGVQRIGTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

```

      10      20      30      40      50      60
m278.pep  LRAITPGAIFSIGAVKVVLIIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC
          |||||
a278      LRAITPGAIFSIGAVKVVLIIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLIC
          10      20      30      40      50      60

      70      80      90     100     110     120
m278.pep  SYSPNTTAPTESRSRFFIAKPKVLPGNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT
          |
a278      SCSPTTAPTESRSRFFIAKPKVLPGNSSISPCIASDKPWMRTIPSVTEITVPRVRTSAFT
          70      80      90     100     110     120

```

```

m279.pep      ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRSTLTA
|| ||||| ||||| |||: |||||::||| ||||| ||||| ||||| ||||| |||||
g279          ITTCPGELKLTASTTSPCADSAQICLTCSSSKPKMAAIAPTPCGTADCISSARRRSTLTA
              70          80          90          100          110          120

              130          140          150
m279.pep      SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g279          SAKSNSAATSAVYSPRLCPATAAGVLPPTSXKX
              130          140          150

```

a279.seq

```
1 ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNN A GGGCTTCGGC
51 GAGTTTGTCT GCGGGCGGGT TCATGAGGCT GCAATGGGA GGTACNGACA
101 CNGGCGAGCG CAGGGCGCGT TTGGCGCCGG CTCTTTTGGC GGCAAGCATA
151 GCGCGCTCGA CGCGCGCGGC ATTGCTCTGA ATCACGACT GTCCGGGCGA
201 GTTGAAGTTG ACGGCTTCAA CCACTTCATC CTGTGCGGAT TCGGCGCAAA
251 TTTGTTTAC CTGTTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA NGCGCAGCAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GCGGCAACN AGTGCGGTGT
401 ATTCGCCGAN GCTGTGTCCG GCAACGGCGG CAGGCGTTTT GCCGCCGCT
451 TCCGAATAG
```

```
a279.pep
1  MTXICGCLIS TVXRASASLS AAGFMRLQWE GTDTGSGRAR LAPASLAASI
51  ARSTAAALPA ITTCPELKL TASTSSCAD SAQICFTCSS SKPRIAAIAP
101 TPCGTADCIS SARXRTSLTA SAKSNAPAAT SAVYSPXLCF ATAAGVLPPA
151 SE*
```

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAMARPTAAALPA					
a279	: :					
	10	20	30	40	50	60
	MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA					
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTFCGTADCISSARRRTSLTA					
a279	:					
	70	80	90	100	110	120
	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTFCGTADCISSARXRTSLTA					
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX					
a279						
	130	140	150			
	SAKSNAAPAATSAVYSPXLCPATAAGVLPPASEX					

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

637

201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KOVAIIROI KREGIKAVFT
 251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNIFALTN
 301 AMKQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng)
 from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLTIAALLTASATAAPLPVVTFSFILGQVAKQIGGERVSIQSLVGNQDTHAYHM					
	::					
g280	MKHLKLTIAALLATAATAAPLPVVTFSFILGQVAKQIGGERVAVQSLVGNQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKLVLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EEGHHDDH-					
	::					
g280	TSGDIKKIRSAKLVLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAE EEGHHDDH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---DHDHDEGHHDHGEYDPHVWNPVLM SAYAQNVAKALIKADPEGKVYYQORLGN YQMQ					
	::					
g280	HDHDHDEGHHDHGEYDPHVWNPVLM SDY AQNVAETLIKADPEGKVYYQORLGN YQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGV SSEAEPSAKQVAAI					
	::					
g280	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGNRYNISFIAPQGV SSEAEPSAKQVAAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHN IK					
	::					
g280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHN VE					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

1	ATGAAACACC	CCAAACTCAC	CCTTATCGCC	GCATTGCTGA	CCACTGCCGC
51	AACTGCCGCC	CCCCTGCCGG	TTGTAACCAG	CTTCAGCATT	TTAGGCGACG
101	TAGCCAAACA	AATCGGCGGA	GAGCGCGTAT	CCATACAAAG	TTTGGTCGGA
151	GCCAAACCAAG	ATACGCACGC	CTATCATATG	ACCAGCGGCG	ACATTAATAAA
201	AATCCGCAGT	GCAAACTCG	TCCTGATTAA	CGGCTTAGGA	CTTGAAGCTG
251	CCGACATCCA	ACGTGCCGTC	AAACAGAGCA	AAGTATCCTA	TGCCGAAGCG
301	ACCAAAGGCA	TCCAACCCCT	CAAAGCCGAA	GAAGAAGGCG	GACACCATCA
351	CGACCACGAT	CATGACCACG	ACCATGACCA	CGAAGGACAC	CACCACGACC
401	ACGCGCAATA	TGACCCAC	GTCTGGAACG	ACCCGTCCT	TATGTCCGCC
451	TATGCCCAA	ACGTGCGCGA	AGCCCTGATA	AAGGCCGACC	CCGAAGGCAA
501	AGTTATTAT	CAACAACGCT	TGGGCAACTA	CCAAATGCAG	CTCAAAAAAC
551	TGCACAGTGA	CGCACAAGCC	GCATTTAATG	CCGTCCCTGC	CGCCAAACGC
601	AAAGTCCTGA	CCGGGCACGA	TGCCTTTTCC	TATATGGGCA	AACGTACCA
651	TATCGAATTC	ATCGCCCCAC	AAGGTGTGAG	CAGCGAAGCC	GAGCCTTCAG
701	CCAAACAAGT	CGCGCCATC	ATCCGACAAA	TCAAACGCGA	AGGCATCAAA
751	GCCGTATTTA	CCGAAAATAT	CAAAGACACC	CGCATGGTTG	ACCGCATCGC

639

```

501 gcacgtcatt ttcctcatcc tcgctggtat gaacctcgta tccggcttcc
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt
601 accgcccgtt tatgggcaag aaatatgggg acgctcatcc tgtgtccgt
651 cctcatcgcc cttttttgcg gtttgatcgg gctgctcatt tcctaccaca
701 tcgaaatccc ttccggcccc gccatcatcc tctgttgag cgtcctttat
751 cttttttccg tcatactcgg caaagaaggg ggcattctgc ccaaatgggt
801 caaaaaccac cgccaccaca ccacctga

```

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

g281.pep

```

1  MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGVGG FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL
101 ISKNGSSVDL LHLFSGSVLA VDIPALQLIA AVSGLTLITL AVIYRPLVLE
151 SIDPLFLKSV NGKGGLWHVI FLILVVMNLV SGFQALGILM SVGIMMLPAI
201 TARLWARNMG TLILLSVLIA LFCGLIGLLI SYHIEIPSGP AILCCSVLY
251 LFSVILGKEG GILPKWFKNH RHHTT*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

m281.seq (partial)

```

1  ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51  CGTCGGCGTA TTCTCGTCA TCGCGCGTAT GAGCCTGA GAAGGACGAT
101 TGAGCCACGC CGTCTGCCCC GGTGCCGCGC TCGGCTACAT GTTTGCCGGC
151 TTGAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGCAG GCATGCTGAT
201 GGCACTGCTT GCGGGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG CGTAGTCTCT
301 GTCAGCAAAA ACGGGAGCAG CGTCGATTG CTCACCTCC TTTTCGGCTC
351 TGTACTTGCC GTCGATATTC CTGCCCTGCA GCTCATCGCC GCGTCTCCA
401 GCCTCACGCT CATTACCCTT GCCGTCATCT ACCGCCCCTG CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCCGTC GCGGGCAAAG GCGGGCTTTG
501 GCACGTCTCT TTTCTCGTCC TGGTCGTCAT GAACCTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TCATGATGCT GCCAGCATT
601 ACCGCCCCGC TGTGGGCGAA GCATATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATCC TTCCGGTCCC GCCATCATCC TCTGTTGAG CGTCTTTAT
751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CC..

```

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

m281.pep (partial)

```

1  MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLFSGSVLA VDIPALQLIA AVSSLTLITL AVIYRPLVLE
151 SIDPLFLKSV GKGGLWHVL FLVLVVMNLV SGFQALGILM SVGLMMLPAI
201 TARLWAKHMG ALILLSVLTA LLCGLSGLLI SYHIEIPSGP AILCCSVLY
251 LFSVILGKEG GILT..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng)

from *N. gonorrhoeae*:

m281/g281

	10	20	30	40	50	60
m281.pep	MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG LSLPAMGLGG					
g281	MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG LSLPAMGVGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL VSKNGSSVDL LHLFSGSVLA					
g281	FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL ISKNGSSVDL LHLFSGSVLA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIA AVSSLTLITL AVIYRPLVLES IDPLFLKSV GKGGLWHVL FLVLVVMNLV					

641

	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1  atgggattgg gtatggaaat cggcaagctg atttggtgct ttttggtgct
51  gatcaatccg tttagcgcgt tgctgcttta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgac ggcggtgcgc tattgaaggt
201 tttgggcata agcgtcgggt cgtttcaggt cggcggcggg attttggtgc
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggcgatt gccgtcgtgc ccatcgccat accgatcacc atcggtcggg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgcgc tgattatcgc ggccggtttg gtggtcagtg cgatttgta
501 tgccatttta atcgttgccg ggaaggtcag ccgcctgctg ggcgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggcgggatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattcccgc aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1  MGLGMEIGKL IVALVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLR GATGLTILNR IMGMLAAVS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1  ATGGGATTGG GCATGGAAT CCGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCGCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTGTGTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGCGCGACGG
551 GGCTGACGAT TTAAACCGC ATTATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLR GATGLTILNR IMGMLAAVS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

643

```

              70      80      90      100     110     120
m282.pep      GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGOARPARNAGAI
a282           GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGOARPARNAGAI
              70      80      90      100     110     120

              130     140     150     160     170     180
m282.pep      AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL
a282           AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL
              130     140     150     160     170     180

              190     200     210
m282.pep      GATGLTILNRIMGMMMLAAVSVEIIVSGLKTIFFPQLAGX
a282           GATGLTILNRIMGMMMLAAVSVEIIVSGLKMIFFPQLAGX
              190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

```

g283.seq
1   atgaactttg ctttatccgt catcacattt accctcgcc ttttctgccc
51  cgtccccgct gccggaaccg ccgtctttac ttggaagac ggcggcggca
101 acagctattc ggatgtgccg aaacagcttc atcccgaacca gagccaaatc
151 ctcaacctgc ggacgctcca aaccaaaccg gcggtcaagc ccaaacctgc
201 cgtcgatacg aatgcggaca gtgcgaagga aaacgaaaag gatatcgccg
251 agaaaaacgg gcagcttgag gaagaaaaga aaaaaattgc cgaaaccgaa
301 cggcagaaca aagaagaaaa ctgccggatt tcaaaaatga acctgaaggc
351 ggtgggaaac tcaaatgcga aaaacaagga tgatttgatc cgtaaatata
401 ataacgccgt aaacaaatac tgccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

```

g283.pep
1   MNFALSVITF TLASFLPVPP AGTAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTLQTKP AVKPKPAVDN NADSAKENEK DIAEKNGQLE EEKKKIAETE
101 RQNKEENCRI SKMNLKAVGN SNAKNKDDLI RKYNNAVNKY CR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

```

m283.seq
1   ATGAACCTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAGA AGAAACTGC CGGATTCAA AAATGAACCT
351 GAAGGCGGTG GGAAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

```

m283.pep
1   MNFALSVIML TLASFLPVPP AGAAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTRQTKP AVKPAQADAG KRTDGAAQEN NPDTAENRQ LEEKKRIAE
101 TERQNKEENC RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

```

              10      20      30      40      50      60
m283.pep      MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTRQTKP
g283           MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP
              10      20      30      40      50      60

```

645

```

501 gggtaatggg cggtagctca ataccgcgtg cggcaacgtc ggtggcaacc
551 aaaattttgc agcggccttt acgcaaattc gtcagcgtgc ggttgcgcca
601 gccctgcggc atatcgccgt gcaggcagtt ggcggcgaaa cctttttcgt
651 acaattcatc cgcgatgact tcggatcatc ctttggtgga cgtgaaaaac
701 acacattggg cgatgttggc atcgcgcagg atgtggtcga gcaggcggtt
751 tttgtggcgc atatcgctgc agtacaacaa ctgtcttcg attttgcctt
801 ggccgtccac gcgttcgact tcgataattt cagagtcctt ggtcagtttg
851 cgcgcagatt tgccgactgc gccgtcccaa gtggcggaga acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

```

g284.pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
51  TVFLKAFFLE TFAARFAAEA FFAREMIAAP AAGFPIAPAA FAERLAACGF
101 AFAGRFLHAFD GQFGQFAVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRFLFR QVVVYDVNG RYVNTACGNV GGNQNFAAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHREFG RENHTLVDVG IAQDVVEQAV
251 FVAHIVAVQQ LLFDALAVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

```

m284.seq..
1  ATGCCGCTCTG AAACTCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51  AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCGTTT GCCTTTGAAG CCTTCGCCGG TTTTTTGTAA
151 ACCGTCTCTC TTAAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTTCG
201 CGCCGAAGCC TTCTTTGCTC GGTTCATGAT CGCCGCGCCA ACCGCCGAT
251 TTACGATCGC CCCAGCCGCC TTTGCCTTTC GGCTTGCCGC CTGCGGATTT
301 GCGTTTGCGG GTCGGTTCCA TGCCTTCGAT GGTCAGTTCG GGCAGTTTTC
351 GGTAAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCGGCCT GCGCGGCCGG TCGCGCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACATC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT ACGCAAATCC ATCAGCGTGC GGTGCGCCA
601 GCCTTGCGCG ATATCGCCGT GCAGGCAGTT TCGCGCGAAA CCTTTTTCGT
651 ACAGTTCATC CGCAATGACT TCGGTCATGG CTTTGGTGA CGTGAAAATC
701 ACGCATTGAT CGATATTGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTTCTTCG ATTTTGCTCT
801 GATCGTCCAC CGGTTTCGACT TCGATGATT CAGGGTCTTT GGTCAGTTTG
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCG CTCGCGGTTG CTTCCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAATCAG CACTTCCAAA
1001 CGTTCAAAAT CAACTTTGCC GCTTGCATC AGGTCCATCA GACGGCCCGG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGCT CAGGGCACGG GTTTGGTAGC
1101 CGAAAGACGC GCCGCCGACG ATGCTGACGG TCGGGAACCA ACGCATATTT
1151 TTGGCATACG CCAGCGCGTT TTTCTCGACT TGAGCGGCA GTTCGCGGGT
1201 CGGGGTCAAC ACCAAAGCAC GCGGCGCTTT GCCCGGTTT TCGCTGCGTT
1251 TGGTCAGTTT TTGCAAAGTC GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

```

m284.pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
51  TVSLKAFFLE TFAARFAAEA FFAREMIAAP TAGFTIAPAA FAERLAACGF
101 AFAGRFLHAFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRFLFR QVVVDNVNG RYVDTACGNI GGNQNFAAAF TQIHQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFVG RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVQNG HFQTFKINFA ALHQVHQFAR
351 RGDNQIDRFA QGTGLVAERR AADDADGAEP THIFGIQORV FLDSLRSQFAG
401 RGQHQSTRAF ARFFAAFGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

647

```

51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFAHFD QQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGFGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNO HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRARAF AKFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

	10	20	30	40	50	60
m284.pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
a284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
	10	20	30	40	50	60
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
a284	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
a284	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
	70	80	90	100	110	120
m284.pep	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVFRLEFQVVVDNVGNGRYVDTACGNI					
a284	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVFRLEFQVVVDNVGNGRYVDTACGNV					
	130	140	150	160	170	180
m284.pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDIG					
a284	GGNQNFAAFAQIHQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHGFGGRENHALIDVG					
	190	200	210	220	230	240
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
a284	IAQDMIEQAVFVAHIVAVQQLFFDFALVVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
	250	260	270	280	290	300
m284.pep	LTVARRCFHGDGFDVVDKAHIQHTVGFVQNHQFQTFKINFAALHQVHQTARRGDNQIDRFA					
a284	LTVFRRGFDDGFDVVDKAHIQHTVGFVQNHQFQAGEIDFAALHQVHQTARRGDNQIDRFA					
	310	320	330	340	350	360
m284.pep	QGTGLVAERRAADDADGAEPHTHIFGIRQRVFLDLSRQFAGRGQHQSRAFARFFAAGQF					
a284	QGAGLVAERCTTDDADGTEPHTHIFGIRQRVFLDLSRQFAGRRQHQRARAFARFFAAGQS					
	370	380	390	400	410	420
m284.pep	LQSRX					
a284	LQSRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

g285.seq
1 atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat ttgggcagta

```

649

```

3451 ttctccggct acggcgcgga cggtaccata ggcggcaaac tgacctgac
3501 cgcgcaaccg ggcggaaatg tgcgtgggg- gggcacggtc cgcgtcatca
3551 aagggcgtra caaagcatac gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgtc caacgacccc aacctgaaca tccgcgcgga
3651 acgcccgcct tcccccgctg gtgcgggctg ggaatatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcctcct caaccgtgcc ggcagcggca gcagcggcga
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc ggcaaatca
3851 acgaccgcat cgggctgggt gatgatttgg gctttaccag caagcgcgc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaaaca ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accggtgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccgttcg tcggcgcgcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

```

g285.pep
1  MTDTPPTDPTD PTENGTRKMP SEHRPAPPK KRRPLLKLSA ALLSVLILAV
51  CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSJET
101 EGADLKISRF RFAWKPSLM RSLHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLPA AVYLDRFETG KISMGTFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSSGASVG LKKPFALDTA IYTKGGFEGE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGS LD LENTKAGFAD RYNGIPVROVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFCG RLDGSIGIGG TTASPKISWQ LGTGTARTDG SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTGGG GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLDDG IRTFETDLG TARNLHIGKA ADIRSLDFTL KGPSGTSRPM
651 RADIKGGRLS LSGGAHVDT AGLTLEGTA QHRIKTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKSIGI LDIGGAFNLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSNLN QHFSWDRKTG ISAKGGARGL HIAELHNFFK PPFEHNLVLN
801 GDWDVAYGHN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNITGSLN ASAQIGGRVG SPSVNAAVNG SSNYKINGN ITVGQSRSD
951 TAPLGGRLN TVADAEAFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYRN QTOGIILNDG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 SMENSVPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GGLTLTAQP GGNVRGVGTG RVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVAGVEIL GSLNSPRITL TANEMSEKD
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRA
1351 QAVARIGSRS SGGELTYTIR FDLRFGSDKK DSAGNGKGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

```

m285.seq
1  ATGACCGATA CCGACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCCTGAT TTTGGCAGTA
151 TGTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACGCCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CACGCCGTGG AGCAGTTCGT CGGGGGCGGC
651 CTCGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACGCCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

```

651

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
 4151 GAAACGGCAA AGGAAATATA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep
 1 MTDAPTDT PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
 51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
 101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPL
 151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
 201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
 251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF
 301 VPSLPDAGLN FDLTAIPSFS DGIALEGSLD LENTHAGFAD RNGIPVRQVL
 351 GGFVIRQDGT VHIGNTSAAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
 401 EDVLQTAFKG RLDGSIIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
 451 GQRKLVLDTV NIAAGQGSIT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
 501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
 551 PRAAVDLRLG RNIKTGSGF GKKGDRLNLN ITAPDLRFG FGLAGSLNVR
 601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
 651 RADIKGSRLS LSGGAHVVDI ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
 701 LDASGGINRE LTRWKGSGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
 751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFEHNLVLN
 801 GDWDVAYGRN ARGYNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRI
 851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFLPA
 901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSD
 951 TAPLGGRLNL TVADAEVFRN FLPVGGTVKG SLNAAVTLGG SIADPHLGGG
 1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
 1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
 1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR
 1151 FAGYGADVTI GGLTLTAQS GGSVRGVGTV RVIKGRYKAY GQDLDTKGT
 1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSEKD
 1251 KLSWLILNRA GSGSSGDNA LSAAGALLA QINDRIGLV DDLGFTSKRS
 1301 RNAQTGEINP AEQVLTGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
 1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNGKKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	: : : : : : : : : :					
g285	MTDTTPTDPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM					
	: : : : : : : : :					
g285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m285.pep	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYLDRFETGKISMKGAFDK					
	: : : : : : : : :					
g285	RRSLHITDISAGDIAIVTKPTPPKEERPPLQGLPDSIDLPAAYLDRFETGKISMGTFDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
	: : : : : : : : :					
g285	QTVYLERLNAAARYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFECE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRAELIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					

a285.seq

1	ATGACC	GATA	CCGCAC	CGAC	AGATAC	CCGAT	CCGACC	GA	ACGGC	CACGG
51	CAAAAT	CGCG	TCTGA	ACAC	GCCCTA	CCCC	GCCGGC	AAAA	AAACG	CCGCC
101	CAGTGT	GTAA	GCTGT	CGCG	GCACTG	CTGT	CTGT	TGAT	TTTGG	CAGTA
151	TGTTT	CCTCG	GCTGG	CTCG	CGGAC	CGGAA	GCGGGT	TTTGC	GCTTC	CGGGCT
201	GTACCA	AAATC	CCGT	CTTGG	T	CGGCG	CGTAAA	CATTT	CTCTC	CAAAAC
251	AAGGCA	CGCT	GCTC	GACGG	TTCAC	CGCG	CAACT	GTGTC	GATAGA	AAATC
301	GAGGGG	GCAG	ACCTT	AAAAT	CAGCC	GCTTC	CGCTT	CGCGT	GGAA	ACCGTC
351	CGAACT	GTAGT	CGCCG	CAGCC	TGCAC	ATTAC	CGAAAT	TTCC	GCCG	GGCACA
401	TGCCAT	CGT	TACCA	AAACG	ACTCG	CGCTA	AAGA	AAGAAC	CCCG	CGGCTC
451	AGCCTT	CCCC	ACAGC	CATAGA	CCTGC	CTGCC	CGCGT	CTATC	TGAC	CGGCTT
501	CGAGAC	CGGGC	AAAAT	CAGCA	TGGGC	CAAGC	CTTTG	ACAAA	CAAA	ACGGTCT
551	ATCTC	GAAAC	GCTGG	ATGCT	TCATAC	CCGTT	ACGAC	CGGCA	AGGAC	ACCGC
601	CTCAGC	CTGA	AGGCT	GCCGA	CACCG	CGTGG	AGCACT	TTCTG	CGGGG	TGACG

655

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3951 CGGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AACTGATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTG TCGGCGGCG AGCTGACATA
4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

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a285.pep
1 MTDAPTDTPTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPL
151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSF DGIALEGLD LENTKAGFAD RINGIPVRQVL
351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGSST AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIKTDDGGF GKKGDRNLN I PDLSRFG FGLAGSLNVR
601 GHLSGDLDDG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRLS LSGGAEVVDL ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKGSI GI LDIGGAFLNK LQNRMTLEAG AERVAASAAN
751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFEHNLVLN
801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFPLA
901 AAQNTGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSEF
951 TAPLGGRLNL TVADAEVFRN FLPVGTQTVK SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRLTV SGNTRLRYS P KGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAAPLPVNMN LTDLDNDGIR
1151 FAGYGADVTI GKKLTLTQAS GGSVRGVGTV RVIKGRYKAY GQDLDTIKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTGVKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNSKKGK*

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m285/a285 99.4% identity in 1389 aa overlap

```

10 20 30 40 50 60
m285.pep MTDAPTDTPTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
|||||
a285 MTDAPTDTPTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
10 20 30 40 50 60

70 80 90 100 110 120
m285.pep AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPSSELM
|||||
a285 AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPSSELM
70 80 90 100 110 120

130 140 150 160 170 180
m285.pep RRSLLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYLDRFETGKISMKGAFDK
|||||
a285 RRSLLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYLDRFETGKISMKGAFDK
130 140 150 160 170 180

190 200 210 220 230 240
m285.pep QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK
|||||
a285 QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK
190 200 210 220 230 240

250 260 270 280 290 300
m285.pep TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAF
|||||

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657

a285	AAQNITGSLNAAAQIGGRVGS	PSVNA	AVNGSSNY	KINGNIT	VGQSR	SFDTAP	LGGRLNL
	910	920	930	940	950	960	
m285.pep	TVADAEVFRN	FLPVGQT	VKGSLNAA	AVTLGG	SIADPH	LGG	SINGDKLYYRNQTQGIILDNG
a285	TVADAEVFRN	FLPVGQT	VKGSLNAA	AVTLGG	SIADPH	LGG	SINGDKLYYRNQTQGIILDNG
	970	980	990	1000	1010	1020	
m285.pep	SLRSHIAGR	KWVIDSL	KFRHEGT	AELSGT	VMENSG	PDVDIG	AVFDKYRILSRPNRLTV
a285	SLRSHIAGR	KWVIDSL	KFRHEGT	AELSGT	VMENSG	PDVDIG	AVFDKYRILSRPNRLTV
	1030	1040	1050	1060	1070	1080	
m285.pep	SGNTRLRY	SPQKGI	SVTGM	IKTDQ	GLFGS	QKSSMP	SVGDDVVVLGEVKKEAAAPLPVNMN
a285	SGNTRLRY	SPQKGI	SVTGM	IKTDQ	GLFGS	QKSSMP	SVGDDVVVLGEVKKEAAAPLPVNMN
	1090	1100	1110	1120	1130	1140	
m285.pep	LTLDLND	GIRFAG	YGADVT	IGGKLT	LTLAQ	SGGSVR	GVGTVRVIKGRYKAYGQDLITKGT
a285	LTLDLND	GIRFAG	YGADVT	IGGKLT	LTLAQ	SGGSVR	GVGTVRVIKGRYKAYGQDLITKGT
	1150	1160	1170	1180	1190	1200	
m285.pep	VSFVGP	LPNDPN	LIRAER	RLSPV	GAGVEI	LGSLNS	PRITLTANEP
a285	VSFVGP	LPNDPN	LIRAER	RLSPV	GAGVEI	LGSLNS	PRITLTANEP
	1210	1220	1230	1240	1250	1260	
m285.pep	GSGSSG	DNAALS	AAAGAL	LAGQIN	DRIGLV	DDL	GFTSKRSRNAQTGELNPAEQVLT
a285	GSGSSG	DNAALS	AAAGAL	LAGQIN	DRIGLV	DDL	GFTSKRSRNAQTGELNPAEQVLT
	1270	1280	1290	1300	1310	1320	
m285.pep	LTGKLYI	GYEYSI	SSAEQ	SVKLI	YRLTR	AIQAV	ARIGSRSSGGELTYTIRFDRFS
a285	LTGKLYI	GYEYSI	SSAEQ	SVKLI	YRLTR	AIQAV	ARIGSRSSGGELTYTIRFDRFS
	1330	1340	1350	1360	1370	1380	
m285.pep	DSAGN	GK	GKX				
a285	DSAGN	GK	GKX				
	1390						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

```

1   CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCCTG CTGGTTCGGC GTAAACATTT CCTCCAAAA CCTCAAAGGC
151 ACACTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATCACCAGCA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAGGCCTT
351 GCCCAGACAG ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAAACAAAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGAGCAG TTCGTCGGGG TCAGCCTCGG

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1   LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLDDGFDGDN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAYYLD RFETGKISMG KTFDKQTVYL
151 ERLNAAARYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGGGTASP KISWQLGTGT
401 ARTDGSIAIA SDPANEQRKL VFDTVNISAG EGSHTAQGYL ELFKDRLLKL
451 LRSRADFDP RIDPQFPAGD INGSIHLAGL LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVGRHLSG DLDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKGSPG TSRPMRADIK GGRLSLSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSGILDIGG AFNLHLQNM
701 TLEAGAEHVA ASAAWQAMG GSLNLQHFSW DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQD DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSNLASAQI GGRVGSPPVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRNLTVADA EAFRNLFPVG QTVKGSNLAA
951 VTLGGSADP HLGGSSINGDK LYRNRQTGI ILDNSSLSRH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 KINGNITVGO SRSFDTAPLG GRNLTVADA EAFRNLFPVG QTVKGSNLAA
1101 PVNMNLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR GVGTVRVIKG
1151 RYKAYQDLD ITKGTVSFVG PLNDPNLNR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEF MSEKDKLSWL ILNRAGSGSS GDNAALSAAL GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGVEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLF GSKKDSAGN
1351 GK GK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

```

1   CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATT CTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GCGACAGCCT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTCCGCGCGG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCGCGCGT CTATCTCGAG CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACCGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTGCGGG GCGGCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGCGCG CCTTCGTGCC
801 TTCCCTGCCC GATGCGGAC TGAATTTGCA CCGTACCGCC ATCCGCTCGT
851 TTTGAGACGG CATCGCGCTG GAAGGTTGCG TCGATTTGGA AAACACCAA
901 GCCGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCGG
951 CTTTGTATC CGGCGAGGAC GCACGGTGCA TATCGGCAAT ACGTCCGCGG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAG CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCGAGCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATT CGACCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGCGGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CGGATTGCGG GCAAGTCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGGTC GATTGCGGC TGGGGCGGAA CATTATTAAC ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGGT GATTGAGCG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CGGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGAGA CATCGGTCG
1801 CTCGATTTCG CGCTCAAAGG TTCGCCGAC ACAAGCCGCC CGATACGGCG
1851 CGACATCAAA GGCAGCGGCC TTTGCTGTG GGGCGGAGCG GCGGTTGTG
1901 ATACCGCGCA CCTGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGGCG CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGAACCTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGCGGCG GCATTC AACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA

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661

g285-1.pep	LKLSAALLSVLILAVCFLGWIAGTEAGLRFGLYQIPSWFGVNISSQNLRKGTLLDGGFDGDN
m285-1	LKLSAALLSVLILAVCFLGWLALGTEAGLRFGLYQIPSWFGVNISSQNLRKGTLLDGGFDGDN
	10 20 30 40 50 60
g285-1.pep	70 80 90 100 110 120
m285-1	70 80 90 100 110 120
g285-1.pep	130 140 150 160 170 180
m285-1	130 140 150 160 170 180
g285-1.pep	190 200 210 220 230 240
m285-1	190 200 210 220 230 240
g285-1.pep	250 260 270 280 290 300
m285-1	250 260 270 280 290 300
g285-1.pep	310 320 330 340 350 360
m285-1	310 320 330 340 350 360
g285-1.pep	370 380 390 400 410 420
m285-1	370 380 390 400 410 420
g285-1.pep	430 440 450 460 470 480
m285-1	430 440 450 460 470 480
g285-1.pep	490 500 510 520 530 540
m285-1	490 500 510 520 530 540
g285-1.pep	550 560 570 580 590 600
m285-1	550 560 570 580 590 600
g285-1.pep	610 620 630 640 650 660
m285-1	610 620 630 640 650 660
g285-1.pep	670 680 690 700 710 720
m285-1	670 680 690 700 710 720
g285-1.pep	730 740 750 760 770 780
m285-1	730 740 750 760 770 780

663

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTTGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCAG
951 CTTTGTCTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCTG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAC CGCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCAGCG ACGGCAGCCT CGCCATTGCA AGCAGCCCGC CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCGGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATC CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GCGAGGCAAT ATCAACGGCT CAATAAACCT TCGCGGCGAA TGGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCCG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGCTC GATTTGCGGC TGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCAGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAATG TACGCGGACA
1701 CCTTTCGGGC GATTTGGACG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCAGCGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCTGTTTCG
1801 CTCGATTTCG CGCTCAAAGG TTCGCCGAC ACAAGCCGCC CGAATCCGCG
1851 CGACATCAAA GGCAGCCGCC TTTGCTGTC GGGCGGAGCG GAGGTGTGTCG
1901 ATACCGCCGA CCTGATGCTG GACGGCACGG CGGTGCAGCA CGCATCCGCG
1951 ACACACGCGC CCATGACGCT GGATGGCAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGAACCTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCCTCGA CATCGCGCGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCGGTA TTGCCCAGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAACGCGC CTTTCAAAC GACCGTATCG GAATCTGCT
2451 TGACGGCGCG GCGCGTTTCG GCGGATTAAC CGCCGATTG GACATCGGCA
2501 ACGCCTTCG CGGCAATATG GCAATGCAAC CGCTCGCGCG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCCGCAGCC TGAATGCCG CGCGCAAAAT GCGCGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTC ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTTCG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGGCAGAAA CTCTATTACC GCAACCAAC CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTGCGAT ATCGCGGCA GGAAATGGGT AATCGACAGC
3001 CTGAATTCG GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTGCGTAT
3051 GGAACACAGC GGACCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCCTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAAC
3201 GGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATGCCG TCCGTGCGCG
3251 ACGATGTCGT CGTATTAGG GAAATCAAAA AAGAGGCGCG GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CCGCTACGGC GCGGACGTTA CCATAGCGCG CAACTGACCC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGGG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTCGGC CGCTCAACG ACCCAACCT CAACTCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGC GCGGTGGAAA TATTGGGCG CCTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCCTCAACC GCGCCGGCAG TGGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGC TTGCGGGGCA AATCAACGAC
3751 CGCATCGGCG TGGTGGATGA TTTGGGCTTT ACCAGCAAAG GCACCGGCAA
3801 CCGGCAAAAC GCGGAACTCA ACCCCGCCGA ACAGGTGCTG ACCGTGCGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCGCCGT ATCGGCAGCC GTTCGTGGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGTTCTCC GGTTCGGACA AAAAAGACTC CGCCGAAAC
4051 AGCAAGGAA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

665

a285-1.pep	VLDTVNIAAGQGS	SLTAQGYLELFKDRLLKLD	IRSFADPSRIDPQLPAGNINGS	INLAGE	
m285-1	VLDTVNIAAGQGS	SLTAQGYLELFKDRLLKLD	IRSFADPSRIDPQLPAGNINGS	INLAGE	
	430	440	450	460	470
a285-1.pep	490	500	510	520	530
	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD				
m285-1	490	500	510	520	530
	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD				
a285-1.pep	550	560	570	580	590
	RLNLNITAPDL	SRFGFGLAGSLNVRGHL	SGDLGGIRT	FETDLSGAARNLHIGKAADIRS	
m285-1	550	560	570	580	590
	RLNLNITAPDL	SRFGFGLAGSLNVRGHL	SGDLGGIRT	FETDLSGAARNLHIGKAADIRS	
a285-1.pep	610	620	630	640	650
	LDFTLKGS	PDTSRPIRADIKGSRLSL	SGGA	EVVD	TADLMLDGTGVQHRIRTHAAMTLDGK
m285-1	610	620	630	640	650
	LDFTLKGS	PDTSRPIRADIKGSRLSL	SGGA	AAVVD	TADLMLDGTGVQHRIRTHAAMTLDGK
a285-1.pep	670	680	690	700	710
	PFKFDLDASGGINRELTRWKGSIGILDIGGA	FNKLQNRMTLEAGA	ERVAASAANWQAMG		
m285-1	670	680	690	700	710
	PFKFDLDASGGINRELTRWKGSIGILDIGGA	FNKLQNRMTLEAGA	ERVAASAANWQAMG		
a285-1.pep	730	740	750	760	770
	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
m285-1	730	740	750	760	770
	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
a285-1.pep	790	800	810	820	830
	NISRQSGDAVLP	GGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM			
m285-1	790	800	810	820	830
	NISRQSGDAVLP	GGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM			
a285-1.pep	850	860	870	880	890
	ANAPLGGRITASL	PDLGLTKPFLPAAAQ	NITGSLNAAQIGGRVGS	PSVNAAVNGSSNYG	
m285-1	850	860	870	880	890
	ANAPLGGRITASL	PDLGLTKPFLPAAAQ	NITGSLNAAQIGGRVGS	PSVNAAVNGSSNYG	
a285-1.pep	910	920	930	940	950
	KINGNITVGQSR	SFDAPLGGRLNLT	VADAEVFRN	FLPVGQTVKGS	LNAAVTLGGS
m285-1	910	920	930	940	950
	KINGNITVGQSR	SFDAPLGGRLNLT	VADAEVFRN	FLPVGQTVKGS	LNAAVTLGGS
a285-1.pep	970	980	990	1000	1010
	HLGGSINGDKLYYRNQTQGI	ILDNGSLRSHI	AGRKKWIDSLKFRHEGTAELS	SGTVGMENS	
m285-1	970	980	990	1000	1010
	HLGGSINGDKLYYRNQTQGI	ILDNGSLRSHI	AGRKKWIDSLKFRHEGTAELS	SGTVGMENS	
a285-1.pep	1030	1040	1050	1060	1070
	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRL	RLRYSPOKGISVTGM	IKTDQGLFGSQKSSMP		
m285-1	1030	1040	1050	1060	1070
	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRL	RLRYSPOKGISVTGM	IKTDQGLFGSQKSSMP		
a285-1.pep	1090	1100	1110	1120	1130
	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGY	GADVTIGGKLT	LTAQSGGSVR		
m285-1	1090	1100	1110	1120	1130
	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGY	GADVTIGGKLT	LTAQSGGSVR		
a285-1.pep	1150	1160	1170	1180	1190
	GVGTVRVIKGRYKAYQDLDITKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS				
m285-1	1150	1160	1170	1180	1190
	GVGTVRVIKGRYKAYQDLDITKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS				

667

451 QNRDDFGHIP VLHRANPHLC PRRFLHARK QKTRHVHTR TSGLHRCTRQ
501 CRCPLGADVP QRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

```
m286.seq
1  ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
51  GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GCGGGGTTTC GCATTGTTCA AAAACAAAAG CCCCACACCC
151 GAATCAGTCA AATTAAACC CAAATCCCC GTCCTCATCG ACACGCAGGA
201 CAGTGAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCACGCAGC
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCGCCGGACA ACGTTAAAC GATGCTCCGC AGTAAGGCT ATTTACAGCAG
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCGCG CACCAATATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTTCA AGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA
501 CTGGCAGCAG CCGGTAGGCA GCGATTTCTG TCAGGACAGT TGGGAAAAACA
551 GCAAACTTTC CGTCTCGGC GCGTAACGC GCAAAGCCTA CCGCTTGCC
601 AAGCTCGGCA ATACGCAGGC GCGCTCAAC CCCGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GCGCACTTTG
701 AAATCACCGG CACACAGCGT TACCCGAAC AAATCGTCTC CGGCCTTGGC
751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA
801 ACAGGCGCTC GAACAACAG GGCATTATTC CGGCGCGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAACT CGAAACCGGC ATCCGCTCG ATTCGGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAATACGA AACACCGCTT
1051 GCGCCCGGCA TCAGCCAGCC GCGCAACTAT CGGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCA AAACCTCGAA AAACGCGCCT
1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
1201 CTGGGGGCGG AATTTCTCGC AGAAGGCCGG AAAATCCCGG GCTCGGCTGT
1251 CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCCTCT TGGAAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CCGCAGCGC
1351 AAAATCGGTA CGACTTTGGG CACATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTAC GCCGAAAAC AAAAACTCG
1451 GCACGTTTCA CATAAGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCGACGTTT CTTAGGGCT GATGTTCCG AGCGCGCGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCGA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTCCCG CGCGGTGTT CACGATATGG GCGATGCCCG
1701 CGCCAATTTC AACGTATGA AGCTGAAACA CGGTCGGGA CTGGGCGTGC
1751 GCTGGTTTCA CCGCTTGC CGTTTTCTC TCGACATCG CTACGGGCAC
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA
```

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

```
m286.pep
1  MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51  ESVKLPKFP VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTKDGAIVTV HITPGPRTKI ANVGVAIGD
151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTOAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGMPYDL DLLDFQQAL EQNGHYS GAS VQADFDR LQG DRVVPKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAIDYYNL FNKG YIGSVV WMDKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTQNL KRAFSGGVWY VRDRAGIDAR
401 LGAEFLAEGR KIPGSVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLGTFL SSTALIRTS RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRLTSGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

669

```

1351 AAAATCGGTA CGACTTTGGG CGCATTCCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCACTTT ATTTCTTCAC GCCCGAAAAC AAAAAACTCG
1451 GCACGTTTCAT CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTAGGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCA ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTC CACGATATGG GCGACGCCGC
1701 CGCCAATTTT AAACGTATGA AGCTGAAACA CGGTTCGGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTTCTT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

```

a286.pep
1  MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51  ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKD GAYTV HITPGPRTKI ANVGVA ILGD
151 ILS DGNLAEY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLG NTRAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLLDFQQAL EQNGHYS GASVQADFDR LQGD RVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKGYIGSVV WDMDKYETTL
351 AAGISQPRNY RGN YWTSNV S YNRSTTQNL E KRAFSGGIWY VRDRAGIDAR
401 LGA EFLAAGR KIPGSDIDL G NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLGAF L SSTALIRTS A RAGYFFTPEN KKLGTFIIRG QAGYT VARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRT LSGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSP LA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

m286/a286 98.7% identity in 615 aa overlap

10 20 30 40 50 60
m286.pep MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVK LKPKFP
|||||
a286 MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVK LKPKFP
10 20 30 40 50 60

70 80 90 100 110 120
m286.pep VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS
| |||||
a286 VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS
70 80 90 100 110 120

130 140 150 160 170 180
m286.pep LTEKD GAYTV HITPGPRTKIANVGVA ILGDILSDGNLAEYRNALENWQQPVGSDFDQDS
|||||
a286 LTEKD GAYTV HITPGPRTKIANVGVA ILGDILSDGNLAEYRNALENWQQPVGSDFDQDS
130 140 150 160 170 180

190 200 210 220 230 240
m286.pep WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPD TATADLNVVDSGRPIAFGDFEITGTQR
|||||
a286 WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPD TATADLNVVDSGRPIAFGDFEITGTQR
190 200 210 220 230 240

250 260 270 280 290 300
m286.pep YPEQIVSGLARFQPGMPYDL DLLLDFQQALEQNGHYS GASVQADFDR LQGD RVPVKVSVT
|||||
a286 YPEQIVSGLARFQPGTPYDL DLLLDFQQALEQNGHYS GASVQADFDR LQGD RVPVKVSVT
250 260 270 280 290 300

310 320 330 340 350 360
m286.pep EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKGYIGSVVWDMDKYETTLAAGISQPRNY
|||||
a286 EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKGYIGSVVWDMDKYETTLAAGISQPRNY
310 320 330 340 350 360

370 380 390 400 410 420

```

671

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151 TNVGNVSVVID GPSQNTLTH CKGDSCNGDN LLDEEAPSKS EFEKLSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGTNKYI IFYTDKPPTR SARSRRSLPA
251 EIPLIPVNQA DTLIVDGEAV SLTGHSGNIF APEGNYRYLT YGAEKLPGGS
301 YALRVQGEPA KGEMLVGTAV YNGEVLHFHM ENGRPYPSGG RFAAKVDFGS
351 KSVDGIIIDSG DDLHMGTKKF KAAIDGNGFK GTWTENGGGD VSGRFYGPAG
401 EEVAGKYSYR PTDAEKGFGF VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTTC CCCTTTCAGC
51  CTGCGGGGGC GCGGGTGGCG GATCGCCCGA TGTCAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTTCCTG AAAAAGAGAC AGAGGCCAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGGCA GCGGGGCAAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AATCAATCAA GCCGCCGTT
551 CTTAGATCC CATCCCCGCG TCAAACCTG CACCTGCGAA TGGCGGTAGC
601 AATTTTGGA GGGTTGATTT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGCCAATA
701 ATTTCTTGGA TGAAGAAGTA CAGCTAAAT CAGAATTGTA AAAATTAAAT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCCGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTACG CTGACGGGGC
1001 ATTCGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGGA AACGGCCGTC CGTACCCGAC CAGGGGCAGG
1201 TTTGCCGCAA AAGTCGATTT CCGCAGCAA TCTGTGACG GCATTATCGA
1251 CAGCGGCGAT GATTTCGATA TGGGTACGCA AAAATTCAAA GCCGCCATCG
1301 ATGGAACCGG CTTTAAGGGG ACTTGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGAAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGCGG ATTCGGCGTG TTTGCCGGCA
1451 AAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1  MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAK
51  EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMANAA
151 DGMQGDPSA GGQNAAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFGRLDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFEVL VADSVQMKGI NQYIIIFYKPK PTSFARFRRS
301 ARSRRSLPAE MPLIPVNQAD TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIIDSGD DLHMGTKQFK AAIDGNGFKG TWTENGSGDV
451 SGKFYGPAGE EVAGKYSYRP TDAEKGFGV FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

          10      20      30      40      49
m287.pep  MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETEAK
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287      MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKDEEA
          10      20      30      40      50      60

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673

```

801 AGACGAGCAA CGAGAGAATT TTGTCGGTTT GGTGCTGAC AGGGTAGAAA
851 AGAATGGAAC TAACAAATAT GTCATCATTT ATAAAGACAA GTCCGCTTCA
901 TCTTCATCTG CGCGATTTCAG GCGTTCTGCA CGGTCGAGGC GGTGCTTCC
951 GGCCGAGATG CCGCTGATTC CCGTCAATCA GGCGGATACG CTGATTGTGCG
1001 ATGGGGAAGC GGTGAGCCTG ACGGGGCATT CCGGCAATAT CTTCGCGCCC
1051 GAAGGGAATT ACCGGTATCT GACTTACGGG GCGGAAAAAT TGTCCGCGCG
1101 ATCGTATGCC CTCAGTGTGC AAGGCCAACC GGCAAAGGC GAAATGCTTG
1151 CGGGCACGGC CGGTGTACAAC GGCGAAGTGC TGCATTTCCA TATGGAAGAC
1201 GGCCGTCCGT CCCCGTCCGG AGGCAGGTTT GCCGCAAAAG TCGATTTCCG
1251 CAGCAATCT GTGGACGGCA TTATCGACAG CGGCGATGAT TTGCATATGG
1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
1351 TGGACGGAAA ATGGCGGCGG GGATGTTTCC GGAAGGTTT ACGGCCCGGC
1401 CGGCGAAGAA GTGGCGGGAA AATACAGCTA TCGCCCGACA GATGCGGAAA
1451 AGGGCGGATT CGGCGTGT TTGCCGCAAAA AAGAGCAGGA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1204; ORF 287.a>:

```

a287.pep
1 MFKRSVIAMA CIVALSAACGG GGGSPDVKS ADTLSKPAAP VVTEDVGEEV
51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAAVSAENTG NGGAATDNP
101 ENKDEGPQND MPQNAADTDS STPNHTPAPN MPTRDMGNQA PDAGESAQPA
151 NQPDMANAAD GMQGGDDPSAG ENAGNTADQA ANQAENNVQV GSONPASSTN
201 PNATNGGSDF GRINVANGIK LDSGSENVTL THCKDKVCDR DFLDEEAPPK
251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VYIKDKSAS
301 SSSARFRRSA RSRRSLPAEM PLIPVQADT LIVDGEAVSL TGHSGNIFAP
351 EGNRYRLTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMEH
401 GRPSPSGGRF AAKVDFGSKS VDGIIIDSGD LHMGTQKFKA VIDGNGFKGT
451 WTENGGGDVS GRFYGPAGEE VAGKYSYRPT DAEKGGFGVF AGKKEQD*

m287/a287 77.2% identity in 501 aa overlap

10 20 30 40 49
m287.pep MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETEA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 MFKRSVIAMACIVALSAACGGGGGGSPDVKSADTLSKPAAPVVTEDVGEEVLPKEKKDEEA
10 20 30 40 50 60

50 60 70 80 90 100 109
m287.pep KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATDNPENKDEGPQNDMPQNAADT
70 80 90 100 110

110 120 130 140 150 160 169
m287.pep DSSTPNHTPDNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDDPSAGGQNAGNTA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGGDDPSAG-ENAGNTA
120 130 140 150 160 170

170 180 190 200 210 220 229
m287.pep AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNTLTHCKGDS
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 DQAAANQAENNVQGGSONPASSTNPNATNGGSDFGRINVANGIKLDSGSENVTLTHCKDKV
180 190 200 210 220 230

230 240 250 260 270 280 289
m287.pep CSGNNFLDEEVQLKSEFEKLSADADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
a287 CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVYIKD
240 250 260 270 280 290

290 300 310 320 330 340
m287.pep KP--TSFARFRRSARSRRSLPAEMPLIPVQADTLIVDGEAVSLTGHSGNIFAPEGNRY
| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 KSASSSSARFRRSARSRRSLPAEMPLIPVQADTLIVDGEAVSLTGHSGNIFAPEGNRY
300 310 320 330 340 350

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675

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

```

      10      20      30      40      50      60
m288.pep  MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGGLPHIVTKCAV
          |||||
g288      MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGGLPHIVTKCAV
          10      20      30      40      50      60

      70      80      90     100     110     120
m288.pep  RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV
          |||||
g288      RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV
          70      80      90     100     110     120

      130     140     150     160     170     180
m288.pep  PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADVFVACTQVF
          |||||
g288      PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADVFVACTQVF
          130     140     150     160     170     180

m288.pep  DTX
          |||
g288      DAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

```

a288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51 TCTAGGCATA CCGTTGCCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTCTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTGCCCT GTGCTGCCAA AGCAGCCATC GGCGGTTTTC CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCGCGCGG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCCGC CCGTGTGCGG CGCGGATTAT AACACGAAAC GCAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TAAAGCCGTC CAAGTCGCCG TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTGC GCAAGTCTTT AATGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

```

a288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHA
151 LFQAGFDKAV QVAVQYGFV ADFVACAQVF NA*

```

m288/a288 97.2% identity in 181 aa overlap

```

      10      20      30      40      50      60
m288.pep  MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGGLPHIVTKCAV
          |||||
a288      MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGGLPHIVTKCAV
          10      20      30      40      50      60

      70      80      90     100     110     120
m288.pep  RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV
          |||||
a288      RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV
          70      80      90     100     110     120

      130     140     150     160     170     180
m288.pep  PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADVFVACTQVF
          |||||

```

677

```

701 ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGA AAAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TGCGCGTGTT GGGTGGCGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
1  ..VSVGAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
51  QAKLVSAQIA LGSAEKKYKR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTTMSS GGYNSSTDTA SNAVYYIARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLII PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTEV
301 KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

m290.pep                                10      20      30
                                      VSVGAQASGQIKILYVKLGQVKKGDLIAE
g290                                PQAAYITEAVRRGDISRTVSATGEISPSNLSVSVGAQASGQIKKLYVKLGQVKKGDLIAE
30      40      50      60      70      80

m290.pep                                40      50      60      70      80      90
INSTSQNTNLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
||||:||||:|: |||||||||||||||||||||||||||||||||||:|||||
g290                                INSTTQNTNIDMEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATSKEDLESAQD
90      100     110     120     130     140

m290.pep                                100     110     120     130     140     150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:|||||||||||||||||||||:||||||||||||| |||||||
g290                                ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPEVEGQTVNAAQST
150     160     170     180     190     200

m290.pep                                160     170     180     190     200     210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
|||||||||||||||||||||||||||||||||||||||||
g290                                PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
210     220     230     240     250     260

m290.pep                                220     230     240     250     260     270
GGYNSSTDASNAVYYIARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
|||||||||||||||||||||||||||||||||||||
g290                                GGYNSSTDASNAVYYIARSFVPNPDGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
270     280     290     300     310     320

m290.pep                                280     290     300     310     320     330
KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
|||||||||||||:|||||||||||||||||||||
g290                                KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKECDKVVISEITAAEQQESGERALGG
330     340     350     360     370     380

m290.pep                                PPRRX
|||||
g290                                PPRRX
390

```

679

```

m290.pep      GGYNSSTDASNAYYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a290          GGYNSSTDASNAYYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               270      280      290      300      310      320

               280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
               : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a290          RAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
               330      340      350      360      370      380

m290.pep      PPRRX
               ||||
a290          PPRRX
               390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg *cctgccgct
51  gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgcgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttgacaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaattct atggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atgcgtaaa gcaaatccc ggtcggcggc agcatctgcg acaatcccg
651 cgcggaacc acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tcccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaac cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSAVASLKR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTTE RAADLNKIDF ASLPLDKAIK EVRNGNKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNFVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPD
251 PTGGNHQKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAGAAA CCTATTCCGC CCAAGATTG AAAGTGTTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CCGCGCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGACAA AGCCATCAA GAAGTGCGCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTG CCGGCCTGCA CCCCAGATGC GCgcgcaagg
551 CGCAAATCTT ATGGTGTcag CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAAATCCC GGTcggcggc AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCC

```

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSWAASLKAR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSFMP
251 QLEEIIRKNQ *

m292/a292 100.0% identity in 260 aa overlap

      10      20      30      40      50      60
m292.pep MKTKLIKILTPFTVLPLLACGQTPVSNANAEPVKAESAGKSWAASLKARLEKTYSAQDL
|||||
a292      MKTKLIKILTPFTVLPLLACGQTPVSNANAEPVKAESAGKSWAASLKARLEKTYSAQDL
      10      20      30      40      50      60

      70      80      90     100     110     120
m292.pep KVLVSSETPVKGIYEVVVSQRIIYTDAEGGYMFVGGELINIDTRKNLTEERAADLNKIDF
|||||
a292      KVLVSSETPVKGIYEVVVSQRIIYTDAEGGYMFVGGELINIDTRKNLTEERAADLNKIDF
      70      80      90     100     110     120

      130     140     150     160     170     180
m292.pep ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
|||||
a292      ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
      130     140     150     160     170     180

      190     200     210     220     230     240
m292.pep ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLSGEQFGFNGTPTLVFPNG
|||||
a292      ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLSGEQFGFNGTPTLVFPNG
      190     200     210     220     230     240

      250     260
m292.pep RSQSGYSFMPQLEEIIRKNQX
|||||
a292      RSQSGYSFMPQLEEIIRKNQX
      250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtctggtc
51  gggtcgggct gtcagaacat catcgaaccg ctttcctcgc gcgttacgac
101 gatattcgcc ttttcgacct acaatttttc cgaagcctgc cggcagccct
151 tggcatcgcc tgccggcggt caagtcgaat cggcggacgc gtggcggtgaa
201 gccgttgaaa aaaccttata tggcgagggg ggcggaatgc agatgcaggc
251 gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301 ccgaggcggt gcgggaagcg gtatgcggac atcggggggc atagtgtatc
351 aatccgtatc cgagttttcc ggttgagca tcgtatgagt atttatgccg
401 tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcgccgctg
451 tttttgaag tgctggtttt gtcggtcctg catacgggac ggggtgtcgcg
501 cgaggcgccg cgcgaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
551 tgatgccgtt tgcggtcggg ctgctgttcc ccaggggaaac tctagagtcg
601 actgcagcag catgccctc...

```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
1  MRITCAPMSL LSAAVWSVRA VRTSSNRFPALRRYSAPFR TIFPKPAGTP
51  WHRVRRFKSN RTRGVKPLK KPYLARGAEC RCRRAWTALS HNIAERARES
101 PRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPPFAVG LLFARGTLES
201 TAAACP...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

683

```

701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

```

a294.pep
1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAFRP TIFPKPAGTP
51 WRRVRRFKSN RRTRGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES
101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

```

m294/a294 94.9% identity in 277 aa overlap

```

m294.pep      10      20      30      40      50      60
MRITCAPMSLLSAAVWSIRVVRTSSNRFPAAFRYSAFQPTIFPKPADTPWHRVRRFKSN
|||||:|||||:|||||:|||||:|||||:|||||
a294          10      20      30      40      50      60
MRITCAPMSLLSAAVWSIRAVRTSSNRFPAAFRYSAFRPTIFPKPAGTPWHRVRRFKSN

m294.pep      70      80      90     100     110     120
RRMRGGKPLKKPYRPRGGGCRRAWTALSHNIAERARESPRRCGKRYADIGGDSDTIRI
|||:|||||:|||||:|||||:|||||:|||||
a294          70      80      90     100     110     120
RRTRGGKPLKKTYRPRRAECRCRRARTALSHNIAERARESPRRYGKRYADIGGDSDTIRI

m294.pep     130     140     150     160     170     180
RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFFEVLVLSVLHTGRVSRARREVEKAMSYR
|||||:|||||:|||||:|||||:|||||:|||||
a294          130     140     150     160     170     180
RVFRLEYRMSIYAVAHIVHLYCAIAFVGGVFFEVLVLSVLHTGRVSCARREVEKAMSYR

m294.pep     190     200     210     220     230     240
AVRVMFVVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK
|||||:|||||:|||||:|||||:|||||:|||||
a294          190     200     210     220     230     240
AVRVMFVVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK

m294.pep     250     260     270
MARSTLTVGWSKYIHAVVFTHMLLIVFLAKAMFYISWX
|||||:|||||:|||||:|||||:|||||:|||||
a294          250     260     270
MARSTLTVGWSKYIHTVVFTHMLLIVFLAKAMFYISWX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

```

g295.seq
1 atgctcggga tggcgcgga cgaaggccag cagggcatcg ccgcgatatt
51 gttgccacgc cgccagcagt tttccgcct cgtcttcgcc ccgataaacg
101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gttttcaaaa
151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
201 tattgccgca cacctgcacg gatgcccgcg ccaatttcgc caaccgcgcc
251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
301 acggatcagg cggcggactt tcagataacc gttcagcgat tttccgaca
351 gccgcgcatt cgccaaaaac agcggcacac ccgctgcggc gcattccttc
401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcgggcg
451 gtgttcgcgc aaaaactgcc gtaccacgt tttttgtca tacggaagat
501 agcggcattg cgcacgggga aacagaactt gcgcggtttc ccgtcccgtc
551 ggggtcatct gcgtcatcag cagcggcgca tcgggaaaaa gccgccgcaa
601 ctgcgctatc aagggtctgg cggcacgcgt ttctccgacc gaaacggcgt
651 gtatccaaac cgcgcgggta acgggattcg gatcgggctt gccgaaacgc
701 tcgtccctat gcgcccggtg tgccggggca cttccggagc gtttgtccaa
751 ataacgccgt atccatatcg gcgcaagcag ccaataca tcataaagcc
801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacggttc
851 ggacggcatt tcggcaacgg aatcaaatat cgtag

```

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

685

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1   ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCGGA CGGCATCAGG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAAC AGCGGCACAC CCGTGCGCCG GCATTCCTTC
401 ATCAGATTGG GCCAGATTTC GGTTCCTATC AAAATGCCGA ACATCGGGCG
451 GTGTTGCGCG AAAAAGTGGC GTACCCACGT TTTTGTGTC TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCGTC
551 GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAGAC GCTGCCGCAA
601 CTCGCGTATC AAAGGTTGGG CGGCACGCGT TTCCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGTA ACGGATTCG GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCCGATA TGCAGGGGCA CTTCGGAGC GTTGTGTCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATT CTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1   MLGMARHDDQ OGIAAILLPR RQOFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRFHLFR RHQVVFGLIA HLHGCRAQFR QPRRIRLRLC QTARQSRGGR
101 TDQAADFQIT V*RFRRQPRI RQQRHTRAP AFLHQIGPDF GFHQNAEHRRA
151 VFAQKLPYPR FVIRKIAAL CIRKQNLGRF PSRRGHLRHQ QRRIGKTLQP
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLG	MAR	HDD	QOR	IAAIL	PRR
a295	MLG	MAR	HDD	QOR	IAAIL	PRR
	10	20	30	40	50	60
	70	80	90	100	110	120
m295.pep	RYD	VVF	GIA	AHL	HGC	RAQ
a295	RHQ	VVF	GIA	AHL	HGC	RAQ
	70	80	90	100	110	120
	130	140	150	160	170	180
m295.pep	RQK	QRH	TRAP	AFPH	QVGP	DFGF
a295	RQK	QRH	TRAP	AFPH	QVGP	DFGF
	130	140	150	160	170	180
	190	200	210	220	230	240
m295.pep	PPR	RGL	RHQ	QRR	IGKT	PPQ
a295	PSR	RGL	RHQ	QRR	IGKT	PPQ
	190	200	210	220	230	240
	250	260	270	280	290	
m295.pep	CRG	TSG	AFV	QIT	PYP	YRR
a295	CRG	TSG	AFV	QIT	PYP	YRR

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1   ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
```

687

201 EGDVRLMYD SLYFHGQOVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
 251 GNYDDEGKV LOEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
 301 AAPQGTVPRA SADGVITFKG RKGgyGNAMV IRHANGVETL YAHLSAFSQA
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPVNPVSV ALPTPELTQA
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

m297/g297 97.9% identity in 430 aa overlap

m297.pep	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERVRPQQRVEQNLPLPSWGGSGVQT
g297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTEGTERVRPQQRVEQKLPLPSWGGNGVQT
m297.pep	AYWVQEAVQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA
g297	AYWVQEAVQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSA
m297.pep	REVQFFTDDEGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEVVP
g297	REVQFFTDDEGERNLVALEKKGGIWRRSASDADMKVLPTLRSVVVKTSARGSLARAEVVP
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQOVAAGDILAAEVVKGGRHQAFY
g297	EIRESLSGIFAGRFSLDGLKEGDAVRLLYDSLYFHGQOVAAGDILAAEVVKGGRTHQAFY
m297.pep	YRSDKEGGGGNYYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY
g297	YRSDKEGGGGNYYDEDEGRVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY
m297.pep	AAPQGTVPRASADGVITFKGRKGGYGNAMVIRHANGVETLYAHLSAFSQAEGNVRGGEVI
g297	AAPQGTVPRASADGVITFKGRKGGYGNAMVIRHANGVETLYAHLSAFSQAQGNVRGGEVI
m297.pep	GFVGSTGRSTGPHLHYEARINGQPVNPVSVLPTPELTQADKAFAAQKQKADALLARLR
g297	GFVGSTGRSTGPHLHYEARINGQPVNPVSVLPTPELTQADKAFAAQKQKADALLARLR
m297.pep	GIPVTVSQSDX
g297	GIPVTVSQSDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1	ATGGCTGTCT	TCCCACTTTC	GGCAAAACAT	CGGAAATACG	CGCTGCGCGC
51	GCTTGCCGTT	TCGATTATTT	TGGTGTCCGC	GGCATAACATT	GCTTCGACAG
101	AGAGGACGGA	GCGCGTCAGA	CCGCAGCGCG	TGGAACAAAA	ACTGCCGCCG
151	CTGTCTTGGG	GCGGCAGCGG	TGTTCAAGACG	GCATATTGGG	TGCAGGAGGC
201	GGTGCAGCCA	GCGGACTCGC	TGGCGGACGT	GCTGGCGCGT	TCGGGTATGG
251	CGCGGGACGA	AATTGCCCGA	ATAACGGAAA	AATATGGCGG	CGAAGCCGAT
301	TTGCGGCATT	TGCGTGCCGA	CCAGTCGGTT	CATGTTTGG	TCGGCGGCGA
351	CGGCGGCGCG	CGCGAAGTGC	AGTTTTTTAC	CGACGAAGAC	GGCGAGCGCA
401	ATCTGGTCGC	TTTGGA AAAA	AAAGGCGGCA	TATGGCGCGG	GTCGGCTTCT
451	GAGGCGGATA	TGAAGGTTTT	GCCGACGCTG	CGTTCGGTCG	TGGTCAAAAC
501	GTCGGCGCGC	GGTTCGCTGG	CGCGGGCGGA	AGTGCCCGTC	GAAATTCGCG

689

	370	380	390	400	410	420
m297.pep	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTCGCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTC CCGCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCCTG TCCGGCGAAA cgcggcgac ggCTCAAGAC GCGGTTTCGG
251 CAGATATGCC GCCTGAAGCC GCCGCATCCG AAGCCGCCCC GCCGGCCGGC
301 GGAACAGAAT GGAAACAAGG CACCGAAGCC GCCCGCTCC GCAGCGGCGA
351 CAAAGTCTTT TTGCGCGGAG ATTCGCTGAT GCAGGGCGTT GCCCTTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCTTGAAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCC GAACGACCCG TGGGATTTC CCGTCGGCAA ACCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCCTG CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAAGTCTTT CGGAACATT GAAAGGCAAA ATCATCTGTA TTCCACCGC
801 GCAAAACTG AGCGGCGGGA AAGGCGGCTA CACCGATTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAATAATA ATGGAATAA TCGTTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATG -

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298.pep

```

1  MKNFLSLFAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKTFL SGETPPTAQD GGSADMPPEA AASEAAPPAG
101 GTEWKQGTAE AAVRSGDKVF FAGDSLMQGV APFVQKSLKQ QYGIESANLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201 KFADEWAQE YLKRVDRIE AAHTRVQVW WLGIPLYMKV KLDGQMRYLD
251 KLLSEHLKKG IILIPTAQL SGGKGRYDTS VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTCCTCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCGGAC GGCTCAAGAC GCGGTTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCCGTCCT TCAAACCGGT
301 GAAACAGAAT GGAAACAAGA CACCGAAGCC GCCCGCTCC GCAGCGGCGA
351 CAAAGTCTTT TTGTGCGGCG ACTCGCTGAT GCAGGGCGTT GCCCTTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGCAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCCTG CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAAGTCTTT CGGAACATT GAAAGGCAAA ATCATCTGTA TTCCACCCAC
801 GCACACCCCT AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAATAATA ATGGAATAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

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691

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751  AAACGCTTT  CGGAATATTT  GAAAGGCAAA  ATCATCCTGA  TTCCACCCGC
801  GCACACCCTG  AGCGGCGGGA  AAGACCGCTA  CACCGACTCC  GTCAACGTCA
851  ACGGCAAACC  CGTCCGCTAC  CGCAGCAAGG  ACGGCATACA  CTTTACCGCC
901  GAAGGACAAA  AACTGCTGGC  GGCAGAAAATA  ATGGAAAAAA  TCGTTTTTGA
951  ACCAAGTACG  CAACCATCAA  GTACACAGCC  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
1  MKNFLSLFAS  ILSALIAVW  FSQNPINAYW  QQTYHRNSPL  EPLAAYGWWR
51  SGAALQENAY  ALSDGIKAF  LSGETPPTAQD  GGSADMPSEA  AAPETAPQTG
101  ETEWKQNTA  AAVRTGDKV  FAGDSLMOGV  APFVQKSLKQ  QYGIESVNLS
151  KQSTGLSYPS  FFDWPKTIE  TLKKHPEISV  LAVFLGPNDP  WDFPVGKRYL
201  KFASDEWAE  YLKRVDRI  LEAAHTRVQV  VWLGIPYMKKA  KLDGQMRYLD
251  KLLSEYLGK  IILIPHTA  HLTSGGKDRY  TDSVNVNGK  PVRYRSKDG  IHFTA
301  EGQKLLAAKI  MEKIVFEP  STQPSSTQP*

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m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFSLGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAFSLGETPPTAQDGGSDMPSEAAAPETAPQTGETEWKQNTTEAAAVRTGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWDFPVGKLYLKFADEWAEYLYKRVDRILEAAHTRVQVWVWLGIPYMKKA					
a298	LAVFLGPNDPWDFPVGKRYLKFADEWAEYLYKRVDRILEAAHTRVQVWVWLGIPYMKKA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLDKLLSEHLKGIILIPHTHTLSGGKDRYTDSVNVNGKPVRYRSKDG IHFTA					
a298	KLDGQMRYLDKLLSEYLGKIIILIPHTHTLSGGKDRYTDSVNVNGKPVRYRSKDG IHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
a298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
1  ATGAACCCCA  AACACTTCAT  CGCATTTTCC  GCCCTGTTCC  CCGCCACGCA
51  GGCAGAAAGC  CTGCCCGTCG  CCTCCGTCAG  CCCCAGACAC  GTTACCGTTT
101  CCCCCTCCGC  CCCCTACACC  GATACAAACG  GGCTGCTGAC  CGACTACGGC
151  AACGCCGCCG  CCTCGCCTTG  GATGAAAAAA  CTCCGATCCG  TCGCACAAGG
201  CAGCGCGCAG  GCCTTCCGCA  TCCTGCAAA  TCGCGACTCG  CATACCGCCG
251  GCGACTTCTT  TACCGACGCC  CTGCGCAAA  GCCTGCAAAA  AACATGGGGC
301  GACGCGCGCA  TAGGCTGGGT  TTACCCCGCC  AACGTCAAAG  GGCAGCGCAT
351  GGCGGCCGTC  CGTCACAGCG  GCAACTGGCA  AAGCTTCACC  AGCAGGAACA
401  ATACCGGAGA  TTTCCCGCTC  GGCGJCATCC  TCGCCCAAAC  CGGCAGCGGC
451  GGCGGCATGA  CCCTGACCGC  GTCTGACGGC  AAAACCGGCA  AACAGCGCGT

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693

g299	MNPKHFIAFSALFAATQAEALPVASVSPDVTVSPSPAPYTDNGLLTDYGNAAASPWMKK
	10 20 30 40 50 60
m299 . pep	LQSV AQSGSETFRILQIGDSHTAGDFFTD SLRRLQKTWGDGJIGWVYPANVKGQRMAAV
	70 80 90 100 110 120
g299	LR SVAQSGSEAFRILQIGDSHTAGDFFTDALRRLQKTWGDGJIGWVYPANVKGQRMAAV
	70 80 90 100 110 120
m299 . pep	RHNGNWQSLTSRNNTGDFPLGGI LAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
g299	RHSGNWQSFTSRNNTGDFPLGGI LAQTGSGGSMTLTASDGTGKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299 . pep	TVNGNTVSANGGGQVLDTGAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
g299	TVNGNTVSANGGGQVLDTGAALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299 . pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299 . pep	LIIGAPESLKN TLGVCGRTPVRLTEVQQMQRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
g299	LIIGAPESLKN TLGVCGRTPVLLTEVQQMQRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299 . pep	GWA AKDGVHFS AKGYRRAEMLADSLEELVRSAAIRQX
	370 380 390
g299	GWA AKDGVHFS AQGYRRAEMLADSLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

```

a299.seq
1  ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTCC CCGCCACGCA
51  GGCAGAAGCC CTACCTGTCG CCTCAGTCAG CCTCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAAA CTCCAATCCG TCGCACAAAG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTACAAAA AACTTGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCGGCCGTC CGGCACAACG GTAAC TG GCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTC CGCTC GGCGGCATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCCTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GGCGGCGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATCTA GTCATCCTTG CCTACGGTAC
801 CAACGAAGCC TTCGGCGACA ACATCGACAT TGCCGATACC GAACAGAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTACCTGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCCTGA CCGAAGTCCA ACAGATGCAG CGGCGCATCG
1001 CCCGT CAGGG GCAGACGATG TTCTGGTCTT GGCAAACGC GATGGGCGGC
1051 GTTTCAGCA TGAAAACTG GCTCAACCAC GGATGGGCGC CCAAAGACGG
1101 CGTACACTTT TCCGCCAAAG GCTACCAACG GTCGCGGGA ATGCTCGCCG
1151 ACAGCCTCGA AGAACTCGT CGCTCCGCTG CAATCAGGCA ATAA

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695

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351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCGTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAATGG TTTTTTATGG
701 CAGCCAGTAC GTTGTGATG GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTTGT CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCCTGAAA CAGGATTGGT
951 TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTATT TTCTTGTGT
1001 TTGCGCTGCC GGGCATTGTT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTGTGCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGGTTTAA TTTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCGCCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTCT GGCTGATTAT GGCAGCGCTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATT CTATGATCTT JCCGTATTCC
1501 GCTTTCTTCT TAATTGCATG GATCGCCTTA TTCTGCATTT GGGTATTTGT
1551 TTTGGGTCTG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:
g302.pep

```

1 MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVDPDRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLLGVGIA EKSGLISALM RLLLTKSPRK LTTFMVVFTE
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGAVFLK
401 EVGLGGSVLF IGFIILICAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPQ
451 VIQAAYRIGD SVTNIIPTMM SYFGLIMATV IKYKKGDAVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFVLGL PVGPGTPTFY PVP*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

```

m302.seq
1 ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51 GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTACGCTT TTTATATTTT TCATGTGTGT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCGACTA TCCGTCCCGG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGTTTTT ATCAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAAT CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCGT
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTAGC TTTGTGATTG
701 CTTTGATTGG TTATTTTGTG ACTGAAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GGCATTCCAA
801 TGAATCACG CCTTTGGAAT ATAAAGGATT AATTGGGGCT GCGGTGGTGT
851 TTGTTGCCTT ATCCGCCCTA TTGGCTTGGA GCATCGTCCC TGCCGACGGT
901 ATTTTGCCTC ATCCTGAAAC AGGATTGGTT TCCGTTTCGC CGTTTTTAAA
951 ATCGATTGTT GTTTTATTTT TCTTGTGTT TGCATGyCG GGmTTGTTT
1001 ATGGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CgTAATGCG

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697

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m302.pep  SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g302      SIVPADGILRHPETGLVAGSPFLKSIVVFIFLLFALPGIVYGRITRSLRGEREVVNAMAE
          310      320      330      340      350      360

          360      370      380      390      400      410
m302.pep  SMSTLXLXLIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGILICAFI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g302      SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGAVFLKEVGLGGSVLFIFIGILICAFI
          370      380      390      400      410      420

          420      430      440      450      460      470
m302.pep  NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIIIPMMSYFGLIMATV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g302      NLMIGSASAQWAVTAPIFVPMMLLAGYAPQVIQAAYRIGDSVTNIIIPMMSYFGLIMATV
          430      440      450      460      470      480

          480      490      500      510      520
m302.pep  IKYKKDAGVGTLSMMLPYSAFFLIAWIALFCIWWFVLGLPVGPGAPTFFYPAPX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g302      IKYKKDAGVGTLSMMLPYSAFFLIAWIALFCIWWFVLGLPVGPGPTPTFFYPVFX
          490      500      510      520      530

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1  ATGCACTCAA TATATTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTCAGCC
251 TGCTCGATGC TGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTATG CGCTTATTGC
401 TCACAAAATC TCCACGCAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACCTG TTTTATATGG
701 TAGCCAGTAC GTTTGTGATT GCTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC TGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCTGAAA CAGGATTGGT
951 TTCCGGTTCG CCGTTTTTAA AATCAATTGT TGTTTTATT TTCTTGTGT
1001 TTGCACTGCC GGGCATTGTT TATGGCCGGG TAACCCGAAG TTTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTGGTGC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTGTTT ATCGGTTTTA TTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGCTA CGCGCCGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATT CTATGATGT GCCGTATTCC
1501 GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATT GGGTATTTGT
1551 TTTGGGCTG CCCGTCGGT CCGGCGCGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1  MHSIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDPRPVG KGRADDGLIH VVSLLDADGL IKILHTVKVN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTSPRK LTFMVVFTG

```

699

g305.seq
 1 ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTG
 101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
 151 CAGCTCGGTG CCGTTTTGGC GGTAGTGTG GAATACCGGC AGCGTTTCAG
 201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
 251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT
 301 GACAAACAAA TCAAAGAGTA TCTGTTTAA CCCTTGAGTG TTGCAGTCAT
 351 GCTGGTTTTG GCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
 401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCG
 451 TTGATGATCG GTGTTGCCCA AGTGTGTTGA CTGGTTCCGG GTACGTCCCG
 501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
 551 CGGCAACGGA GTTTTCATT TTCTGGCCG TTCCGATGAT GGTGTCAGCA
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
 651 CGGTTTGATT TTGATAGGCT TTATGCTGCT TTTTGTGTTCC GGTGTTGTTAG
 701 CGGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCCGTTT
 751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGGTTGTC
 801 GGGCTGGATA AGTTGGGAAT GA

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
 51 QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAIAP IPAAVMGLLF
 101 DKQIKEXLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA
 151 LMIGVAQVFA LVPGTSRSGS TVMGGMLWGI ERKTATEFSF FLAVPMMVAA
 201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
 251 AYYRIVFGIV IILWLSGWI SWE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)
 1 AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTG
 101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
 151 CAGCTCGGTG CAGTTTTGGC GGTAGTGTG GAATACCGGC AACGTTTCAG
 201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
 251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT
 301 GGCawACAAA TCAAAGAGyA TCTGTTTAA CCCTTGAGTG TTGCAGTCAT
 351 GCTGGTTyTG GrCGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
 401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
 451 TTGATGATCG GCGTTGCCCA AGTGTGTTGA CTGGTTCCGG GTACGTCCCG
 501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA
 551 CTGCGACAGA ATTCTCGTTT TTCTTGCTG TGCCGATGAT GGTGCGGCA
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
 651 CGGTTTGATT CTGATAGGCT TTATGCTGCT CTTTGTGTTCA GGCTTGTTAG
 701 CGGTAAAAGC GTTGTGAGG TTTGTTTCGG GTAC...

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
 51 QLGAVLAVVF EYRQRFNSVL HGLGKDRKAN RFVLNLAIAP IPAAVMGLLF
 101 GXQIKEXLFN PLSVAVMLVL XGFXILWVEK RQSRAPKIA DVDALRPIDA
 151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
 201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHNKVFEIAIQLGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHNKVFEIAIQLGAVLAVVF					
	10	20	30	40	50	60

701

	70	80	90	100	110	120
m305.pep	130	140	150	160	170	180
	XGFXILWVEKQSRAPK	IADVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI				
a305	GGFFILWVEKQSRAPK	IVDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI				
	130	140	150	160	170	180
m305.pep	190	200	210	220	230	240
	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAFVSGLVAVKALLR					
	190	200	210	220	230	240
m305.pep	FVSG					
	!!!					
a305	FVSKKNYIPFAYYRIVFGIAIIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

```

g306.seq
1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTTCGGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAGGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGCGGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TGCGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAAGA
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGCAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAAG  AAATGAAAAA  CTTTGGGCAA  GCGGAAGCC  AACGCATTAT
651 CTGCAATGG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTCCGA  AGTGGTCGGC  TATCAGCGCG
751 GACATAAAAC  GCTTTACCGC  GTGCAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```

g306.pep
1  MFMNKFSSQSG  KGLSGFFFL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREEDP  QQAVRKKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEEK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMKNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRE
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```

m306.seq (partial)
1  ..GGTTGTTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCGmAwAA  CCAGCyTAAG
151 GAAGACATCC  AACCTGAwCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAAwGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGACGCG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAAW  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAAGCT
451 TCAAAAGAAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTGCCG
551 CCGCCAAAGA  AGTGCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```

703

```

601 GAAGTGCAGA AAATGAAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
701 ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTCGGTTAT CAGGCGGGAC
751 ATAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
801 A

```

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```

a306.pep
1 MFMNKFSQSG KLSGFFFFGL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
51 PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD QQAVRKKALT EEREQTVGEK AQKKDAETVK
151 QQAVKPSKET EKKASKEEKK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

m306/a306 93.7% identity in 252 aa overlap

```

m306.pep          10      20      30      40
                  GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPK
                  |||||||||||||||||||||||||||||||||||||||||||
a306              MFMNKFSQSGKLSGFFFFGLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK
                  10      20      30      40      50      60

m306.pep          50      60      70      80      90      100
                  NQXKEDIQKPADQNALSEPDAATEAEQSDAEKAADKQPVADKADEVEEKAGEPEREEDP
                  || ||||| ||||||||||||||||||||||||||||||||||||||||||| |||||
a306              NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD
                  70      80      90      100     110     120

m306.pep          110     120     130     140     150     160
                  QQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
                  |||||||||||||||||| |||||||||| |||||||||| |||||||||| |||||||
a306              QQAVRKKALTEEREQTVGEKAQKKDAETVKQAVKPSKETEKKASKEEKKAEKEKVAPKP
                  130     140     150     160     170     180

m306.pep          170     180     190     200     210     220
                  TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTRARKGSVPNWQSWAY
                  |||||||||||||||||| |||||||||| |||||||||| |||||||||| |||||
a306              TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTAGARKGSVPNWQSWAY
                  190     200     210     220     230     240

m306.pep          230     240     250
                  LPRWSVIRRDIKRFTGCKAAICLPMRX
                  ||||||||||||||||||
a306              LPRWSVIRRDIKRFTGCKAAICLPMRX
                  250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

```

g307.seq
1  atgaaaacct tcttcaaaac cctttcgacc gcgtcactcg cgctcatcct
51  cgcagcctgc ggcggtcaaa aagacagcgc gcccgagcc tctgccgccg
101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
151 accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201 ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtgc
251 gcccgaaatc ggcatggcg gagggcgagt tggacatcaa cgtcttccaa
301 cacaaacctt atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351 cgaagccttc caagtgccga ccgcgccttt gggactgtat ccgggcaaac
401 tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgcccaac
451 gacccgtcca acttcgcacg cgccttggtg atgctgaacg aactgggttg
501 gatcaaaact aaagacggca tcaatccgct gaccgcatcc aaagccgaca
551 tcgcggaaaa cctgaaaaac atcaaaatcg tcgagcttga agccgcacaa
601 ctgccgcgca gccgcgcca cgtggatttt gccgtcgta acggcaacta
651 cgccataagc agcggcatga agctgaccga agccctgttc caagagccga

```


705

```

51  VGDFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFQH
101 KPYLDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLNKI  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEGYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                                QWLKDVTEAYNSDAFKAYAHKRFEYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEYKSPA
          220      230      240      250      260      270

                                39
m307.pep      AWNEGAAX
          |||||
a307      AWNEGAAX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTCT  GTTTTTTCAC  TATAATAGCC  GGTGTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCCTGAAGG  CTTTGGAACT
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGCGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCGGA
401 CGCTTGCTTC  TGTCGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGCGGCGCG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAGCCGCGA
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVYRIL  GVADNLYPCL  SDFCFFTIIA  GLPLQAVLWE  RMMVRRLLI
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADVFHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFQDNLTRA
151 ADVVLKERRR  LVLVRETPLE  NLAHLNLMKR  VTEMGGVVP  PVPAMYRKPQ
201 TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTCT  GTTTTTTCAC  TATAATAGCC  GGTGTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCCTGAAGG  CTTTGGAACT
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTTC  TGTCGCGCAC  GGCTTCGGCG  ACAATCTGCT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GWAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

m308.pep (partial)

707

m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
a308	MLNRIFYRILGVADNLYPYLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASEYARDEVYALADFVHPIGNIGACIASGTF					
a308	GVKALKLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF					
	70	80	90	100	110	120
m308.pep	KTDGMLVAPCSMRTLASVAHGFQDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMNR					
a308	KTDGMLVAPCSMRTLASVHGFQDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMNR					
	130	140	150	160	170	180
m308.pep	XTEMGGVVFPVPFAMYRKQTADDIVAHVSAHALSLFGIDTPDPAEWQGMMA					
a308	VTEMGGVVFPVPFAMYRKQTADDIVAHVSAHALSLFGIDTPDPAEWQGMADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTAAATC GGGTATTTTA TCGGATATTG GGTGTGCCG ACAATTTGTA
51  TCCGTGTTTA TCGGATTCTT GTTTTTCAC TATAATAGCC GGTGTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCCTGT TCGATGCCGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCCTG CGATGTACCG CAAGCCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFTTIIA GLPLQAVLWE RMMVRRLLII
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMNR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFGID TPLAELWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTAAATC GGGTATTTTA TCGGATATTG GGTGTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTCTT GTTTTTCAC TATAATAGCC GGTGTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCCG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCCGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCCTG CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFTTIIA GLPLQAVLWE RMMVRRLLII

```

709

```

m308-1      KTDGMLVAPCSMRILASVAHGFGDNLTRAADVVLKERRRLVLMVRETPNLNLAHLDNMKR
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPPVPAMYRKQPOTADDIVAHSVAHALSLFGIDTPDSA EWQGMADX
              |||||
m308-1      VTEMGGVVFPPVPAMYRKQPOTADDIVAHSVAHALSLFGIDTPDSA EWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

```

g311.seq
1  atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgcgtgccc gcgcgctttg ggggtgtttg
101 gtttggaaac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggcg gcattctgat tgaacagtc agggcgggcg gtaaaacggt
201 tgcctggttc ggtatcggca tcaatttcgt gctgcccagc gaagtggaaa
251 acgccgcttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccc ccgtattgct ggaaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgctgtt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgttct
501 gcacttgga acggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggttcg
601 gaacgttttt tgctgttggg aggcgggaac agccggtcca agtgggcgtg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgcgc taccgcgatt
701 tgcgcctttt gggcgcgagc tgggcggaaa aggcggtatg aaatgtccgc
751 atcgtcggtt gcgccgtgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgcga caggctttgg
851 gcatacgcaa ccactaccgc caccgcgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgtcgt
951 cagttgcggc acggcggtaa cggttgacgc gctcaccgat gacggacatt
1001 atctcggcgg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
1151 gcggctcgat aatgatgatg cacggccgtt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggccggcgcg cgaaagtcgc
1251 cgaagccctg ccgcctgcat ttttggcgga aaataccgtg cgcgtggcgg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

```

g311.pep
1  MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGGILLETV RAGGKTVAVV GIGINFVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLET LLAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGT VKG VDGRGVHLHLE TAEGEQTVVS GEISLRPDNR SVSVKRPDS
201 ERFLLLEGGN SRLKAWAVEN GTFATVGSAP YRDLSPILGAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSR RFS RNACVVVSCG TAVTVDALTD DGHYLG GTIM PGFHLMKESL
351 AVRTANLNRP AGKRYPFPTT TGNASVSGMM DAVCGSIMMM HGRLKEKNGA
401 GKPVDV IITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

```

m311.seq (partial)
1  ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTGCGCCT GTTGCGGCAG TGGCGTGTCC GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCArATTAA GGGCCCAATG ATTTGGTTGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAACCGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG CCGGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAAT
351 CAGCCTGCGG TCCGACnACA GGCCGGTTTC CTGnCGAAG CGGCGGGATT

```

711

```

                240      250      260      270      280      290
m311.pep      WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR
                |||||
g311          WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR
                300      310      320      330      340      350

                300      310      320      330      340      350
m311.pep      HAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPVVDVIITGGGAAKVAEA
                |||||
g311          PAGKRYPFPTTTGNAVASGMMDAVCGSIMMHGRLEKKNAGKPVVDVIITGGGAAKVAEA
                360      370      380      390      400      410

                360      370      380      389
m311.pep      LPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEH
                |||||
g311          LPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX
                420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1   ATGTTCAAGT   TTGGCTGGGT   GTTTGACCGG   CCGCAGTATG   AGTTGGGTTC
51  GCTGTCGCCT   GTTGCGGCAG   TGGCGTGCCG   GCGCGCTTG   TCGCGTTTGG
101 GTTTGAA AAC   GCAAATCAAG   TGGCCAAACG   ATTTGGTCGT   CGGACGCGAC
151 AAATTGGGCG   GCATTCTGAT   TGAACCGGTC   AGGACGGGCG   GCAAAACGGT
201 TGCCGTGGTC   GGTATCGGCA   TCAATTTCGT   GCTGCCCAAG   GAAGTGGAAA
251 ACGCCGCTTC   CGTGCAATCG   CTGTTTCAGA   CGGCATCGCG   GCGGGGAAAT
301 GCCGATGCCG   CCGTGTGCT   GGAAACGCTG   TTGGCGGAAC   TTGATGCGGT
351 GTTGTGCAA   TATGCGCGGG   ACGGATTTGC   GCCTTTTG   GCGGAATATC
401 AGGCTGCCAA   CCGCGACCAC   GGCAAGGCGG   TATTGCTGTT   GCGCGACGGC
451 GAAACCGTGT   TCGAAGGCAC   GGTAAAGGC   GTGGACGGAC   AAGGCGTTCT
501 GCACTTGGA   ACGGCAGAGG   GCAAACAGAC   GGTGCTCAGC   GCGGAAATCA
551 GCCTGCGGTC   CGACGACAGG   CCGGTTTCCG   TGCCGAAGCG   GCGGGATTTC
601 GAACGTTTT   TGCTGTTGGA   CGGCGGCAAC   AGCCGGCTCA   AGTGGGCGTG
651 GGTGGAAAC   GGCACGTTTC   CAACCGTCGG   TAGCGCGCCG   TACCGCGATT
701 TGTCGCCTTT   GGGCGCGGAG   TGGCGGAAA   AGGTGGATGG   AAATGTCCGC
751 ATCGTCGGTT   GCGCGGTGTG   CGGAGAATTC   AAAAAGGCAC   AAGTGCAGGA
801 ACAGCTCGCC   CGAAAAATCG   AGTGGCTGCC   GTCTTCCGCA   CAGGCTTTGG
851 GCATACGCAA   CCACTACCGC   CACCCGAAG   AACACGGTTC   CGACCGTTGG
901 TTCAACGCCT   TGGGCAGCCG   CCGCTTCAGC   CGCAACGCCT   GCGTCGTCGT
951 CAGTTGCGGC   ACGGCGGTAA   CGGTTGACGC   GCTCACCGAT   GACGGACATT
1001 ATCTCGGGGG   AACCATCATG   CCCGGTTTCC   ACCTGATGAA   AGAATCGCTC
1051 GCCGTCCGAA   CCGCCAACCT   CAACCGGCAC   GCCGTAAGC   GTATCCTTT
1101 CCCGACCACA   ACGGGCAATG   CCGTCGCCAG   CGGCATGATG   GATGCGGTTT
1151 GCGGCTCGGT   TATGATGATG   CACGGGCGTT   TGAAAGAAAA   AACCGGGGCG
1201 GGCAAGCCTG   TCGATGTCAT   CATTACGGGC   GCGGCGCGCG   CAAAAGTTGC
1251 CGAAGCCCTG   CCGCTGCAT   TTTTGGCGGA   AAATACCGTG   CGCGTGGCGG
1301 ACAACCTCGT   CATTACGGG   CTGCTGAACC   TGATTGCCGC   CGAAGGCGGG
1351 GAATCGGAAC   ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1   MFSFGWVFDR   PQYELGSLSP   VAAVACRRAL   SRLGLKTQIK   WPNDLVVGRD
51  KLGGILIETV   RTGGKTVAVV   GIGINFLPK   EVENAASVQS   LFQTASRRGN
101 ADAAVLLET   LAELDAVLLQ   YARDGFAPFV   AEYQAA NRDH   GKAVLLLLRDG
151 ETVFEGTVKG   VDGQGVHLE   TAEGKQTVVS   GEISLRSDDR   PVSVPKRDRS
201 ERFLLLDG   SRLKAWVEN   GTFATVGSAP   YRDLSP   WAEEKVDGNVR
251 IVGCAVCGEF   KKAQVQEQLA   RKIEWLPSSA   QALGIRNHYR   HPEEHGSDRW
301 FNALGSRFRS   RNACVVVSCG   TAVTVDALTD   DGHYLG   PGFHLMKESL
351 AVRTANLNRH   AGKRYPFPTT   TGNASVSGMM   DAVCGSVMM   HGRLKEKTGA
401 GKPVDVIITG   GGAAKVAEAL   PPAFLAENTV   RVADNLVIH   LNLNIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

```

801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGGACGG CGAAACCGTG TCGGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGCACCTTGA AACGGCAGaa ggcGAACAGa cggtcGtcag
951 cggcGaaaTC AGccTGCGGc CCGacaacag gtcggtttcc GTgccgaagc
1001 gGccggatTC GgaacgttTT tTGCTgttgg aaggcgggaa cagccggctc
1051 aAGTGGGcgt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGGcCC
1101 gtaCCGCGAT TTGTGCGCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAATC CAAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TCGTCTCGTC TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCCCT TCCCGACCAC AACGGGCAAC GCCGTGCGAA GCGGCATGAT
1551 GGACGCGGTT TCGGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1  MTLVKPSHWR VLAELADGLP OHVSQLAREA DMKPOQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWAFDRPOY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIEVVRAG
201 KGTVAUVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVVDG
301 RGVVLHLETAE GEQTVVSGEI SLRPDNRVS VPKRPDSERF LILEGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIWG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAAL GIRNHYRHPE EHGSDRWFNA LGSRRFRSRNA
451 CVVVSCTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRPAKG
501 RYFPFTTTGN AVASGMMDAV CGSIMMMHGR LKEKNAGAKP VDVIIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1  ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGCTC CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCCGCGCA CACACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGGCGC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGACAAA GGCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAAGTGGTC CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGCGCA GTGGCGTGTC GGCGCGCCTT
501 GTCGCGTTTA GGTTTGGATG TGCAGATTAA GTGGCCCAAT GATTTGGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGCG
601 GGCAAAACGG TTGCCGTGGT CCGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTGTTGCA ATATGCGCGG GACGGATTTC CGCCTTTTGT
801 GGCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCACCTTGA AACGGCAGAG GGCAACAGAG CGGTCGTGAG
951 CGGCGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GCGGGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTGCGCTT TGGGCGCGGA GTGGGCGGAA AAGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGGCTGTGT GCGGAGAATT CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTGCGCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACGG GTTGTGAAC ATGATTGCCG

```

```

m311-1.pep  VDVIIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEHIX
              |||||
g311-1      VDVIIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHAX
              550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1  ATGACGCTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGAATCACCT
351 GCAAAATAAG GGCAGGGGGC GTCAGGGGCG GAAGTGGTCG CACTGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTTGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGGGCA GTGGCGTGCC GCGCGGCCTT
501 GTCCGCTTTG GGTTTGAAAA CGCAAATCAA GTGGCCAAAC GATTGGTTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAACCGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTCTG TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CGGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGAAA TGCCGATGCC GCCGTGTTGC TGGAAACGCT GTTGGCGGAA
751 CTGTATGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGCGGCTT TGCATTGGA AACGGCAGAG GGCAAAACAG CGGTGCTCAG
951 CGCGGAAATC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCCGAAGC
1001 GCGGGGATTG GGAACGTTT CTGCTGTTGG ACGCGGCAA CAGCCGCTC
1051 AAGTGGCGGT GGGTGGAAAA CGGCACGCTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGCGGAA AAGGTGGATG
1151 GAAATGTCCG CATCGTCGGT TGGCGCGTGT GCGGAGAATT CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGACGCC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACCGGACAT TATCTCGGGG GAACCATCAT GCCCGTTTC CACTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGTAAG
1501 CGTTATCCTT TCCCGACCA AACGGGCAAT GCCGTCGCCA CGGCATGAT
1551 GGAATGCGGT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAGAAA
1601 AAACCGGGG GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGG GACAACCTCG TCATTACCGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGCGG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1  MTLVKPSHWR VLAELADGLP QHVSQARMAD MKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGROGRKWS HRLGECLMFS FGWVDRPQY
151 ELGSLSPVAA VACRRALSRL GLKTOIKWPN DLVVGRDKLG GILIVRTVG
201 GKTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEQTVRGVDG
301 QGVHLLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAWVNGTF ATVGSAFYRD LSPLGAEMAE KVDGNVRIWG CAVCGEFKKA
401 QVQEQARKI EWLPSAQAL GIRNHYRHE EHGSDRWFNA LGSRRFSRRA
451 CVVVSCTGAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPPTTGN AVASGMMDAV CGSVMHHRG LKEKTGAGKP VDVIIITGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

```

a311-1/m311-1 98.5% identity in 591 aa overlap

```

              10      20      30      40      50      60
a311-1.pep  MTLVKPSHWRVLAELADGLPQHVSQARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
              |||||
m311-1      MTLVKLSHWRVLAELADGLPQHVSQARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
              10      20      30      40      50      60

              70      80      90      100     110     120
a311-1.pep  LVRPLAVFDAEGLRELTERS GFQALKHECAS...DEILELARIAPDKAHKTICVTHLQSK
              |||||
m311-1      LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              70      80      90      100     110     120

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717

```

901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAGGCAGG CGTGTTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCCGTC TGCTCCGTTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCGCGCGA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAACCAC CGCCGTGCGC
1201 ATTATTCGGT TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTGGGGC TACGCGCCTG TAATGCCGCG AAAAGAAGGT TCGTGCGAAG
1301 TGTTTCGTCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1 MSIQSGEILE TVKMVADRNF DVRTITIGID LHDICISTDID VLNQNIYNKI
51 TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FCGAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1 ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51 CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCGGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAAC
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAAGGGA TGTGCGcTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCTGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACcGTc AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAAATTTGT CGTGTCTTGC AACCGGTGG AAGACAACCC GTTTWTGGCG
601 GGCGCGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTCG GCGTATCCGG
651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAACTG CTTTCAAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCCGCGA AGCcTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTCGCCGA CCCCGCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGCCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAATC
1051 GAAGCCATGA CCGCCGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGGG CATATTGCC GACGAAGCCG
1151 CCATCGGCAt GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CAcGGTCGAG TTCGGCGGCT TGTGGGgCTA
1251 CGCGCCTGTG ATGCCGGTCA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDICISSDIN VLNQNIYNKI
51 TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQ
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCX SIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FCGAKIVVFC NAVEDNPFXA
201 GAFHGSGLAV INVGVSGPGV VKAALENS DA TTLTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCGTHGTTA
301 ALALLNDAVK KGGMMASAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIIVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTV EFGLLGYAPV MPVKEGSCEV FVNRGGRI PA PVQSMKN*

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719

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301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATTG GCGGCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGCGCGCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTCTGTC AACGCGGTGG AAGACAACCC GTTTATGGCG
601 GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCGCGCT
651 ATCCGGCCCG GGTGTCTGTA AAGCCGCGTT GGAAAATTCG GATGCAACGA
701 CATTGACCGA AGTTGCCGAA GTTGTGAAGA AAACCGCCTT CAAAATTACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGCGGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGTT TGAGCGTCTG CGGTACGCAC
901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGGCGCG TTTATCCCGG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAAGCAGG CGTGCTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTCCGGTCG GCTTGGATAT
1101 GATTGCCGTT CCCGGCGACA CACCGCGCA CACCATTTCG GGCATCATTG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATTCCGG TAACCGGTAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 CCTGTTGGGC TACGCGCCTG TAATGCCGGT AAAAGAAGGC TCATGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATACCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

```

a312.pep
1  MSIQSGEILE TVKMOVADQNF DVRTITIGID LHDICISTDID VLNQNIYNKI
51  TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGC AKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DATTLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGGMA SSAVGLLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

m312/a312 96.7% identity in 451 aa overlap

```

          10      20      30      40      50      60
m312.pep  MSIQSGEILETVKMOVADQNF DVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
          |||
a312       MSIQSGEILETVKMOVADQNF DVRTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT
          10      20      30      40      50      60

          70      80      90     100     110     120
m312.pep  AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVVAQTLDKAAKAIGVSFIGGFSSALV
          |||
a312       AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVVAQTLDKAAKAIGVSFIGGFSSALV
          70      80      90     100     110     120

          130     140     150     160     170     180
m312.pep  QKGMSPSDEV LIRSIPEAMKTTDIVCXSSINIGSTRAGINMDAVKLAGETVKRTAEITPEG
          |||
a312       QKGMSPSDEV LIRSIPEAMKTTDIVCSSINIGSTRAGINMDAVRLAGETIKRTAEITLEG
          130     140     150     160     170     180

          190     200     210     220     230
m312.pep  FGC AKIVVFCNAVEDNPFXAGAFHGSG--DAVINVGVSGPGVVKAALENSDDATTLTEVAE
          |||
a312       FGC AKIVVFCNAVEDNPFMAGAFHGSGEADAVINVGVSGPGVVKAALENSDDATTLTEVAE
          190     200     210     220     230     240

          240     250     260     270     280     290
m312.pep  VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTFPVGDSVARILEEMGLSVCGTH
          |||
a312       VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCGTH

```


721

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLSDSAIAA					
g313	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFQFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFQFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIALLVLFHRKSNIVKLLLEGRESKIGGSRX					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNILNLKIGKESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

```
a313.seq
1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTGGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGCGCGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCACAAAC TGCCTTGGTC
301 TGC CGCTTGA TTTGGCTTGT GATGGCATTG GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCCCC CCTTGCCGCA CTGTTTTTTA
401 TGCCGCATAC TTCCTGGATT TTCGCAACCC TCGCAATCGC CATATTGGTG
451 TTGCTCCGCC ATAAGAGCAA CATCCTCAAC CTGATTAAAG GCAAAGAAAG
501 CAAAATCGGC GAAAAACGCT GA
```

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

```
a313.pep
1  MDDPRTYGS NPGATNVLR S GKKKAAALT L LGDAAKGLV A VLLARVLQEP
51  LGLSDSAIAA VALAALVGH M WPVFFGFKG G KGVATALGV L LALSPTTALV
101 CALIWLVMF QFKVSSLAAL TATIAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNILN LIKGKESKIG EKR*
```

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLSDSAIAA					
a313	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFQFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFQFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIALLVLFHRKSNIVKLLLEGRESKIGGSRX					
a313	TATIAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNILNLKIGKESKIGEKRY					
	130	140	150	160	170	

723

```

|||||
g401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.pep HRIHLLNPRDVVPESNMPAFPLARNKVDVDATVANMKALRKVGTTPYSDEEIAKAPEALA
|||||
g401  HRIHLLNPRDVVPESNMPAFPLARNKVDVDATVANMKALRKVGTTPYSDEEIAKAPEALA
      130     140     150     160     170     180

      190     200
m401.pep NKSELDVVAYLQGLGLALKNVRX
|||||
g401  NKSELDVVAYLQGLGLALKNVRX
      190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1  ATGAAATTAC AACAAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GGCAGCAACA CAGCCGGCGT CGGGCGTGAA GCCTTACAA
151 GCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCGG TCGGGAACG GAGCGTTACG
251 GTCATTACTC TGTGCGCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTC CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAATC GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
1  MKLQQLAE EK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PLARNKVDV
151 DATVANMKAL RKVGTTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

      10      20      30      40      50      60
m401.pep MKLQQLAE EK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYNALQVAGRDIY
|||||
a401  MKLQQLAE EK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYNALQVAGRDIY
      10      20      30      40      50      60

      70      80      90      100     110     120
m401.pep IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
|||||
a401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.pep HRIHLLNPRDVVPESNMPAFPLARNKVDVDATVANMKALRKVGTTPYSDEEIAKAPEALA
|||||
a401  HRIHLLNPRDVVPESNMPAFPLARNKVDVDATVANMKALRKVGTTPYSDEEIAKAPEALA
      130     140     150     160     170     180

      190     200
m401.pep NKSELDVVAYLQGLGLALKNVRX
|||||
a401  NKSELDVVAYLQGLGLALKNVRX
      190     200

```

651	TGCTCTTCAA	AATATTGCTG	ACCGTCCGGA	TAgGCTGATT	GAAAACAAAC
701	ACGGCATTGT	TGCGGTTTAC	CATAGAGATG	GTGATAAGGT	TGTTTATGGG
751	GCGAATGTAT	ACGACGGCGC	ATACAATACC	GATGTATTCA	ATAGTGTCAA
801	CGGCATCGAA	CGTGCCATTC	TGCTACCCCT	CCTGAAGTCT	GGCATAACGC
851	GCATTTTCGT	CGTTGGACTC	AGTACAGGTT	CGTGGGCGCG	CGTCTTGCTA
901	GCCATTCCGG	AAATGCGAGT	GATGATCGTT	GCGGGAATCA	ATCCGGGCTA
951	CCGTAGCCTT	ATCGCGGACG	AGCCGCAAAT	CGCCCCGCTT	TTGCAGGACA
1001	AACGTGTTGA	AATTGTATTG	GATGACGGTA	GGAAATGGCT	CGCTCGCCAT
1051	CCTGTAGAAA	AATTCGACCT	GATTTTGATG	AATACGACTT	GGTACTGGCG
1101	TGCCTATTCC	ACCAACCTGT	TGAGTGCGGA	ATTTTTAAAA	CAGGTCGAAA
1151	GCCACCTTAC	CCGGATGTGT	ATTGTAATGT	TTAATACCAC	GCACAGCCCG
1201	CATGCTTTTG	CTACCGCCGT	ACACAGTATT	CCCTATGCAT	ACCGCTATTG
1251	GCATATGGTA	GTCGGCTCGG	CAACCCCGGT	AGTTTTCCCT	AATAAAGAAC
1301	TGCTCAAGCA	ACGTCTCTCC	CGGTTGATTT	GGCCGGAAG	CGGCAGGCAC
1351	GTATTTGACA	GCAGCACCGT	GGATGCTGCA	GCACAAAAGG	TGTCTCTCTG
1401	TATGCTGATT	CAGATGACCG	acACtTCCGC	TGGGGCGGAA	TTTATTACCG
1451	ACGATAATAT	GATGTGAGAA	TACAATAACG	GCAGAGGGAT	TTAA

m402.ppt

1	MDIVNTKPNP	SLIYMXSFLS	GLLSLGLIEVL	WVRMFSFAAQ	SVPQAFSFTL
51	ACFLTGLIAGV	AYFGKRICRS	RFVDIPFIGQ	CFLWAGIADF	LILGAAWLLT
101	GFSGFVHHAG	IFITLSAVSX	XLIFPLVHHV	GTGDNKSGRQ	VSNVYFAXVA
151	GSALGPLVLG	FVILDFLSTQ	QIYLLLCXIS	AAVPLFCTFL	QKSLRNLNVS
201	VAVSLMFGIL	MFLLPDSVFQ	NIADRPDLRI	ENKHGIVAVY	HDGGRDKVVYG
251	ANVYDGAYNT	DVFNSVNGIE	RAYLLPSLSK	GIRRIFVUGL	STGSWARVLS
301	AIPEMQSMIV	AEINPAYRSL	IADEPQIAPL	LQDKRVEIVL	DDGRKWLRRH
351	PDEKFDLILM	NTTWYWRAYS	TNLLSAEFLK	QVQSHLTPDG	IVMFNTHTSP
401	HAFATAVHSI	PYAYRYGHMV	VGSATPVVFF	NKELLKQRLS	RLIWPESGRH
451	VFDSSTVDAA	AOKVVSRLMI	OMTEPSAGAE	VITDDNMIVE	YKYGRT*

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/g402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNSTLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPPQAFSFTLACFLTGI	AVG				
	: : :					
g402	MDMVNTKPNSTVINMLSFLTGLLSLGIEVLWVRMFSFAAQSVPPQAFSFILACFLTGI	AVG				
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSINVYFAXVAGSALGPVLIGFVILDFLSTQQIYYLLICXIS					
g402	GLIFPLVHHVGTGDNKSGRQVSINVYFANVAGSALGPVLIGFVILDLLSTQQIYYLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSRLRNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSRLRNAVSVAVSLMFGILMFLLPDSVFQNIAGRDPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVYGANVDGAYNTDVFSNVNGIERAYLLPSLKSGIRRIFFVVGLSTGSWARVI					

727

```

51  ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

m402/a402 99.0% identity in 497 aa overlap

```

              10      20      30      40      50      60
m402.pep      MDIVNTKPNSTLIYMXSFLSGLLSLGIEVLWVRMFSAQSVPAFSTLACFLTGI
a402           MDIVNTKPNSTLIYMLSFLSGLLSLGIEVLWVRMFSAQSVPAFSTLACFLTGI
              10      20      30      40      50      60

              70      80      90      100     110     120
m402.pep      AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVV
a402           AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR
              70      80      90      100     110     120

              130     140     150     160     170     180
m402.pep      XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS
a402           GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQQIYLLICLIS
              130     140     150     160     170     180

              190     200     210     220     230     240
m402.pep      AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY
a402           AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY
              190     200     210     220     230     240

              250     260     270     280     290     300
m402.pep      HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS
a402           HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS
              250     260     270     280     290     300

              310     320     330     340     350     360
m402.pep      AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
a402           AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
              310     320     330     340     350     360

              370     380     390     400     410     420
m402.pep      NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
a402           NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
              370     380     390     400     410     420

              430     440     450     460     470     480
m402.pep      VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSTVDAAAQKVSRMLIQMTEPSAGAE
a402           VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSTVDAAAQKVSRMLIQMTEPSAGAE
              430     440     450     460     470     480

              490
m402.pep      VITDDNMIVEYKYGRGIX
a402           VITDDNMIVEYKYGRGIX
              490

```

729

```

51 DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYET AETTSGLTGT LTTSLSLTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSCKIK PTEGLMVDFF DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGPX *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRF AVEQELVAASARA AVKMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRF AVEQELVAASARA AVKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGT					
m406	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGT					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406.pep	LTTSLSLTLNAPALSRTQSDGSGSRSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
m406	LTTSLSLTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSCKIKPTEGLMVDFFSDIRPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSCKIKPTEGLMVDFFSDIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406.pep	SHEGYGYSDEAVRQHRQGPX					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCGGCTT CTGCCAGAGC TGCCGTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```

```

101  tcgtcaaacg attcggacac caagccgctg tctcggtcga ggccgagggg
151  cagctgggtc atgtcgttcg agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggg cagaccattt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgat acgtgccgc
501  cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaacgga tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggatgc gtaaccggcg atcggcgga
651  taatttcgcg tttcagttcg tcgtcttgtt tgtcaattc caacaaggct
701  ttcgggtgga tgccgatttg gcggtgatg ataaattcca tacgcgcaa
751  gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801  tgccgacgtt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacatcgg taatttgcac gtccagcagg ccggcataga taaagccggg
901  atcgcttcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggtcgcatt gccgcagccg acgacggcag gaatacccag ttcgcgcgcg
1001 atgatggcgg cgtggcaggt gcgtccgcg cggttggta cgtggcgga
1051 agcacgttcc atcacgggtt cccaatccg atcggtcatt tcggtaacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cgggaagcat ttaatacagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgcacaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttggga tttgacggtt tcggggcgcg cttgcaggat gtatagtttg
1301 ccgtccagcg cgtcgcgtcc ccattcgata tccatcggcg gcccgtagtg
1351 tttttcgatg gtcagcgctg agtgtgccaa ctcgggtgat tcttcgctcg
1401 taatggagaa gcggttcgcg tcttcttcgg ggaattcgac gttggttacc
1451 gatattgcgg cttcggcttt gtcggtgaaa atcattttga tgtgttcga
1501 acccatgggt ttgcgcagga tggcggggtt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgatc gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

```

g501.pep
1  MVGRTLTLADT DIFVLLAAGG DGKMQHHFDG RVAFVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAADQV GVFGFEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVVKF QQGRVDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDFDGCFWH IVQGDIGNLY VQQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDBG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHLALTD FLTDGTTFAQ
401 DGFFAVDGVA AQVAAFFLG FDGFGAGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQRVVCQ LGDFFVNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGF EHI KFVRVDRALY DVFAQTVRGG NKDDLVLVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

```

m501.seq
1  atggtcggac sggccttgac cgcagatgcc gacatatttg tctcgttcg
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc agggttgcgt
101  tcgtcaaacg attcggatac caagccgctg tcgcggtcga gaccgagggg
151  cagttgggtc atgtcgttcg agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggcttt
301  gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  caacgttggg caacccattt tcatcgcgga cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgat acgttgccgc
501  cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaacgga tgcggccaat gtcgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcggg
651  taatttcgcg ttttaattcg tcgtcttgtt tgtcaattc caacaargct

```

733

g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAADNFRFQFVVLVFKFQQGFRVDADL
	190 200 210 220 230 240
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFFRCFRHIVXGDIIGNLYVQQTGIDKAG
g501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFFRCFRHIVXGDIIGNLYVQQTGIDKAG
	250 260 270 280 290 300
m501.pep	IAFGTGYGNFLTVPQQFGCIAAADNGRNAQFTRDGGVAGTAAAVGNDGRSTFHHGFPPIR
g501	IAFGTGYGNFLTVPQQFGCIAAADNGRNAQFTRDGGVAGTAAAVGNDGRSTFHHGFPPIR
	310 320 330 340 350 360
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAHALTDFTLDGAAFAFYGFVAVDGEAAQVAVALFLG
g501	IGHVGNQYVAGFDGIHLGSI FNQAHALTDFTLDGAAFAFYGFVAVDGEAAQVAVALFLG
	370 380 390 400 410 420
m501.pep	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGGQCVMRQLSNFFVGNGEAVAVFLGDID
g501	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGGQCVMRQLSNFFVGNGEAVAVFLGDID
	430 440 450 460 470 480
m501.pep	VGYGFTGFCFVGKXNHFVFXTHGFTQDGLARFERGFEXXKFVRVDRTLVDVFAQTVRGG
g501	VGYGFTGFCFVGKXNHFVFXTHGFTQDGLARFERGFEXXKFVRVDRTLVDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	NKDDLIVXGFGVEGEHHT
g501	NKDDLIVXGFGVEGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq (partial)

1	ATGGTCGGAC	GGGCTTGAC	CGCAGATGCC	GACATATTTG	TTCTGCTTGC
51	GGCAGGCGGA	GATGGCAAGG	TGCAGCATCA	CTTTGACGGC	AGGGTTGCGT
101	TCGTCAAACG	ATTCGGATAC	CAAGCCGCTG	TCGCGGTCGA	GACCGAGGGT
151	CAGTTGGGTC	ATGTCGTTCG	AGCCGATGGA	GAAGCCGTCG	AAGTATTGCA
201	GGAATTGTTC	CGCCAATACC	GCGTTGCTCG	GCAGCTCGCA	CATCATAATC
251	AGGCGCAGGC	CGTTTTTGCC	GCGTTCCAAG	CCGTTTTCTT	TCAGGGCTTT
301	GACAACGGCT	TCGGCTTCGC	CCAAAGTGCG	GACGAACGGA	ATCATGATTT
351	CAACGTTGGT	CAACCCCAT	TCATCGCGGA	CGCGTTTCAA	GGCTTTGCAT
401	TCCAAGGCGA	AACAGTCTTT	GAAGTTGTCT	GCGACATAAC	GCGCCGCACC
451	ACGGAAGCCC	AACATCGGGT	TTTCTTCATG	CGGTTCGTAT	ACGTTGCCGC
501	CGACCAGGTT	GGCGTATTCG	TTGGATTTGA	AGTCGGACAT	ACGGACGATG
551	GTTTTACGCG	GATAAACCGA	TGCGGCCAAT	GTCGCCACGC	CTTCGGCGAT
601	TTTATCGACG	TAGAAGTCGA	CAGGGGACGC	GTAACCGGCG	ATACGGCGGG
651	TAATTTCCGC	TTTTAATTCG	TCGTCTTGTT	TGTCAAATTC	CAACAAGGCT
701	TTGGGGTGGA	TACCGATTTG	GCGGTTGATG	ATAAATTCCA	TACGCGCCAA
751	GCCGATGCCT	TCGCTGGGCA	GGTTGGCGAA	GCTGAATGCG	AGTTCGGGAT
801	TGCCGACGTT	CATCATGACT	TTTACAGGTG	CTTAGGCAT	GTTGTCCAAA
851	GCAACATCGG	TAATTTGTAC	GTCCAGCAGG	CCGGAGTAGA	TGAAGCCGGT
901	ATCGCCTTCG	GCACAGGATA	CGGTAACCTC	TTGACCGTTT	TTAGCAATT
951	CGGTTGCATT	GCCGCAGCCG	ACAACGGCAG	GAATACCCAG	TTCGCGCGCG

735

	370	380	390	400	410	420
m501.pep	IGHVGN EYVAGFDGIHLGSI FNQAH LALTDFLTDGAAFA XYGFVAVDGEAAQVAVALFLG					
a501	: : : : : : : : : : : :					
	370	380	390	400	410	420
	VGHVGNQYVAGFDGIHLGSI FNQAY LALTDFLTDGAAFAQDGF FAVDRKAAQVAAAFLLG					
m501.pep	430	440	450	460	470	480
	FYGFGLTGLQDVEFAVQAVASPFDIHRAAVVFFDGCVMRQLSNFFVGNGEAVAVFLGDID					
a501	: : : : : : : : : : : :					
	430	440	450	460	470	480
	FDGFGLTGLQDVEFAVQAVASPFDVHRAAVVFFDGCVMRQLGDFVGNGEAVAVFFGDID					
m501.pep	490	500	510	520	530	540
	VGYGFTGFCFVGKNHFDVFXTHGFTDGG LARFERGF EHXKFVRVDR TLYDVFAQTVRGG					
a501	: : : : : : : : : : : :					
	490	500	510	520	530	540
	VGYRFAGFCFVGKNHFDVFXAHGFAQDGRFACFQRGF EHFVFGIDCALYDVFAQTVGXS					
m501.pep	550	559				
	NKDDLIVXGFGVEGEHHTX					
a501	: : :					
	DKDDLIVTGFIEGEHH					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

```

g502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcccgttt gtcacctgac
51  cgtcgccgtc gcttccgcac aggcggggcgc ggtagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca aaccgtccaa
151 agcaaaaaga aaacccaac cgcgcacggc acgttcaaaa tcctgcgccc
201 gggcctcttc aaatgggaat acactttgcc ctacagacag actattgtcg
251 gcgacggtca aaccgtttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcgcgggc agccccgccg ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcaacg cccaaacgca acaacgccgg
451 ctaccaatac atccgcacgc gttcaaaagg cggcaacctc gccgccatgc
501 agcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

```

g502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51  SKKKTQTAHG TFKILRPGLF KWEYTLPIYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNTK ALESSYTLKE DGSSNGIDYV RGNAQTQRRR
151 LPIHPHRLQR RQPRRHAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

```

m502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcccgttt gtcacctgac
51  cgtcgccgtc gcttccgcac aggcggggcgc ggtagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca amccgtccaa
151 wgcaaaaaga aaacccaac cgcgcacggc acgttcaaaa tcctgcgacc
201 gggcctcttc aaatgggaat acaccaaact t.acaggcaa accatcgtcg
251 gcgacggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc cataggcgsc agccccgccg ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagctacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgcccggta
451 ccaatacatc cgcacgcggt tcaaaggcgg caacctcgcc gccatgcagc
501 tyaa

```

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

```

m502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51  XXXKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGX SPAAILSNTK ALESSYTLKE DGSSNGIDYV GNAQTQRRR
151 PIHPHRLQRR QPRRHAA*

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

```
g502-1.seq
1  ATGatGAAAc  cgcaCaacct  gttccaaTtc  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTGGACGCG  CTCAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGCCC
201 GGGCCTCTTC  AAATGGGAAT  ACACTTTGCC  CTACAGACAG  ACTATTGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATCGGCGGC  AGCCCCGCGC  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGTTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CGGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GGCGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAAA
601 GCGGTGGACG  TGTGAGCAA  CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

```
g502-1.pep
1  MMKPHNLFQF  LAVCSLTAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTVO
51  SKKKKTQTAH  GTFKILRPGL  FKW EYTL P YRQ  TIVGDGQTV  WLYDVL AQVT
101 KSSQDQAI  GGSPAAILSN  KTALESSYTL  KEDGSSNGID  YVRATPKRNN  AG
151 YQYIRIGF  KGGNLAAMQL  KDSFGNQTS  ISFGGLNTNP  QLSRGAFKFT  PPK
201 GVDVLSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

```
m502-1.seq
1  ATGATGAAAC  CGCACAACT  GTTCCAATTC  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTAGACGCG  CTTAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGACC
201 GGGCCTTTTC  AAATGGGAAT  ACACCAAACC  TTACAGGCAA  ACCATCGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATCTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATAGGCGGC  AGCCCCGCGC  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGCTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CTGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GGCGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAAA
601 GCGGTGGACG  TGTGAGCAA  CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

```
m502-1.pep
1  MMKPHNLFQF  LAVCSLTAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTVO
51  SKKKKTQTAH  GTFKILRPGL  FKW EYTK P YRQ  TIVGDGQTV  WLYDVL AQVT
101 KSSQDQAI  GGSPAAILSN  KTALESSYTL  KEDGSSNGID  YVRATPKRNN  AG
151 YQYIRIGF  KGGNLAAMQL  KDSFGNQTS  ISFGGLNTNP  QLSRGAFKFT  PPK
201 GVDVLSN*
```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTAVAS	QAQAGAVDALKQFNNDADG	ISGSFTQT	VQSKKKQT	TAH	
g502-1	MMKPHNLFQFLAVCSLTAVAS	QAQAGAVDALKQFNNDADG	ISGSFTQT	VQSKKKQT	TAH	
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQ	TIVGDGQTVWLYDVL	AQVTKSSQDQAI	GGSPAAILSNKT		
g502-1	TFKILRPGLFKWEYTL	PYRQTIVGDGQTVWLYDVL	AQVTKSSQDQAI	GGSPAAILSNKT		
	70	80	90	100	110	120
m502-1.pep	TFKILRPGLFKWEYTKPYRQ	TIVGDGQTVWLYDVL	AQVTKSSQDQAI	GGSPAAILSNKT		
g502-1	TFKILRPGLFKWEYTL	PYRQTIVGDGQTVWLYDVL	AQVTKSSQDQAI	GGSPAAILSNKT		
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYV	LATPKRNNAGYQYIRIGF	KGGNLAAMQLKDSFGNQTS	ISF		
g502-1	ALESSYTLKEDGSSNGIDYV	RATPKRNNAGYQYIRIGF	KGGNLAAMQLKDSFGNQTS	ISF		
	130	140	150	160	170	180

```
m503.pep
  1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNI
 51  ASAAEMRSLR PLCARNAR*
```

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	60
m503.pep		MSAPPASATILFHAASISASSCSGKGVSKIHWRI	SLP	TRASSATSSTSNFASAAEMRSLR			
			::				
g503		MSAPSASVILFHAASISASSCSGKGVSKIHWRI	SLP	TRASSETSTSNFARAAEMRSLR			
		10	20	30	40	50	60
		69					
m503.pep		PLCARNAR					
g503		PLCARNAR					

```
a503.seq
1  ATGTCCGCGC  CGCCGGCATT  GGCAACCATT  TTGTTCCATG  CCGCTTCGAT
51  TTCGGCATCG  AGCTGTCGG  GGAAGGGCGT  GTCCAAAATC  CATTTGGCGGA
101 TTTCTTTGCC  GACGCGTGCC  AGTTCGGCAA  CGTCTTCGAC  ATCTAATTTT
151 GCCAGTGC CGGAAATGCG  TTCGTCAGA  CCGTTGTGTG  CGAGGAATGC
201 GCGGTAG
```

```
a503.pep
  1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNE
 51  ASAAEMRSLR PLCARNAR*
```

```

      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRISLPTRASSATSTSNFASAAEMRSLR
          |||||
a503       MSAPPASATILFHAASISASSCSGKGVSKIHWRISLPTRASSATSTSNFASAAEMRSLR
          |||||

      69
m503.pep  PLCARNARX
          |||||
a503       PLCARNARX

```

g503-1.seq

```
1  ATGGCGCGGT  CGTTGTACAG  GGAGGCGAAA  ACGTGGCGCA  TCGCTTTTTT
51  AACGTTATCC  AAGCCATTGA  TATTCAGGAA  GGTTCCTGTT  TGGCGGGCAA
101 ATGATGCGTC  GGGCAGGTCT  TCGGCGGTTG  CGGAGAGCG  TACGGCAACG
151 GAAATGTCCG  CGCGCTCGGC  ATCGGTAATC  ATTTTGTTCC  ATCGCGCTTC
201 GATTTCGGCA  TCGAGCTGTT  CGGGGAAAGG  CGTGTCCAAA  ATCCATTGGC
251 GGATTCTTTT  CCCACGCGGT  GCCAGTTCGG  AAACGTCTTC  GACATCCAAT
301 TTTGCCAGAG  CGGCGGAAAT  GCGTTCGTTC  AGACCGTTGT  GTGCGGAGAA
351 TCGCGCGTAG
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

g504.seq

```

1 atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51 cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgcaccat ccgcgtgaac
151 catcctttga ccttgcacgg catcacgatt tatcaggcga gttttgccga
201 cggcgggttc gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttggaa
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa ataccaccaat
451 atcggccctt ccatcgtgta ccgcatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattatTTTT
551 ggctgaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaag gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgaccggtt cgcggggtgc gcttttggtc tatctcggct cggatttggt
1101 ggttttgggt acagtattta tgttttatgt gcccaaaaaa cgggcgtggg
1151 tattgttttc aaacdgcata atccgttttg ctatgtcttc ggcccgcagc
1201 gaacgggatt tgcagaagga atttccaaaa cagctcgaga gcttgcacgc
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

g504.pep

```

1 MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51 HPLTLHGITI YQASFADGGS DLTFAWNLK DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMALAEEN
251 TLNIFAQKGY LGLDEFITSN IPKGQDDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLLSH MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPKK RAWVLFNSKI RFAMSSARSE
401 RDLQKEFFKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

m504.seq..

```

1 atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51 cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgcaccat ccgcgtgaac
151 catcctttga ccttgcacgg catcacgatt tatcaggcga gttttgccga
201 cggcgggttc gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttggaa
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa ataccaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccgggttt gcaggacacg gattatTTTT
551 ggattaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaag gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcctc gggtttgcag

```

743

g504 YLGSVLLVLGTVFMFYVPPKKRAWVLFNS-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
 370 380 390 400 410

m504.pep DLNHD
 |||||
 g504 DLNHD
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq

1	ATATTGGTTC	AGGACTTGCC	TTTTGAAGTC	AACTGAAAA	AATTCCATAT
51	CGATTTTAC	AATACGGGTA	TGCCGCGCGA	TTTTGCCAGT	GATATTGAAG
101	TAACGGATAA	GGCAACCGGT	GAGAACTCG	AGCGCACCAT	CCGCGTGAAC
151	CATCCTTTGA	CCTTGACACG	CATCACGATT	TATCAGGCGA	GTTTGCCTGA
201	CGGCGGTTCG	GATTTGACAT	TCAAGGCGTG	GAATTTGGGT	GATGCTTCGC
251	GCGAGCCTGT	CGTGTGAAG	GCAACATCCA	TACACCAGTT	TCCGTTGGAA
301	ATTGGCAAAC	ACAAATATCG	TCTTGAGTTC	GATCAGTTTA	CTTCTATGAA
351	TGTGGAGGAC	ATGAGCGAGG	GCGCGGAACG	AGAAAAAGC	CTGAAATCCA
401	CGCTGAACGA	TGTCCGCGCC	GTTACTCAGG	AAGGTAAAA	ATACACCAAT
451	ATCGGCCCTT	CCATTGTTTA	CCGTATCCGT	GATGCGGCAG	GGCAGGCGGT
501	CGAATATAAA	AACTATATGC	TGCCGGTTTT	GCAGGAACAG	GATTATTTTT
551	GGATTACCGG	CACGCGCAGC	GGCTTGCAGC	AGCAATACCG	CTGGCTGCGT
601	ATCCCTTGG	ACAAGCAGTT	GAAAGCGGAC	ACCTTTATGG	CATTGCGTGA
651	GTTTTTGAAA	GATGGGGAAG	GGCGCAAACG	TCTGGTTGCC	GACGCAACCA
701	AAGGCGCACC	TGCCGAAATC	CGCGAACAAT	TCATGCTGGC	TGCGGAAAAAC
751	ACGCTGAACA	TCTTTGCACA	AAAAGGCTAT	TTGGGATTGG	ACGAATTTAT
801	TACGTCCAAT	ATCCCGAAAG	AGCAGCAGGA	TAAGATGCAG	GGCTATTTCT
851	ACGAAATGCT	TTACGGCGTG	ATGAACGCTG	CTTTGGATGA	AACCATACGC
901	CGGTACGGCT	TGCCCGAATG	GCAGCAGGAT	GAAGCGCGGA	ATCGTTTCCT
951	GCTGCACAGT	ATGGATGCGT	ACACGGGTTT	GACCGAATAT	CCCCGCGCTA
1001	TGCTGCTGCA	ACTTGATGGG	TTTTCCGAGG	TGCGTTCGTC	GGGTTTGCA
1051	ATGACCCGTT	CCCCGGGTGC	GCTTTTGGTC	TATCTCGGCT	CGGTGCTGTT
1101	GGTATTGGGT	ACGGTATTGA	TGTTTATGT	GCGCGAAAAA	CGGCGGTGGG
1151	TATTGTTTTT	AGACGGCAAA	ATCCGTTTTG	CCATGTCTTC	GGCCCGCAGC
1201	GAACGGGATT	TGCAGAAGGA	ATTTCAAAA	CACGTCGAGA	GTCTGCAACG
1251	GCTCGGCAAG	GACTTGAATC	ATGACTGA		

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep

1	ILVQDLPEFEV	KLKKFHIDFY	NTGMPRDFAS	DIEVTDKATG	EKLERTIRVN
51	HPLTLHGITI	YQASFADGGS	DLTFKAWNLG	DASREPVVLK	ATSIHQFPLE
101	IGKHKYRLEF	DQFTSMNVED	MSEGAEREKS	LKSTLNDVRA	VTQEGKKYTN
151	IGPSIVYRIR	DAAGQAVEYK	NYMLPVLQEQ	DYFWITGTRS	GLQQQYRWLR
201	IPLDKQLKAD	TFMALREFLK	DGEGRKRLVA	DATKGAPAEI	REQFMMAEN
251	TLNIFAQKGY	LGLDEFITSN	IPKEQQDKMQ	GYFYEMLYGV	MNAALDETIR
301	RYGLPEWQQD	EARNRFLLS	MDAYTGLTEY	PAPMLQLDQ	FSEVRSSGLQ
351	MTRSPGALLV	YLGSVLLVLG	TVLMFYVREK	RAWVLFSDGK	IRFAMSSARS
401	ERDLQKEFPK	HVESLQRLGK	DLNHD*		

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLE	IRVNHPLTLHGITI				
a504	ILVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLE	IRVNHPLTLHGITI				
	10	20	30	40	50	60
m504.pep	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
a504	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
m504.pep	MSEGAEREKSLKSTLXDVR	AVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ				
a504	MSEGAEREKSLKSTLXDVR	AVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ				
	130	140	150	160	170	180
m504.pep						
a504						

745

m505.seq (partial)

```

1  GGCATGTTTC GTTTACAATT CAGGCTGTTT CCCCCTTTGC GAACCGCCAT
51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151 TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCCGAC CCCAAACCGG TCAAAGCCGT TTTTGGGAA ACGGCAAAAG
251 GCGGTTTGGA ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
351 CAAACACGAA GGGCTGCTAT TCATCAGGCC GCACATCGGC AGCTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
451 TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTCGCGGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
601 ACGTCCCCTC CCCTCAAGAA GCGGGGGAAG GCGTATGGGT GGATTTCTTC
651 GGCAAACCTG CCTATACCAT GACGCTGGCG GCAAATTGG CACACGTCAA
701 AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GCGGACAAAG
751 GTTTCGATTT GCACATCCGC CCGCTCCAAG GGAATTGAA CCGGACAAA
801 GCCCATGATG CCGCGGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
851 TTTCCGACG CAtATC...
```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1  MFR LQFRLFP PLRTAMHILL TALLKCLSL PLSCLHTLGN RLGH LAFYLL
51  KEDRARI VAN MRQAGLN PDP KTVKAVFAET AKGGL ELAPA FFRK PED IET
101 MFKA VHGEH VQQA LDKHEG LLFITPHIGS YDLGG RYISQ QLPF PLTAMY
151 KPPK IKAIDK IMQAGR VRGK GKTAPT SIQG VKQI IKA LRS GEATIV LDPH
201 VPSPQEGGEG VWVDFG KPA YMTLAAXLA HVKG VKT LFF CCERLP GGQG
251 FDLH IRPVQG ELNGDKA HDA AVFN RNAEYW IRRFP THI...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505 ~g) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505 . pep	MFR LQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARI VAN					
g505	MFR LQFRLFPPLRTAMHILLTALLKCLSLSLSCLHTLGNRLGH LAFYLLKEDRARI VAN					
	10	20	30	40	50	60
m505 . pep	70	80	90	100	110	120
	MRQAGLN PDPKTVKAVFAETAKGGL ELAPAF FRK PED IETMFKA VHGEHVQQA LDKHEG					
g505	MRQAGLN PDPQTVKAVFAETAKCGL ELAPAF FKK PED IETMFKA VHGEHVQQA LDKGEG					
	70	80	90	100	110	120
m505 . pep	130	140	150	160	170	180
	LLFITPHIGSYDLGG RYISQQLPFLTAMYKPPK IKAIDKIMQAGR VRGKGKTAPT SIQG					
g505	LLFITPHIGSYDLGG RYISQQLPFLTAMYKPPK IKAIDKIMQAGR VRGKGKTAPT GIQG					
	130	140	150	160	170	180
m505 . pep	190	200	210	220	230	240
	VKQI IKA LRSGEATIV LDPHVSPQEGGEGVWVDFG KPAYMTLAAXLAHVKG VKT LFF					
g505	VKQI IKA LRAGEAT IILDPHVSPQEGG -GVWADFFG KPAYMTLA AKLAHVKG VKT LFF					
	190	200	210	220	230	
m505 . pep	250	260	270	280	289	
	CCERLP GGQGF DLH IRPVQGE LNGDKA HDA AVFN RNAEYW IRRFP THI					
g505	CCERLPD GQGFV LHIRPVQGE LNGNKA HDA AVFN RTEYWI RRP TQYLFMYNRYKTP					
	240	250	260	270	280	290

747

m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCTGTTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCCACCCC AAAACGGTCA AAGCCGTTTT TCGGGAACG GCAAAAGGCG
251 GTTTGGAAC TCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAATAACCG CGCTACCAG CATACAAGG GTCAACAAA
551 TCATCAAAGC CTTGCGTTTC GCGGAAGCAA CCATCGTCTT GCGGACCCAC
601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGTC ACATCCGCC CGTCCAAGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCTATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCILHTLGN RLGHIAFYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDLET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFFLTAMY
151 KPPKIKAI D KIMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPOEGG EG VVWDFFGKPA YTMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQ G ELNGDKAHDA AVFNRAEY W IRRFPTQYLF MYNRYKMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

```

      10      20      30      40      50      60
m505-1.pep MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCILHTLGNRLGHIAFYLLKEDRARIVAN
g505        MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCILHTLGNRLGHIAFYLLKEDRARIVAN
      10      20      30      40      50      60

      70      80      90     100     110     120
m505-1.pep MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDLETMFKAVHGW EHVQQALDKHEG
g505        MRQAGLNPDPTQTVKAVFAETAKGGLLELAPAFFRKPEDLETMFKAVHGW EHVQQALDKHEG
      70      80      90     100     110     120

      130     140     150     160     170     180
m505-1.pep LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI D KIMQAGRVRGKGKTAPTSIQG
g505        LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI D KIMQAGRVRGKGKTAPTSIQG
      130     140     150     160     170     180

      190     200     210     220     230     240
m505-1.pep VKQIIKALRSGEATIVLPDHVPSPOEGGEGVVWDFFGKPAYTMTLAAKLAHVKGVT LFF
g505        VKQIIKALRSGEATIVLPDHVPSPOEGGEGVVWDFFGKPAYTMTLAAKLAHVKGVT LFF
      190     200     210     220     230

      250     260     270     280     290     299
m505-1.pep CCERLPGGQGF DLHIRPVQ GELNGDKAHDA AVFNRAEY W IRRFPTQYLFMYNRYKMPX
g505        CCERLPDGGGFV LHIRPVQ GELNGDKAHDA AVFNRAEY W IRRFPTQYLFMYNRYKTPX
      240     250     260     270     280     290

```

m505-1/a505 99.7% identity in 298 aa overlap

```

      10      20      30      40      50      60
m505-1.pep MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCILHTLGNRLGHIAFYLLKEDRARIVAN
a505        MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCILHTLGNRLGHIAFYLLKEDRARIVAN
      10      20      30      40      50      60

      70      80      90     100     110     120

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749

```

201 RPFRELAALD GFVQVALMAF AVVGDDDFCSF FVGQVFNPLL AAEMEFHPKT
251 FARFVPEAVG MRTEAVHMAV AGGNTAVAHH DGNLVQGFQ QRPEVPVVC
301 GTHIGARIAF DGFVQVGEFA RVAQEEHGRV VADHIPVAFF GIEFQRKTAD
351 VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGGOAVL IVGNGRAVVH
451 GQMGYGAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLS
501 TFYFPFAKTM DAIIRQDFRY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

m506.seq

```

1 ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTCT
51 TGCCGAACAA TGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAGGCGC
101 CGCGGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCGC TTGATTTTCA AAGGCGGTTC GGCGAATCG GGTGTTGCT
201 GCCATTGGCC GAAGCTGTyG GGTTCGTAGT GCGGCAGGCT GCCGyAGTTG
251 CCGTCGCGCG GGCCTTGCCC GTyGCGsTgr TTgCTGTgAA CAsGGCAACG
301 CGGACGATTG ACGGGAATTT GCGGGAAGTT TACGCCCAA CGGTAGCGTT
351 GTGCGTCGCG GTAATTGAAC AAACGCGCTT GCAGCATTTT ATCTsGGCTG
401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTTCG GATTGCGGTT CTCAAACGGA TGATAAGGTA
501 CTTTTTCCGC GTCTGCTTCA GGCATGACTT GGATGTACAT CGTCCATTTC
551 GGAAACTCGC CGCGTTCGAT GGCTTCsTAT AAGTCGCGCT GATGGCTTTC
601 GCGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTGCGTC AGGTTTTTAA
651 TGCCTTGTG GGTGCGGAAA TGGAATTTCA CCCAAAAACG CTCGCTGCT
701 TCGTTCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA TATGGCGGTA
751 GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT TGGTGCACTG
801 CTTCCGGCAG CAGCGTCCAG AAGTCCAGT TGTTTGTGGC AGAGCGCATA
851 TTGGTGC GGTGCGCTTT GACGGCTTTG TTCAGGTCGG GGAACCTACG
901 CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC ACATCCAGT
951 TGCCTTCTTC GGTATAAAAT TTCAAGGCAA AACCGCGGAT GTCGCGTTCT
1001 GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC GGGCGAACAT
1051 CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TCCTTTGGCG TGCATACGGC
1101 GTTCGGGGAT GACTTCGCGC ACGAAGTCGG CGAGTTTTTC AGTCATCGCT
1151 CTTGTTCTCT TTCTCAGGTT GGTCAAATGG GGGTAAACGG CTTACAGTAC
1201 GATTTGGCGG AAAGCGTATT CGTAACCGGT TTCTTGATTG CAATAAATTT
1251 CTTGAATCGA CATTTTATTT CCCTTTTGTA AAAACTATGG ATGCGACTAT
1301 ACGCCAAGAT TTTGCTATT AA

```

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

m506.pep

```

1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHVQ EQGARLAEIV VIVLAVVPVC
51 RVAVDFQRRF GESGLLLPLA EAVGFVVRQA AXVAVGAALP VAXXAVNXAT
101 RTIDGNLAEV YAQTVALCVG VIEQTRLQHF IXAGADTGNE VARCEGGFLH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRYFFR VCFRHLDDVH
201 RPFRLAAFD GFXXVALMAF AVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIKFQKKTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGKRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVH
451 GQMGYRAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLS
501 TFYFPFVKTM DATIRQDFRY *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/g506

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQEQGARLAEIVVIVLAVVPVCRVAVDFQRRF					
	: : : : : : : : : : : : :					
g506	MAVFDEVGRIAHGCGGVVKQSLFLRVVHVQEQGARLAEVVVIVLAVVPVCRVAVDFQRRF					
	10	20	30	40	50	60

751

```

651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTGTG GGTGCGGAAA TGGAAATTTCA CCAAAAACG
751 CTCGCCTGCT TCGTTCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGSTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCACTG CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTGTTGGC
901 AGAGCGCATA TTGGTGCGCG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCCA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGCGCGCG CGTTGTTTCT
1351 GGTACAGATG GTTACAGGCG ATTTGGAGGT ANTCATCGCT CTTGTTCCCT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAAT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQARLAEIV VIVLAVVPVR
51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRHDLVDH
201 RPFRLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAAVAHH DGNLVQCFGQ QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAF GIELQRKTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRVVH
451 QMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

```

10 20 30 40 50 60
m506.pep MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a506 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVRRVAVDFQRRF
10 20 30 40 50 60

70 80 90 100 110 120
m506.pep GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a506 GEVGLLLPLAEAVGFVVRQAADVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVALRVG
70 80 90 100 110 120

130 140 150 160 170 180
m506.pep VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a506 VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ
130 140 150 160 170 180

190 200 210 220 230 240
m506.pep VKRMIRYFFRVCFRHDLDVHRPFRKLAAFDGFXVALMAFAVVGDDFGGFFVGQVFNALL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a506 VKRMIRHFFRIGFRHDLVDHVRPFRKLAAALDGFVQVALMAFTVVGDDFGGFFVGQVFNALL
190 200 210 220 230 240

250 260 270 280 290 300
m506.pep GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAAVAHHDGNLVQCFGQQRPEVPVVC
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a506 GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAAVAHHDGNLVQCFGQQRPEVPVVC
250 260 270 280 290 300

```


753

51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLFVFG NLHRPFRQLG
 101 LFFFDLQLVF FKLHADLLLL LMNALXLRRL CLLVAFDALV QVLLMADLFF
 151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng) from *N. gonorrhoeae*:

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLFGMGKLLLLQRQFAAD					
	: : : : :					
g507	MLLPALQQGGGFLSGGGFGLVGVQGLVFLFQTTFALFVLGNLFGMGKLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m507.pep	AVCLVLLGLEGGVERGLGFFQFGQTLFVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL					
	: : : : :					
g507	AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLLFFDLQLVFLKLHADLLLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m507.pep	LMNALXLRRLCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG					
	: : : : : :					
g507	LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLAQHAAFVAQFVYCLLLRLFGSLQG					
	130	140	150	160	170	180
m507.pep	VYFVV					
	:					
g507	VYFVI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

a507.seq

1	ATGCTCTTGC	TGGCTTTGCA	ACAAGGCGGC	AGCTTCCTGC	GCGGCGGCGG
51	TTTCGGCTTC	GTCAGGCAGA	TTCAAGGGCTT	GGTTTTCCTG	TTTCAGACGA
101	CCTTTGCGCT	CTTCGTGCTT	GGCAACGGTT	TGTTGCGCAT	GGGCAAGCTG
151	CTGCTGCTTC	AACGCCAGTT	CGCGGCGGAT	GCGGTTTGCC	TCGTCCTGCT
201	GGGTTTGAA	GGCGGCATTG	AGTGTGGCTT	GGGTTTCTTC	CAATTCGGGC
251	AGACGCTCTT	CGTGTTCGGC	AACCTGCATC	GCCATTCCG	CCAATTCGGT
301	TTGCTTTTCT	TCCGCCTGCA	ACTCGTTTTC	TTCAAGCTGC	ACGCGGATTT
351	GCTGCTGCTC	CTGATGGATG	CGCTGCATCT	GCGCTGCGC	CGCTGCTTG
401	TCGCGTTCGA	TGCGTTGGTG	CAGGTTTTGC	TGATGGCGGA	TTGTTCTTC
451	CAAACGGGCA	ATCTGTTCGC	GCAACAGGCC	GCGTTTGTG	CCCAATTCGT
501	GCACGCGCTG	CTGCTGCGAC	TGTTGCGCAG	TCTGCAAGGC	GTGTACTTCG
551	TCGTTTAA				

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep

1	MLLLALQQGG	SFLRGGGFGF	VRQIQGLVFL	FQTTFALFVL	GNLFGMGKL
51	LLLQRQFAAD	AVCLVLLGLE	GGIECGLGFF	QFGQTLFVFG	NLHRPFRQFG
101	LLFFRLQLVF	FKLHADLLLL	LMDALHLRLR	RLLVAFDALV	QVLLMADLFF
151	QTGNLFAQHA	AFVAQFVHRL	LLRLFGSLQG	VYFVV*	

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLFGMGKLLLLQRQFAAD					
	: : : : :					
a507	MLLLALQQGGSFLRGGGFGFVRQIQGLVFLFQTTFALFVLGNLFGMGKLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

755

	10	20	30	40	50	60
m508.pep	MVAFGVDQG	FFLLQQGGLGGG	LKLRQLGLQGLHFS	VLLPALFLNL	REFLLHNNI	FFVQGL
		:			:	
g508	MVAFGVDQGL	LLLLQQGGLGGG	LKLRQLGLQGLYAG	VLLPALFLNL	REFFLHGDV	FFVQRV
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLD	VLLVVELGFIGEG	KLLLAFLPVEGL	LFLKLGDLLP	VVFLFLVFE	VDGDFG
	:	:			:	
g508	YGFQQLVELD	VLLVVELGFIGEG	KLLPAFLPVQGL	LEPGLLPVVL	FLRVEFVDG	DFG
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFQ	QKLRRLFQTA	LLLLAAVRGGL	LVFEFGGFL	QGN	DVV
					:	
g508	KPVLAVGFQ	QKLRRLFQTA	LLLLAAVRGGL	LVFEFGGFL	QSSD	DVV
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```
a508.seq
1  ATGGTAGCGT  TTGGCGTTGA  TCAGGGCTCT  CTGCTGCTGC  AACAGGGCGG
51  TTTGGGTGGC  GGCCTGAAGC  TCGGGCAGCT  TGTTTGTGAC  GGGTTGTGAC
101 CGGGCGTATT  GTTCCCTACC  TGCTCCTGA  ATCTGCGCGA  GTTCTCCTG
151 TACGACAATA  TATTCTTCGT  CCAAACCTCG  TACGGCTTCG  CTCAACTCTT
201 CGAGCTTGAT  GTGCTGCTCG  TCGTTTGGGA  ACTCGGTTTC  ATAGGCGAGG
251 GCAAGCTCTT  GCTGGCGTTC  CTGCCAATCG  AAGGTTTGT  GTTCAAGCTG
301 GGCAATTTGC  TGTGGTAGT  TTTGTTTTG  CTGGTTGAGC  TTGTGGACGG
351 CGACTTCGGC  AAGCCCGTAT  TGGCGGTTGG  CTTCCAACAG  GGCAAGCTGC
401 GCCTGTTTCA  GACGACCTTG  CTGCTCTTGG  CGGCTGTGCG  CGGCGGTTTG
451 CTGCTGGTGT  TCGAGTTCGG  CGGCGGCTTC  CTGCAAAATG  GCGATGTGCT
501 CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```
a508.pep
  1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLYAGVLFPT LLNLREFLL
51  YDNIFVQTL YGFAQLFELD VLLVLELGF IGEGKLLLAFL LPIEGLLFKL
101 GNLLLVVFL LVLVDGDFG KPVLAVGQQ GKRLRFQTL LLLAAVRGL
151 LLVFEFGGFL LQNGDVV*
```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508.pep	MVAFGVDQGGFLL	LQQGGLGGGLKLRQL	GLQGLHFSVLLPALF	LNLRREFLLHN	NIFFVQGL	
a508	MVAFGVDQGGFLL	LQQGGLGGGLKLRQL	GLQGLYAGVLPPT	LLNLREFLLYD	NIFFVQTL	
	10	20	30	40	50	60
m508.pep	YGFAFFFKLDVLL	VVLELGFIGEGKLL	LAFLPVEGLLFKL	GDLLPVVFLFL	VEFVDGDFG	
a508	YGFAQLFELDVL	LVLELGFIGEGKLL	LAFLPIEGLLFKL	GNLLVVLFL	VELVDGDFG	
	70	80	90	100	110	120
m508.pep	KPVLAVGFQQGL	RRLFQTALLLLA	AVRGGLLVFE	FGGGLFQGN	DVVX	
a508	KPVLAVGFQQGL	RRLFQTALLLLA	AVRGGLLVFE	FGGGLFQGN	DVVX	
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509.seq

m509.pcp

Homology with a predicted ORF from *N. gonorrhoeae*

m509/q509

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVVFACVLAQVERH					
	: :					
g509	MVAVCDERAVQRTLVQAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVVFACVLAQVERH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m509.pep	HVKAIEHGYGTDDEVQCQTAFAFGKQTAAVVDKGTLOFFQI IQKLLCRSIRLEKAEFAAHTQTER					
	: : : : : :					
g509	HVEAEHGHGTDDEVQCQTAFAGKQAAAVVDKGTLOFFQI IEKFLGRSIRLEKAEFAAHAQTER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m509.pep	ARFAHSARHNVDGAAGVFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
	: : : :					
g509	ARFAHSARHNVDGAAVRFFGAGDFFVRRECQCCHYVVVDFAADGKRQFAVKFVEFAAV					
	130	140	150	160	170	180

a509.pcp

1	MVAVCDERTV	QWTLMAQFAQ	QGGFLLLFVE	AVVVVQACVL	EKLGNHIGVF
51	ACVLAQVERH	HVEAEHGYGT	DEVQCTAFGK	QAAAVVDKGM	LQFFQIIEKF
101	LCRSIRLEKA	EFAAHTQTER	ARFAASHARNH	VNGATVGVFF	GAGGFGVGRF
151	VQQRHHIAVD	FDAADQERQF	AVEFVEFATV	KTEHGIGVAA	EKGTKQGFGRN
201	ERIAVAVAAD	PAADFEDVRN	ADIGIGRLKV	VFHLAVELGQ	GPKKAHRKDG
251	HAVVDFVDDA	EFVAARFAGL	PQAQQDSVDV	AAQPCQRVGI	GTAFALPQQR
301	ADAAVEIQEL	LALHFRGVRG	QNGNGNRIVF	LPLHRFAVGF	PRFEPADGRF
351	QAAFRAAASF	FVGLDLAAAFV	VHVFGDQVNL	GEQAAGQ* ¹	VGLLVQLRLQ
401	YFFNQCRRAV	SGSQEFDRFD	NQRRGFFVQE	VEQGLFQKFR	VRRQSRVLWI
451	VQNMLQLHDS	LIAVNTVNVQ	QMPPHCQTVH	TLTARVPKCR	LKLNAAARRQR
501	YNRPRQLFXE	HHHDNDRTRP	RCRIPAAVQP	PHPLGRNWHR	RAAETFRRAY
551	EGRRLRFLRX	RGPCPISPLP	ASAR*		

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGHNHIGVFACVLAQVERH					
a509	: : : : : : : : : : : :					
	MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVFQACVLEKLGHNHIGVFACVLAQVERH					
	10	20	30	40	50	60
m509.pep	70	80	90	100	110	120
	HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAEFAAHTQTER					
a509	: : : : : : : : : : : : :					
	HVEAEHGYGTDEVCQTAFGKQAAAVVDKGM LQFFQII EKFLCRSIRLEKAEFAAHTQTER					
	70	80	90	100	110	120
m509.pep	130	140	150	160	170	180
	ARFAHSARHNHVG DGA AVGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
a509	: : : : : : : : : : : :					
	ARFAHSARHNHVGNGATVGFFGAGGFFVGRFVGQRHHIAVDFDAADGERQFAVEFVEFATV					
	130	140	150	160	170	180
m509.pep	190	200	210	220	230	240
	EAEHGIGVAAEGKAQGFGRNKR IAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
a509	: : : : : : : : : : : : : :					
	KTEHGIGVAAEGKTQGFGRNER IAVAVAADPAADFEDVRNADIGIGRLKVVFHLAVELGQ					
	190	200	210	220	230	240
m509.pep	250	260	270	280	290	300
	GF EKAHREDGHAVVDVFVDAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGAAAFALRQQC					
a509	: : : : : : : : : : : : :					
	GF KKAHRKDGHAVVDVFVDAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGITAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360

761

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQKRGYSCAKRDSA	FWQALSISAILRAKSPIAKS	PPFREVFNRSWTTLSAAIMT			
g510	MPSRTPQKRGYSCPKRDSA	FWQALSISVILRAKSPIAKS	PPFREVFNRSWTTLSAAIMT			
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLS	IPTACNSVSFSSAGVLT	VS	RGVXDFXVDLFDVHPLILIAA		
g510	IFSLSATRPPSRMASALPLS	IPTACNSVSFSSAGVLT	VS	RGVHDFD	VDLFDVHPLILIAA	
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

1	ATGCCTTCGC	GGACACCGCA	GGGAAAAAGG	GGTTATTCCT	GCGCCAAGCG
51	GGATAGTGCT	TTTGGCAGG	CGTTGTCCAT	ATCGGCTATT	TTACGCGCAA
101	AATCGCCGAT	TGCCAAATCG	CGCCGTTCA	GGGAGGTTT	CAACAGGTCG
151	TGGACGACGT	TGAGCGCGGC	CATAATGACG	ATTTTTTCGC	TGTCCGCGAC
201	GCGTCCGCCT	TCGCGGATGG	CTTCGGCTTT	GCCGTTGAGC	ATTCCGACTG
251	CCTGCAACAG	TGTGTCTTT	TCTTCTGCCG	GCGTGTGAC	GGTCAGCCGG
301	G.CGTGCATG	ACTTCGATGT	GGACTTGTTT	GATGTTTCATC	CTTTAATCCT
351	TATTGCTGCG	TTTCTGCCG	TTGGGGGAGG	CGCGCTGCCA	GTGCGCTGA

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

1	MPSRTPQGKR	GYSCAKRDSA	FWQALSISAI	LRAKSPIAKS	PPFREVFNRS
51	WTTLSAAIMT	IFSLSATRPP	SRMASALPLS	IP	TACNSVSF SSAGVLTVSR
101	XVHDFD	VDLFDVHPLILIAA	FPAVGGGALP	VR*	

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQKRGYSCAKRDSA	FWQALSISAILRAKSPIAKS	PPFREVFNRSWTTLSAAIMT			
a510	MPSRTPQKRGYSCAKRDSA	FWQALSISAILRAKSPIAKS	PPFREVFNRSWTTLSAAIMT			
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLS	IPTACNSVSFSSAGVLT	VS	RGVXDFXVDLFDVHPLILIAA		
a510	IFSLSATRPPSRMASALPLS	IPTACNSVSFSSAGVLT	VS	RGVHDFD	VDLFDVHPLILIAA	
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

1	atgaaagtgc	ttgttttagg	tgcgggtggt	gccggcgat	cctccgtgtg
---	------------	------------	------------	-----------	------------

763

250 260 270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
1  ATGAAAGTGC TTGTTTTAGG TGCTGGTGTT GCCGGCGTAT CTTCCGCGTG
51  GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAACCAGT TTTGCCAAGC CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTGGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCGCTG
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATCTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GCGTGCCGT ACCGCCGTCT
501 GAAGCCCGAA GAATGCGCAG AATTGAGGCC TGCCTGGCA CGCGTTACCG
551 CCAAATTGCG CGGCGCGCTG CACCTGCCCG CAGACGCGAC CGGCGACTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAGGAAA AGGGCGTACG
651 GTTTCATTTC AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAAACCGT TGAAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAAGT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
1  MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
51  YTPWAAPGI PTKALKWLFK SHPPLFRPD GSLYQIEWLW QMLQHCTAAR
101 YQINKERMVR MSEYSREMF RFEAQTMNF EGRKKTGLQI FRQTKVEEAA
151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK QGGLKQMPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVVPYRRLKPEECAEFEPALARVTAK
a512                                |||
                                130      140      150      160      170      180
                                TGMNFEGRKKGTGLQIFRQTKVEEAAKQDIAVLERYGVVPYRRLKPEECAEFEPALARVTAK

                                40      50      60      70      80      90
m512.pep                                IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGLK
a512                                |||
                                190      200      210      220      230      240
                                IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQTISRIDHNGLRIKTVETKQGGLK

                                100      110      120
m512.pep                                QMPLSARSVASAGRFWRWSWISICPFIPSKAIPX
a512                                |||
                                250      260      270
                                QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
1  ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
51  TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151 GATTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301 AAAAGCCATT GGCTGATTAC CGCGTTTTTC CGTATGCTGG TTTTGGCGTG
351 GGTCTATTTC GCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

765

```

1  ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51  CGATCCGATG TGGTCATACT TGGTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACCACGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTTG TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTGGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCGAAGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTGTGTCGC CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTCG CGATACCSTC AAAGCGGCGT
551 GGGGTTGGGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCG CGGAAATCGT
651 CGTCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTCAGAT TTTTTCGGGC
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTA CTGCGCG GTCTGATTTT
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CCTGTATTCC AACGAGGCGG
851 GTATGGGTTT CGCGCCGAAC GCCGCCGCCG CCGCCGAAGT GAAACACCGT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTG ATACCATCAT
951 CGTTTGTCT TGCACGCGCT TCATCATCTT GATTACCAA CAGCCTTACG
1001 GCGATTGAG CGGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCCGCT ATCCTGTTTA TGTTCGCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CCTTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 .AAATGGGCA AAGACCCGA GTTCAAACCT TCCGAACATC CGGGCGTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```

a513.pep
1  MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLFFTVTG FVQFRLFGRS
51  IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGGPGA
101  VFWMWVTALI GMSSAFVESS LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151  WLGVLFALSL IFCFGVFVEA VQTNTIADTV KAAWGWEPHY VGVALVILTA
201  PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNIPI PDVFGQIFSG
251  AFKFDAAAGG LLGGLISQTM MMGIKRGlys NEAGMGSAPN AAAAAEVKHP
301  VSQGMQMLG VFVDTIIVCS CTAFIILIIY QPYGDLSGAA LTQAAIVSQV
351  GQWGAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401  WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYTAKL
451  KMGKDPEFKL SEHPGLKRRI KSDVW*

```

m513/a513 100.0% identity in 191 aa overlap

```

m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
|||||
a513
260 270 280 290 300 310
DAAAGLLGGLISQTM MMGIKRGlys NEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

40 50 60 70 80 90
m513.pep
TIIVCSCTAFIILIIYQPYGDLSGAALTQAAIVSQVGQWAGFLAVILFMFAFSTVIGNY
|||||
a513
320 330 340 350 360 370
TIIVCSCTAFIILIIYQPYGDLSGAALTQAAIVSQVGQWAGFLAVILFMFAFSTVIGNY

100 110 120 130 140 150
m513.pep
AYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMADMMGIMAWINLVAILL
|||||
a513
380 390 400 410 420 430
AYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMADMMGIMAWINLVAILL

160 170 180 190
m513.pep
LSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX
|||||

```

767

```

1  ..GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51  GGIEEDGVAA CRDAAAESA QSAAGGGLTD GFGAVHIRMA AGGIVPVVAL
101 HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151 LVQGGFLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201 AGDVGDFDGL VLQGFGEVVG STGAFAFAD VNGNVQRLVL LELDLXDXAQ
251 PHADALSQXF AEIGFGGGCA RRFCQVERAA AEVEEFGSGV VEQHRNLSXX
301 CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

m515/g515

```

                                10      20      30
m515.pep                      GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                ::|  |||||
g515                          AEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m515.pep                      VERAAGECADEVSDKTARNGGIEEDGVAAACRDA'AAESAQSAAGGGLTDGFGAVHIRMAA
                                |||||: |||||
g515                          VERAAGECADEVSDQPARNGGIEEDGVAAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
                                90     100     110     120     130     140

                                100     110     120     130     140     150
m515.pep                      GGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
                                |||||: |||||
g515                          GGIVPVVALHSVFVGGDDAAGNAVVRALPVCCKTVGVAVNVLSGLHRRAFGVFDAVR
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m515.pep                      VQGGFLFALFCQADGGXRIQIPFVVKVGVAADVCHQTGIGKSGATVFGGVAGDVGDFDGV
                                || |||||: || |||||
g515                          VQRCLFALFCQADGGFRIQIPFVVKVGVAADVLRHQLGVGKSGATVFGGVAGDVGGGADGV
                                210     220     230     240     250     260

                                220     230     240     250     260     270
m515.pep                      LQGFGEVVGSTGAFAFADVNGNVQRLVLELDLXDXAQPHADALSQXFAEIGFGGGCAR
                                ||: ||||: |||||
g515                          AQGLFGEVVGAGAAFAFADVNGNVQRFVLELDLDFDAQAHADALSERFAEVFGGGRAR
                                270     280     290     300     310     320

                                280     290     300
m515.pep                      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAF
                                |||||: ||
g515                          CFCQVERAAAEVEEFGSGVVEQHNNLSWWSVVAF
                                330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

a515.seq

```

1  ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCCT CCGCATCAAA
151 ATAGCTGCTG CCGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAACCGTA GGTGTTGCCG

```


769

```

51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCCGCCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGGGC GGTGTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCGTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGG
551 TAAACGTATT GGTAGTGTCG GGTGTGACCG GCCGCGCCTT CGGAGTTTTC
601 GATGCGGCTG TCCGTGTCCA ACGCTGCGCT TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGCGGTG TGGCGGGCGA TGTGCGGCGC GCGCGGACG GTGTGCGGCA
801 GGCCTTGTTC GGAGAAGTCG GCGGTGCGCG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGATTGTGCC TGCTGGAACG CGATTGTGTC
901 GATTTCGCCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCGCTGAAGT
951 CCGCTTCGGC GCGGTGCGC CCCGCTGCTT TTGCCAAGTC GAGCGTGGG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTTCTTGGT GGAGCGTTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNVNLNHEA RRGNTFRIK
51  IAAAEERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERRA GECADSVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVAVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFLVLELDF
301 DFAQAHADAL SERFAEVGFG GGRARCFQVQ ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVAFF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGGGC GGTGTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGG
551 TAAACGTATT GGTAAATGGC GGTGTGACCG GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCGCGGTG TGGCGGGCGA TGTGATGCGC GGCTTTGACG GTGTCTTGCA
801 GGGCTTTTTC GGAGAAGTCG GCAGTACTGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTCC TGCTGGAACG CGATTGTGTC
901 GATTTCGCCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEIEA FDNVNLNHEA RCGNNAFRK
51  IAAAEERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERRA GECADSVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHVAVVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGGF FALFCQADGG FRIQIPFVVK VGVADVFCQV TGIKSGATV
251 FGGVAGDVVG GFDGVLQGF GEVGTGAAG AFADVNGNVQ RLVLELDF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

```

          10      20      30      40      50      60
g515-1.pep  MVQIQVVRAAGVARGLHSEFARAVTAEIEAFDNVNLNHEARRGGNTFRIKIAAAERAGDV
            |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m515-1      MVQIQVVRAAGVARGLHTEFARAVTAEIEAFDNVNLNHEARCGNNAFRIKIAAAERAGDV
          10      20      30      40      50      60

```

g516.seq

1	atgttggttc	gtaaaacgac	cgccgcggtt	ttggcggcaa	ccctgatact
51	gaacggtgt	acgatgatgt	tgcgggggat	gaacaacccg	gtcagcctaaa
101	caatcacccg	caaacacggt	gacaaagacc	aaatccgcgc	cttcggtgtg
151	gttgccgaag	acaaatgccca	attggaaaag	ggcagctcgg	tgatgatggg
201	cgggaaatac	gtgttcgcgc	tcaatcccca	agatccgcgc	aagctgacgg
251	gccttttgaa	ggccgggttg	gacaagccct	tccaaatagt	tgaggatacc
301	ccgagctatg	cccgccacca	agccttcgcg	gtcaaatctg	aagcgcccg
351	cagccagatc	ttcagtagcc	gaggtctttg	cctgcgctat	gataccggca
401	gacctgacga	catcgccaag	ctgaaacacg	ttgattttaa	agcggtcaaa
451	ctcgacaatc	ggaccattta	cagcgcgtgc	gtatccgcga	aaggcaataa
501	ctacgccacg	ccgcaaaaac	tgaacgcgca	ttatcatttt	gagcaaatgt
551	tgccgcgcga	tatttattat	acggttactg	aaaaacatac	cgacaatatc
601	aagctgtttg	gaaatatctt	atatacgccc	cccttgttga	tattggatgc
651	ggcgcgcgcg	gtgctggctc	tgcctatggc	tctgatttga	gccgcgaatt
701	ccctgacaaa	atga			

q516.ppt

1	MLFRKTTAAV	LAATLILNGC	TMMLRGMNPN	VSQITIRKHV	DKDQIRAFGV
51	VAEDNAQLEK	GSLVMMGGKY	WFAVNPEDSA	KLTLGLKAGL	DKFPQIVEDT
101	PSYARHQALP	VKFEAGQSQN	FTSGGLCLRY	DTGRPPDIAK	LKQLEFKAVK
151	LDNRHTIYTRC	VSAAKPGYSAT	PQKLNPADYHF	EQSPADPIYY	TVTEKHTDKS
201	KLFGNIYLYTP	PLILDLAAAA	VLVLPMALIA	AANSSDK*	

m516.seq

1	ATGTTGTTCC	GTA AACGAC	CGCCGCCGTT	TTGGCGGCAA	CCTTGATGCT
51	GAACGGCTGT	ACGTTGATGT	TGTGGGGAAT	GAACAACCCG	GT CAGCGAAA
101	CAATCACCCG	CAAAACGCTT	GACAAAGACC	AAATCCGCGC	CTTCGGTGTG
151	GTGCGCGAAG	ACAATGCCCA	ATTGGA AAA	GGCAGCCTGG	TGATGATGGG
201	CGAAAATATC	TGTTTCGTGC	TCAATCCCGA	AGATTCCGGC	AAGCTGACGG
251	GCATTTTGAA	GGCAGGGCTG	GACAAACCCT	TCCAAATAGT	TGAGGATACC
301	CCGAGCTATG	CTCGCCACCA	AGCCTTCGCG	GTCAA ACTG	AATCGCCTGG
351	CAGCCAGAAT	TTCAGTACCG	AAGGCCTTTG	CCTGCGCTAC	GATACCGCAA
401	AGCCTGCCGA	CATGCCCAAG	CTGAACACG	TCGGGTTTGA	AGCGCTCAAA
451	CTCGACAATC	GACCAATTTA	CACGCGCTGC	GTATCCGCCA	AAGGCAATAA

773

```

1  MLFRKTTAAV LAATLM1GC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFFVNPEDSA KLTGILKAGL DKQFQMVPEPN
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIACL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVADIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDVAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

              10      20      30      40      50      60
m516.pep      MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHV1DKDQIRAFGVVAEDNAQLEK
              10      20      30      40      50      60
a516           MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHV1DKDQIRAFGVVAEDNAQLEK
              10      20      30      40      50      60

              70      80      90      100     110     120
m516.pep      GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN
              70      80      90      100     110     120
a516           GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKQFQMVPEPNRFA-YQALPVKLESPASQN
              70      80      90      100     110

              130     140     150     160     170     180
m516.pep      FSTEGLCLRYDTPDKPADI1AKLKQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
              130     140     150     160     170     180
a516           FSTEGLCLRYDTPDRPADI1AKLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
120           130     140     150     160     170

              190     200     210     220     230     239
m516.pep      EQSVADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARKX
              190     200     210     220     230     239
a516           EQSVADIYYTVTKKHTDKSKLFENIAYTPTTLILDVAVGAVLALPVAALIAATNSSDKX
180           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1  atgcatacggg ttccagacgg cattggagtg tcagtcgtgt tctgccgatt
51  cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcacg
151 tgcgtctttc aatcccgaatt tgatgttttt gggcaggtcg atttggtctg
201 tgcgcgccgt aatgacggct ttcgcgccga agccgatgag ggtcaggaac
251 attttcattt gttcgggctt ggtgttttgc gcttcgtcga ggatgatgta
301 tgcgcgcgtt agcgtcctgc cgcgcataata ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagagggcat cataaagcgg acggaggttag gggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.pep
1  MHRVSDGIGV SVVFCRFVGF DDFLHQRM1PD NVFAGEGMEI QSCHAVQFLT
51  CVFQSRFDVF GQVDLAGVAG NDGFRAEADA Q1QEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGLIKR TEVGVD1FLGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1  ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51  CGTAGGCTTC GACGATTTT1T TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGGAATA CAGCCCTTCC ACGTTGTGCA GTTTCTCACG
151 CGCATCTTTT AATCCC1GATT TGATGTTTTT GGGCAGGTGCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAAGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GCGGAGCGGG GCGATTTC1CAA
351 TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

775

	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
	: : : : :					
a517	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGRPHX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1   atgacgtttt cggcggcaaa gctcaacatt tcggcactga tgttgtgtct
51  ttcggcagga atgaccgttt tactttccgc ttttttactg ctccgaccgg
101 aaggcagcat cttattcaac catTTTTTca gcataaatat tctgaccoga
151 agagcggcat ctccacgggc aaccgtgttc agactgcata aggcggtacg
201 attccacaag atgccgaaaa ccataagcaa aatgcgtaga aactacgccg
251 tccgaatcac gccgcctcct cggcggcaaa cgcttcatta taacagattg
301 ccccttaaaa aatcagaccc tgctttgtg g.jgagtctg aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1   MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RLHQAVRFHK MPKTISKMRN NYAVRITPPP RAATLHYNRL
101 PLKSDPAFV AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1   ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTTGTGTCT
51  TCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCA GCATAAATAT TCTGACCCGA
151 AGAGCGGCAT CTCCACAGGC AACCCTGTTT AGACGCATC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCG TAGAACTAC GCCGTCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTT TGTGGCAGAG TCTGAAATTT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1   MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPQATVF RRHQARFARC RTINKRRRNY AVRITPPSXA ATRHYNRLPS
101 AAGLVRERRR RCAVILSNR KKSDPAFVAE SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep      MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR RAASPRATVF
||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||
g518          MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR RAASPRATVF
              10      20      30      40      50      60

              70      80      90      100     110
m518.pep      RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRERRRRCVILSN
| ||| || : ||:| ||||||||| ||| |||||
g518          RLHQAVRFHKMPKTISKMRNRYAVRITPPRAATLHYNRLPL-----
              70      80      90      100

120      130
m518.pep      GRKSDPAFVAESEI
||||| |||||
g518          --KKSDPAFVAESEI
              110

```

```
m519.seq (partial)
1    TCCGTATTCG GCGGTATGGA GTTGGACAAA ACGTTTGAAG AACCGCACGA
51   AATCAACAGT ACTGTTGTGT CGGCTTTGGA CGAGCGCGCC GGGgCTTgGG
101  GTGTGAAGGT TTTGCGTTAT GAGATTAAG ACTTGGTTCC CCGCGAAGAA
151  ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAAACGCGC
201  CCGTATCGCC GAATCGAAG GTCCGTAAT CGAACAATC AACCTTGCCA
251  GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGCGCA GGCTCAGGCT
301  GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351  AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
401  TCCGTCAAAT TGCCGCGCGC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451  AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501  AAAGCAAGAT ACGTGATTA TGCCCGCAA TGTTCCGAC ATCGGCAGCC
551  TGATTCTTGC CCGTATGAAA ATTATCGACA CGAGCAAAAC CGCCAAATAA
```

```
m519.pep      (partial)
  1  ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51  ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGSQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEAYYVA AFNNLAKESN TLIMPANVAD IGLSLIAGMK IIDSSKTAK*
```

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

```

m519.pep          10          20          30
                   SVIGRMELDKTFEERDEINSTVVAALDEAA
                   |||||
g519              YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
                   90      100      110      120      130      140

m519.pep          40          50          60          70          80          90
                   GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
                   |||||
g519              GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
                   150      160      170      180      190      200

m519.pep          100         110         120         130         140         150
                   IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAEAIRQIAAALQTQGGADAV
                   |||||
g519              IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAEANRQIAAALQTQSGADAV
                   210      220      230      240      250      260

m519.pep          160         170         180         190         200
                   NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK
                   |||||
g519              NLKIAGQYVAFKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSPEAKTAK
                   270      280      290      300      310

```

```
a519.seq
1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTGTGTT TCGGCTTCAA
51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGCTTTTCCA TCGCGCCCTC AGCGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCCGCTG AAAGAAATTC CTTTAGACGT
```

779

801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTCTGCGC GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
 51 IDRVA YRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLR YEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGCTGCC GTCGCCGTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
 101 GCGGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGTTTCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCAACAGTAC TGTGTGTGCG GCTTTGGACG AGGCGGCCGG GGCCTGGGGT
 451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
 551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTGAGCGCG AAGCCGAAAT CCAACATCC GAAGGCGAGG CTCAGGCTGC
 651 GGTCAATGCG TCAATGCGG AGAAATCGC CCGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCGG AAGCCAATGC CGAAGCCATC
 751 CGTCAAAATTG CCGCCGCCCT TCAAACCCAA GCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTCTGCGC GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
 51 IDRVA YRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLR YEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS					
m519-1	MEFFIILLVAVAVFGFSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	KRARIAESEGKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					

781

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in *E. coli* as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in *E. coli*. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1   atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctggtgcc gttaataatg ccggcgatgg
101 atttaatcct gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt tttgtttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccg tgccgccgaa caattcgacc aagacatcga cgtctttacg
351 cgcgaacagt tcgaacggat cttttgacaa ggcgggcgga cgggccgatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgcccaa ggcgcgggaa atttcctctg cgttgtcccg caacacggca
501 gccgcaccgc cgccgaccgt acctaaacct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1   MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCCLP FSMAFNTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1   ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTCGCG
51  CATTTCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTTCGT TGCCGTATTC GGCAGCAGT TTTTGTGTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTGG

```

151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKYX					
a520	CLLASLCLLVSRKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCGGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC GGCGGACGGG CAGATTGGC GGGCTTTTTC
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSILTAAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGTCG GACCAGTTTCG
301 AACGGATCTT TGACAAAGGC TGCGGACGGG CAGGTTTGTG GGGCTTTTTC
351 TTTACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```


785

```

151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCTGC CCCAAACTCC
201 CGAACCGGCA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
301 CAAGCACCTG TAAATAACAG CAGACGCTCC ATTCTcgaag caGaattaag
351 cAatgaacgc aaagccctGa ctGaAGCCCA AAAAATGTTA TCACAagcac
401 gtCtGGCAAA AGGCGgcaAC AtcaaCCatc aaaAaatcaa cgcattgtaa
451 AGCAATGTTt tggacAGACA GCAAAATaTC Caagcactgc aaaGAgAATt
501 GGGACGTATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>:

g521n.pep

```

1 MKSKLPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSchSTDl
51 PPIGNYSSER YILPQTPEPA PPSNGGQAV KYKAPVKTVS KPAKSNTPPQ
101 QAPVNNRRS ILEAELSNER KALTEAQKML SQARLAKGGN INHQKINAL*
151 SNVLDQRQNI QALQRELGRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1473>:

m521.seq

```

1 ATGAAATCAA AACTCCTCTT AATCCTAATC AACTTTTCCC TGATTTCAAG
51 CCCATTGGGT GCGAATGCGG CCAAAATCTA sACCTGCACA ATCAACGGAG
101 AAACCGTTTA CAUCAsCAAG CCGTCCAAA GCTGCCACTC AACCGATTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACGCC
201 CGAACCGGTA TCATCACCGT CAAACGGCGG ACwGGTTGTC AAATATAAAG
251 CCCCGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGTCTGGC AAAGGGCGGC AACATCAACC ATCAAGAAAT AAATGCATTA
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATTCAAGCCC TGCAAAGGGA
501 ACTGGGGCGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

m521.pep

```

1 MKSKLLILILI NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSchSTDl
51 PPIGNYSSER YIPPQTPEPV SSPNGGXVV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDQRQN IQALQRELGR M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

m521/g521

	10	20	30	40	50	60
m521.pep	MKSKLLILILINFLISSPLGANAAKIXTCTINGETVYTXKPSKSchSTDLPPIGNYSSER					
	: : : : : : : : :					
g521	MKSKLPLILILINLSLISSPLGANAAKIYTCTINGETVYTTKPSKSchSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRSILETELSNE					
	: : : : : : : : :					
g521	YILPQTPEPAPSPSNGGQAVKYKAPVKTVSKPAKSNTPP-QQAPVNNRRSILEAELSNE					
	70	80	90	100	110	
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDQRQNIQALQRELGRMX					
	: : : : : : : : :					
g521	RKALTEAQKMLSQARLAKGGNINHQNINALXSNVLDQRQNIQALQRELGRMX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1475>:

a521.seq

```

1 ATGAAATCAA AACTCCCTT AATCCTAATC AACTTTTCCC TGATTTCAAG

```

787

301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKMWEQP
 101 LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKQCVAD LKSE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng) from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKMWEQPLDRLSEKQIRSFGLGAQEQ					
	: : :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKMWEQPLDGLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	: : :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG
 51 CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTTGG GCATGGGTCA
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCAATG CGCGATGTCC
 151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCCTGA AGAATATTCC
 201 GTTGGCCGAA AAATGGCAA ACGATTGCG GGCCCGCGGT TTAGATTCAA
 251 ACAATACCG CTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKMWEQP
 101 LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKMWEQPLDRLSEKQIRSFGLGAQEQ					
a522	SCVKNIPFAEKWQNDLRARGLDSNNTRLTVDYCKMWEQPLDRLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120

g523 LIVRKEGNLLIIANPX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

a523.seq
1 ATGACTGTAT GGTGTGTTGC CGCTGTTCC GTCTTAATCA TCGAATTATT
51 GACGGGAACG GTTTATCTTT TGGTGTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTTGGTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

a523.pep
1 MTVWFVAAVA VLIIELLTGT VYLLVVSAA AGSGIAYGLT GSTPAAVLTA
51 ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFYR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGTVYLLVVSAAAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTVWFVAAVAVLIIELLTGTVYLLVVSAAAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFVRGTHWQAQNTGQEELEPGTRA				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTTHWQAQNTGQEELEPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIIITHPX				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

g525.seq
1 atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca
51 agcggcggtt gccgaaatgg ttcaaatcga agcgggcagc taccgcccgc
101 tttatctgaa aaaagatacc ggcctgatta aagtcaaacc gttcaaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 ccccaaatgg caaaaaggca ggatcgggtt caaacaggca gaaccgctt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggcaaatgaa aacagccggt taccaatatt tcctgggttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcctccgcc acgcagaaaa aacggctcaa acgaaccgg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaagca cgcgccgaac tactgggtg tttatgatat
551 gcacgggctg a

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

g525.pep
1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKKRLKRT
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
  1 MKFTRLLEFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

          10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
          ||::||: | |||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525       MKFTRLLEFLCAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
          10      20      30      40      50      60

          70      80      90      100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525       AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
          70      80      90      100     110     120

          130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525       AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCRQXVARTTGA
          130     140     150     160     170     180

m525.pep  FMICTGX
          |||||
a525       FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
  1 ATGAAGTACG TCCGGTTATT TTTCTCGGC ACGGCACTCG CCGGCACTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAAGACC GCCCGAACTA CTGGGGTGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAAC TGGGCTTCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
  1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRITLDWYA DGGRKGLHDV GKDRPNYWG VYDMHGLIEW TEDFNSSLLS
201 SGNANAQMFC SGASVGASDS SNYAAFLRYG IRTSLQSKYV LHNLGFRFAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
  1 ATGAAGTATG TCCGGTTATT TTTCTCGGC GCGGCACTCG CCGGCACTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

793

This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKFTRLRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AOGKRLPTID EWEFAGLASA TCKNGSNEPG
151 YNRTILDWYA DGRKDLHDV GKGRPNYWG VYDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF					
a525-1	MKFTRLRLFLCAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSPSYAPKAGELKQPVNTVSWFAANAYCA					
a525-1	AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGDLKQPVNTVSWFAANAYCA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m525-1.pep	AOGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWG					
a525-1	AOGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGDRKDLHDVGKGRPNYWG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWETEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV					
a525-1	YDMHGLIEWETEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV					
	190	200	210	220	230	240
	250					
m525-1.pep	LHNLGFRCTSRX					
a525-1	LHNLGFRCTSRX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atggttttac cagtctcctt ttttcagcct gtccagttgg cggcgggtcgc
51  gcttggtcgg tctgcccgcg ggaatggcgg aagtgatcgc gctgaattgg
101 tcgagctggt tgcactcttc cctcaatgct gccgttttcg cgtctctctc
151 atacagaagc cgcgcctcgg gtgcccggcg gcgttggtgg ttcaaacctt
201 taaccttgat tttatgggga aggggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tgggtttact gtttttgact ttcgagccgt ttacttgaac
301 cctacccagt tcgatatgct tttgcgcaag ggaacgggtc ttgaaaaaac
351 gtgccgccca aagccatttg tccagccgca tggcggaaga atcgtgcttg
401 tctttcatac gattttggtt gaaataattg aatttgtttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLPSVFFQP VLAAVALGR SAVGMGSDA AELVELFALF PQCCRFRVFF
51  IQKPRLCRA ALVVQTFNLD FMGKIERQV DNIADVYGFT VPDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTGCG
51  GCTTGGTGCG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTWTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT

```

795

	70	80	90	100	110	120
m527.pep	ALVVQTFN	DFIGKXNXASVXXI	ADVYGFTV	FDLRAVYLNPT	QFQFVLLR	KGTGLEKTCRP
			:			
a527	ALVVQTFN	LDFIGKIERQVDNI	ADVYGFTV	FDLRAVYLNPT	QFQFVLLR	KGTGLEKTCRP
	70	80	90	100	110	120

	130	140	150
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX		
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX		
	130	140	150

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaaattc gggtaataaa atatacggca acggctgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcggggtg gtatgagtgt ttgtccttgt
101 cgggctggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggccgagaga gtccgctgtc tttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatctt
251 actttttag gaaaataggg aagtttgaag cctgcgggtt ggattggcgt
301 acgcgtgacg gcaaaccttt ggttgagagg ttcaaacagg aaggtttcga
351 ctgttttgaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGGA
351 CTGCTTGGA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m528.pep	MEIRAIKYTA	MAALLAFTVAG	GCRLAGWYEC	SSLTGWCKPR	KPAAIDFWDI	GGESPPSLGD
g528	MEIRVIKYTA	AALFAFTVAG	GCRLAGWYEC	LSLWCKPR	KPAAIDFWDI	GGESPLSLED
	10	20	30	40	50	60

	70	80	90	100	110	120
m528.pep	YEIPLSDGNS	SVRANEYESA	QKSYFYRKIG	KFEXCGLDWR	TRDGKPLIET	FKQGGFDCLE
g528	YEIPLSDGNS	SVRANEYESA	QKSYFYRKIG	FEACGLDWR	TRDGKPLVER	FKQEGFDCLE
	70	80	90	100	110	120

797

```

51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGTA
351 CTGCTTGGAA AAGCAGGGGT TCGGCGCAA CGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51 GGESPPSLGD YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

          10      20      30      40      50      60
g528-1.pep MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90      100     110     120
g528-1.pep YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:
m528-1      YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90      100     110     120

          130
g528-1.pep KQGLRRNGLSERVRWX
          |||:||||| |||:
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1 ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCGCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAG AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

          10      20      30      40      50      60
a528-1.pep MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90      100     110     120
a528-1.pep YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:
m528-1      YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90      100     110     120

          130
a528-1.pep KQGLRRNGLSERVRWX
          |||:||||| |||:
m528-1      KQGLRRNGLSERVRWX
          130

```

799

```

|||||
m529 MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
      10      20      30      40      50      60
      70      80      90      100     110     120
g529.p GSGAVRAGDLEKRRTPAVQQPADAGSIEKRQRRPLRAATAANAWLVVDGKSPAEISAAFX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m529 GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLER-DGSQRWLVVDGKSPAEIWPLLK
      70      80      90      100     110
m529 AFWQENGFDIKSEEPaIGOMETEWAENRAKIPQDSLRLRLFDKVLGGIYSTGERDKFIVR
      120     130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1523>:

```

a529.seq
1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTGCGACCG CCTGATCAAA CTCGAAGTCC CACCTGATTG GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTTC GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGTGTCGC GCCTCGAGCG CGACGGGACG
301 CAACGCTGGC TCGTTGTCGA CGGCAAGTCT CATGTCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG TGCCAAAATC
451 CCCCAGACA GCTTGGCGCG CCTATTCGAC ACAGTCGGTT TGGGCGGCAT
501 CTACTCCACC GGCGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGCGCT TTCCGACATC TTCTTCGCCC ACAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTTGGGCG
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCGCACCGC GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCTTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCCGAG CCTGTGCGCA ACGGCTCGCG CATCGTCTGT
1051 CTAACAAAG ACGGCAGCGC ATATGCCGCG AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TGCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1524; ORF 529.a>:

```

a529.pep
1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAEVLKSV KGVRLERDGS
101 QRWLVVDGKS HAEIWPLLKA FWQENGFDIK SEEPaIGOME TEWAENRAKI
151 PQDSLRLRLFD TVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGKDKDQTTV WQSPSPDPNL EAAFLTRFMQ YLGVDDQQA NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRALAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPGLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELR*

```

m529/a529 99.2% identity in 375 aa overlap

```

      10      20      30      40      50      60
m529.p MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a529 MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
      10      20      30      40      50      60
      70      80      90      100     110     120
m529.p GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVVDGKSPAEIWPLLKA
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a529 GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVVDGKSHAEIWPLLKA
      70      80      90      100     110     120
      130     140     150     160     170     180

```


g530	MSASAAMTGLIWVIVSSCVMDIKVFVMLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA	60
	10 20 30 40 50 60	
m530.pep	ERAAGGRAVRICPGRIPPISVRRGWVVRTWCPKSESVGR	99
	: : : : :	
g530	ERAAGARAVRIRPRRIPPISVRRDWVVRTWCRCSESAGR	99

```
a530.seq
1   ATGAGTGCGA  GCGCGGCAAT  GACGGGTTTG  ATATGGGTCA  TCGTGTCA TC
51  CTGTGTGATG  GATATTAAAG  TGTTTGTTGC  GTTATGCGGT  CGGAACGTT
101 CGGACGGCAT  GGCTATATTT  AAAGTTGTCC  TGAGGCTTTC  AGGGCGGCGC
151 GGACTTTTGC  CTGTCCGCCT  TCCGTCAGCG  GAACGAGCCG  CAGGCGGACG
201 TGTGGTTTCG  ATCTGCCCAT  GCGGATACCC  GCCCATTTCC  GTGCGGCGGG
251 GCTGGGTTCC  CAGAACCATG  TGTGCTAAAT  CGGAATCAGC  CGGTGTTGA
```

a530.pep

```
1  MSASAAMTGL IWVIIVSSCVM DIKVFVALCR PNGSDGMAIF KVLRLSGRR
51 GLLPVLRLPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESAGR*
```

	10	20	30	40	50	60
m530.pep	XSASAAMTGLIWVIVSSCVM	DIKVXVAXCRPNGSDGMXI	FKVVLRLSGRRGLLXVRFP	S A		
a530	MSASAAMTGLIWVIVSSCVM	DIKVFALCRPNGSDGMAI	EKKVVLRLSGRRGLLPVRLP	S A		
	10	20	30	40	50	60
	70	80	90	100		
m530.pep	ERAAGGRAVRICPGRIPIPIS	VRRGWVRTWC RKSES VGRX				
a530	ERAAGGRAVRICPGRIPIPIS	VRRGWVRTWC RKSESAGR X				
	70	80	90	100		

```
g531.seq
  1  ATGACCGCCC  TACTCGTCAT  CCTCGCCCTC  GCCCTGATAG  CCGTCGGCAC
51  GGCAGGCATC  GTCTATCCCG  CCCTGCCCCG  CTGGCATTG   ATGTTTGC CG
101 GAACATGGCT  GCTTGCCTAT  GCCGGCGGCT  ATCAAATCTA  CGGCGCAGGC
151 ATCTTGTGGA  CGGTCCGACT  CATCAGCCTT  GCGCGCATAC  TGCGCGACTA
201 TATGGCAGGC  ATGTTGGGGG  TAAATAACAC  TGGGGCAGCG  AAATCGCCGC
251 TCCGAGGTGC  ATTGCCCGGC  AGCATCATCG  GCATATTTTT  CTCCTTCCC
301 GGACTAATAC  TCGGCCCTT  TATCGGCGCG  GCGGCAGGCG  AACTGATCGA
351 TCGGCGCAAT  ATGCTTCAGG  CAGGTAAAGC  GGGCTTGGGT  ACGCTGTTGG
401 GGCTTGTCTG  CGGCACGGCG  TTCAAAATCG  CTGCGCCGGT  ATCCATCTTG
451 TTTATCCTGT  TGGTGAATA  CATCGCATAC  CTGTTTTAA
```

g531.pep

1	<u>MTALLVILAL</u>	<u>ALIAVGTAGI</u>	<u>VYPALPGLAL</u>	<u>MFACTWLLAY</u>	<u>AGGYQIYGAG</u>
51	<u>ILWTVGLISL</u>	<u>GGILADYMG</u>	<u>MLGVKYTAG</u>	<u>KLAVRGALAG</u>	<u>SIIGIFSLLP</u>
101	<u>GLILGPFFIGA</u>	<u>AAGELIDRRN</u>	<u>MLQAGKAGLG</u>	<u>TLLGLVVGTA</u>	<u>FKIGCAVSIL</u>
151	<u>FILLVKYIAY</u>	<u>LF</u>			

m531.seq

```
1  ATGACCGTAC  TGACCGTCAT  CCTCGCCCTC  GCCCTGATAG  CCGTCGGCAC
51  GGCGGGCATC  GTTTACCCCG  CCCTGCCCGG  ATTGGCATTG  ATGTTTGGCG
101 GAACATGGCT  GCTTGCCAT  GCCGGCGGCT  ACCAAATCTA  CGGCGCGGGC
151 TGTTTGTGGA  CGGTGCGACT  CATCAGCCTT  GCCGGCATA  TGCGGGACTA
201 TTTGGCAGC  ATATGGGGGA  CAAAATATA  CGGAGCGGGC  AAGCTCGCCG
251 TTCGCGGCG  ATTGCGCGC  AGCATCATCG  GCATATTTT  TCCTCTTCCC
301 GGAATAATAC  TCGGTCCCTT  TATCGGCGCG  GCGGCAGGCG  AACTGATCGA
```

803

```

|||||
a531      AGILADYVAGIWGTYGTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN
              70      80      90      100      110      120

              130      140      150      160
m531.pep   MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
              |||||:|||||
a531      MLQAGKAGLGTLLGLIVGTAFAKIGCAVSILFILLVKYIAYLFX
              130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acaggcggat tcgcctgatt tgggtgtacgg
51  tttggaagac aggccgccgt tcggtaatgc gctcttgagc gcggttaccc
101 atcttttggc gattttcgtg ccgatgatta cgcgcgcgt gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgatctcgg tgctcgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggtaaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGSVGSGML SIQRYRHDC
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTGCGTTC GGGGATGCTG TCCATCCAGT CGGTGAATTT TTCGTTGTTT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATCGCATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGGCATT ACCGATTTCG GCGGCGGCTT CGGCGCGAAG GCGGACGGCA
551 CGTTGCGCTC GATGAAAAAC TTGGGCGTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCG CTGTTGCGCA TGAGCGGCAT
651 TGCGGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTTAAATACG GTTTTGCTTT CACTGGCAC GCGTTTATG TGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGCGCGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCTG
901 CGCGGCGGCG TGTTGGCTGA CGGCTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTACAG
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTG
1051 GTGCTGTGTT GTCTGTTCCC CGTTGTCGGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTGCGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTGCG CGTTTGAGCC
1251 GGAAGTGTGTT AAAAACCTGC CCGTCTGTG CCAAACTCT ATTCCGCGC
1301 GCGGCATTAC GGCAGTCTTG CTGAATTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGVPVSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVF GAFVLCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```

805

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVVL IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
251 FKYGFAFDWH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEYTKRL
301 RGGVLADGLV SVIATLGS LPLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGFMVLMFG LIAIAGVRIL VSHGIRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

```

          10      20      30      40      50      60
m532.pep  MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
a532      MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
          10      20      30      40      50      60

          70      80      90     100     110     120
m532.pep  AYLVSAMVASGVGTYLQVNRFGPVGSGMLSISQSVNFSFVTVMIALGAGMKEGGLTKDAM
a532      AYLVSAMVASGVGTYLQVNRFGPVGSGMLSISQSVNFSFVTVMIALGAGMKEGGLTKDAM
          70      80      90     100     110     120

          130     140     150     160     170     180
m532.pep  ISTLLGVSVFVGAFLVCFSAWLLPYLKKVITPTVSGVVVVLIGLSLVHVGITDFGGGFGAK
a532      ISTLLGVSVFVGAFLVCFSAWLLPYLKKVITPTVSGVVVVLIGLSLVHVGITDFGGGFGAK
          130     140     150     160     170     180

          190     200     210     220     230     240
m532.pep  ADGTFGSMENLGLASLVLLIVLVFNCMKNP LLRMSGIAVGLIAGYIVALFLGKVDFSALQ
a532      ADGTFGSMENLGLASLVLLIVLVFNCMKNP LLRMSGIAVGLIAGYIVALFLGKVDFSALQ
          190     200     210     220     230     240

          250     260     270     280     290     300
m532.pep  NLPLVTLVPVPFKYGFADFWDHAFIVAGAI FL LSVFEAVGDLTATAMVSDQPIEGEYTKRL
a532      NLPLVTLVPVPFKYGFADFWDHAFIVAGAI FL LSVFEAVGDLTATAMVSDQPIEGEYTKRL
          250     260     270     280     290     300

          310     320     330     340     350     360
m532.pep  RGGVLADGLVSVIATLGS LPLTTFAQNNGVIQMTGVASR HVGKYIAVILVLLGLFPVVG
a532      RGGVLADGLVSVIATLGS LPLTTFAQNNGVIQMTGVASR HVGKYIAVILVLLGLFPVVG
          310     320     330     340     350     360

          370     380     390     400     410     420
m532.pep  RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF
a532      RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF
          370     380     390     400     410     420

          430     440     450     460
m532.pep  KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX
a532      KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX
          430     440     450     460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

g535.seq

```

1  atgccctttc ccgttttcag acaantattt gcttngtcc tgetacggtt
51  ttttgccgta ggtcggattc tcgaatccga catttccaac agcggttttt
101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatattaca tcgcttccaa ttctgcaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagttga tggtcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttgcggc tgtttgaagt

```

807

Following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1547>:

This corresponds to the amino acid sequence <SEQ ID 1548; ORF 535.a>:

m535/a535 88.7% identity in 256 aa overlap

[illegible]

```

301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
451 CTTTCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

```

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

```

m537.pep (partial)
1 MKSLFIRLLL LGSAAGVFIH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN
51 RIRAQIGLHK LAHAPVLENS ARRHASVLTN NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
151 LSLDRHTDE SGAA...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

```

m537/g537

      10      20      30      40      50      60
m537.pep MKSLFIRLLL LGSAAGVFIHTQXQSLPAGELVYPSAPQIRDGGDALHYLNRIHQIGLHK
||||| ||||||| ||||||| ||||||| ||||||| |||||||
g537      MKSLFIWLLL LGSAAGVFIHTQNQSLPAGELVYPSAPQIRDGGDALHYLNRIHQIGLHA
      10      20      30      40      50      60

      70      80      90     100     110     120
m537.pep LAHAPVLENSARRHASVLTNPNEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
||||| ||||||| ||||||| ||||||| ||||||| |||||||
g537      LAHAPVLENSARRHARYLTNPNEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
      70      80      90     100     110     120

      130     140     150     160
m537.pep TEEEAESSDSDIRTQQRQVGLMSAIYHRLSLDRHTDESGAA
||||| ||||||| ||||||| |||||||
g537      TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAVRENGKTVLVFNQGN
      130     140     150     160     170     180

g537      GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE
      190     200     210     220     230     240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

```

a537.seq
1 ATGAAATCCC TTTTATTCG GCTGCTCTG TTGGGTTCGG CGGCCGGCGT
51 TTTCTATCAT ACCCAAACCC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGCG CCCAAATCGG TTGACACAAG CTGGCACACG CGCCGGTTTT
201 GGAAATTCG GCCCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
451 CTTTCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGTGCG
501 CGAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG
551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
601 TACCGCAACG CCGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT
651 GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC
701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
751 ACGGGCAATC CTGCCAGCAT TGATTTTTCG GAGGCGGCAG GCAAAATATC
801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCGTCA
851 GGGTTTTTAA CGCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACCGC
951 GGTATTTCGAT TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
1001 TTAGAACCCG AAAACCCGAT TACCTTATT TTGAGGTAAA CGGCGGCGAG
1051 AACTTGGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GGCGCGGACG
1101 CTGGTGTTTG GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

```

q538.pcp

1	MSGRTGRNSA	TQAQPERVML	VGVLMDKDDT	GSNAARLNGF	QTALAEAVEL
51	VKAAGGDSVR	VETAKRDRPH	TALFVGTGKA	AELSEAVAQ	GIDLVVFNHE
101	LTPTQERNLE	KILQCRVLDR	VLGLIAIFAR	RARTOEGRLQ	VELAQGLSLHA
151	GLRLIRGYGHL	QSQRGGIGMK	GPGETKLETD	RRLTAHRINA	LKQLQLANLKK
201	QRALRRKSRE	SGRIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDQLFATLD
251	TTARRLYISP	ACSIDLTDTV	GFVSDLPHLK	ISAFSATLEE	TVQADVLLHV
301	VDAAARNSSGQ	QIEDVENVLQ	EIHADHDPIC	KVYNKTDLLP	SEBQNTGIWR
351	DAAGKIAA VR	ISVAENTGID	ALREAIAYEC	AAAPNTDETE	MP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

m538.seq

1	ATGACAGGCA	GAACAGGCGG	CAACGGCAGT	ACCCAAGCGC	AACCCGAACG
51	CGTCATGCTG	GTGGGCGTAA	TGTTGGACAA	AGATGGTAGC	GGCAGTAGTG
101	CCGCCCTCT	GAACGGTTTT	CAGACGGCAT	TGGCGGAAGC	TGTCGAGCTG
151	GTCAAAGCGG	CGGGCGGCGA	TTCCGTGCGC	TGGGAGACTG	CNAAACGCGA
201	CGGTCCGACC	ACCCGCGTGT	TTGTGCGCAC	GGGCAAGGCG	CGGGAGCTGT
251	CAGAAGCAGT	TGCCGCAGAC	GGCATCGATT	TGGTCGTATT	CAACCACGAA
301	CTCACGCCCA	CGCAGGAACT	CAACCTTGAA	AAAGAACTSA	AATGCCCGCT
351	ATTGGACAGG	GTAGGGGCTG	TTCTGGCGAT	TTTCGCTCGC	CGCGCCCGCA
401	CGCAGGAAGG	CAGGCTGCAA	GTCGAGTTGG	CCTCAATTGAG	CATTATTGGC
451	GGACGCTTCA	TACGCGGTTA	CGGCCATCTG	CAGAGCCAGC	CGCGCGGTAT
501	CGGCATGAAA	GGCCCCGGCG	AAACCAAAC	GGAACCGAC	CGCCGATTGA
551	TCGCCCATCG	GATCAATGCC	TTGATAAAAC	AGCTTGCCAA	CCTCAAAAAA
601	CAGCGCGCCC	TGCGCCGCAA	GTCnCGGAA	TCGGGCACAA	TCAAACCGTT
651	TGCGCTGCTG	GGCTATACAA	ATGTCGGAAA	ATCAGCCCTG	TTCAACCGCG
701	TGACAAAGTC	GGGCATATAT	GCAAAGGACA	AGCTTAGTCC	CGAATGCAGC
751	ATTATCCTGA	CCGATACCGT	CGGATTGCTn	AGGCATCTCG	CGCAcAAACT
801	GATTTCGCCG	TTTTCTgCC .A	CGCTGGAAGA	AACCGCGCAA	GCCGATGTGC
851	TGCTGTCAGT	GCTGTAGTCC	CGCGCTCCGA	CACAGCGGACA	CGAGATTGAA
901	CACGTGAAAA	ACGTACTGCA	AGAAATCCAT	GCCGGCGATA	TTCCTGTCAT
951	cAAGGTGTAC	AACAAAACCG	ACCTGCTGCC	GTCTGAAGAA	CAAAACACGG
1001	GCATATGGCG	CGACGCTGCG	GGAAAAATTG	CCGCGCTCCG	CATTTCCGTT
1051	GCTGAAAAAT	CCGGTATAGA	CGCAATCGCG	GAAAGcATTG	CCGAGTCTTG
1101	TGCCGCCCGA	CAAAACACAG	ACGAAACCGA	AATGCCATGA	

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

m538 . pep

1	MTGRTGGNGS	TQAQPERVML	GVMLDKDGT	GSSAARLNGF	QTALAEAVEL
51	VKAAGGDSVR	VETAKRDRPH	TALFVGTGKA	AELSEAVAAD	GIDLVPVFNHE
101	LTPTQERNLE	KELKRCVLDR	VGILIAIFAR	RARTQEGRLQ	VELAQLSHLA
151	GLRTFGYGH	LQSQRRGGMK	GPGETKLETD	RRLIAHRINA	LILQLANLKK
201	QRALRRKSRE	SGTIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDKLSPECS
251	IILDTVGFV	SDLPHKLISA	FSXTLLEATA	ADVLHVVDAA	AAPNSGQQIE
301	DVENVLQDEI	HAGDIPCIKY	NKTDLLPSEE	QNTGIWRDAA	GKIAAVRISV
351	AENTGIDALR	EAIAESCAAA	PKTDTEMP*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng)

from *N. gonorrhoeae*:

m538/q538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTS SAARLNGFQTALAEAVELVKAAGGDSVR					
	: : :					
q538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRVLDR					
	: : : : :					
q538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRVLDR					

813

201 ORALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILDTV GFVSDLPHKL ISAFSATLEE TAQADVLLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVM LDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
a538	MTGRTGRNGSTQAQPERVMLVGVM LDKDGTGSSATRLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHETPTQERNLEKELKCRVLDR					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHETPTQERNLEKILQCRVLDR					
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHETPTQERNLEKELKCRVLDR					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHETPTQERNLEKILQCRVLDR					
	70	80	90	100	110	120
m538.pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
a538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
a538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
a538	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
a538	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
m538.pep	AKDKL-----SPECSIILDTVGFVSDLPHKLISAFSXTLEETAQADVLLHV					
	:					
a538	AKDQLFATLDTTARRLYISPECSIILDTVGFVSDLPHKLISAFSATLEETAQADVLLHV					
	250	260	270	280	290	300
m538.pep	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVNKTDLLPSEEQNTGIWRDAAGKIAAVR					
a538	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
m538.pep	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVNKTDLLPSEEQNTGIWRDAAGKIAAVR					
a538	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
a538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

1	atggaggatc	tgcaggaaat	cgggttcgat	gtcgccgccg	taaaggtagg
51	tcggcagcgc	gaacatcatc	gtctgcatca	tacccagtcc	ggcaacggca
101	aggcggacga	tgtattgttt	gcgttccttt	tggttgccgg	cttcgatttt
151	ttgcgcgtca	tagggtgcgg	cgggtgtagc	tgtctgccgg	attttcaaca
201	gaatgtcggg	gaggcggatt	ttgccgtcgt	cccagacgac	gcggcagcgg
251	tgcgtgctgt	aattgaggtc	gatgcggacg	atgccgtctg	tgcgcaaaag
301	ctgctgttcg	atcagccaga	cgcaggcggc	gcaggtaatg	ccgctgagca
351	tcagcactgc	ttcgtgcgtg	ccattatggg	ttccacaaa	gtcggattgg
401	acttcgggca	ggcgtacag	gcggatttgg	tcgaggattt	cttcggggcgg
451	cagttcgggt	tttttcgcgt	cggcgggtcg	tcgtttgtaa	taactgcccc
501	agccggaatc	gatgatgctt	tgtgcgactg	cctgacagcc	gacgcagcag
551	gttttcgggt	cttcgccttc	gtacgggacg	gtcagatgca	ggttttcggg
601	aacgtccagc	ccgcagtggg	aacagggttt	tttcatggca	tttcgggtttc

815

	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAGVGFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGFHKVGLDFGQVVQADLVEDFLGRQFGFFRVGGASFVITAQAGIDDALCDCLTA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGFVAFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
g539	DAAGFAVFAFVADGQMVFQVGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSSTFSTSSICCPFLGA					
g539	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISWAWISCSSTFSTSSICCPFLRA					
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRRAVVSRAKS					
	310	320	330	340	350	360
g539	WSFAYMPDLVSRLNRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCCGCCCGG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTCTCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGCTGCGG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCAGACA
351 TTAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCTGACAG GCGGATTTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTTGCGCGT CGGCGGTGCG TTGTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GCGCAGCAG
551 GTTTCGCGGT CTTCGTTTTC GTAACGGACG GTCAGATGCA GGTTCGCGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTTT TTTTCATGGC TTTTCGGTTT
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTT
751 CCCGCGCGT CGCGCCATAT GCCCGTGTTC TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CCGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTGAGGATA ATGCTGCATT CCGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GGCAGAAAAG TGGTCTTTCG CATATATGCC
1101 CGACTTGGTC AGCCGTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIFD VAAVKVGRQR EHHRLHHFQP GNGEADDVLF AFFLVGGFDF

```



```
m540.seq (partial)
1 ..CCGAACCCGA TGCCGCTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTGT
51 CCACCCGGAT GGGGGCAGTG TCGTATTGTG TCGATTCTGC CCGCTAATAC
101 AGCAGCCCGA GTTTGATGGG GATTCTGCCC TGTGATTGTC TGTGGGCATT
151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCCTGC TGGTAGAAGT
201 TTTTCAGTTT GCTGATTTC AATCATGCGC CGTGCCCGGC GCCTTTGCGC
251 CAGTTGAAAT CCCAATACAC CACATCATCG TAAGCGCGCG CGGC GCGGTG
301 TCCGCAGTCG TTGATTTCGC CCATATTTT CCAGCGTGA
```

```
m540.pep      (partial)
1      .PNPMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL*FAVGI
51     GIPQGIGTTA IFLLVEVFTF ADFNHARAAA AFAPVEIPIH HIIVRRGGAV
101    SAVVDLRHIF PA*
```

```

m540/g540
                                     10      20      30
m540.pep                          PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                                     |||
g540      GNGVFYQNGKLANAVSACRLPNRQTFPVVPVNPMPSEPSDGIGCLFVHSDGCRFVLCRFV
               10      20      30      40      50      60

               40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFVAVGIGIPQGIGTTAIFLLVEVFTTFADFNHARAAAAFAPVEIPIH
               |||
g540      AVIQHAEFDGDASLRFVAVGVGIAQGIRAAVFLLVFVFAFADFNFHTRAAAFAPVEVPIG
               70      80      90      100     110     120

               100     110
m540.pep      HIIVRRGGAVSAVVDLRHIFPAX
               |||
g540      HIIVRRGGTVSAVVDLRHIFPAX
               130     140

```

```
a540.seq
1  ATGCCGTCCT CCCGACGCGG CAACGGGGTG TTTTATCAAA ACGGCAAAC
51  TGCCAATGCG GTTTCGATT GCAGATTGCC AAACCGGCAA ACCTTTCCCG
101 TGCCGATGCC GAACCCGATG CCGTCTGAAC CTTACAGACG CATCGGGTGT
151 TTATTGTGCC ACCCGGATGG GTGCAGGTTT GTATTGTGTC GATTCGTGCG
201 CGTAATACAG CACGCCGAGT TTGATGGGGA TTCTGCCCTG TGATTGCGG
251 TGGGCGTTGG AATCCCTCAG GGAATAGGCA CAACCGCAAT ATTCTGCTG
301 GTAGAAGTTT TCACGTTTGC TGATTTCATC CATACGCGCG CTGCCGCCGC
351 CTTTCGCGCA GTTGAATACC CAATACACCA CATCATCGTA AGCGCGGCG
401 GCGCGGCGCG CGCATGCGTT AATCTGGTTC ATGTTTTTCC A
```

a540.pep (partial)

```
1  MPSSRRNGV FYQNGLANA VSDCLRLNQR TFPVMPNPM PSEPSDGIGC
51  LFVHPDGCRF VLCRFVAVIQ HAEFDGDSAL *FAVGVGIPQ GIGTTAIFLL
101 VFTTFADFN HTRAAAFAP VEIPIHHIIV RRGAAAAAVV NLVHVEP
```

819

```

|||||
g542      ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```

a542.seq
1  ATGCCGAAAT GGTGCGCAT ACGGCGTTGC AGCGTCCTTT CGCTGATGTT
51  CAGCGTGTCT GCCAGCCGGT TGACTTGATG TGCGCCGCCG GCAAACGCCG
101 CATTCAAGAT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG GCGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTT
301 GGGGGCAAAT CCCATA1CCT GACCGGTTTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

```

a542.pep
1  MPKWSRIRRC SVLSLMFSVS ASRLT*CAPF ANAAFRMLK SSDGIASASA
51  VCPAAGPMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTAF RQDAAKPRRF
101 GGKSHILTGS R*

```

m542/a542 94.6% identity in 111 aa overlap

```

              10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSVSASRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
|||||
a542           MPKWSRIRRC SVLSLMFSVSASRLTXCAPANAAFRMLKSSDGIASASAVCPAAGPMPS
              10      20      30      40      50      60

              70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
|||||
a542           ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

g543.seq
1  atggtttgtc ggttatttgc cgcggttttt ggctttcaac tcggcaatca
51  gcccgtcgat gccttttggt ttgatgattt cgcgcaattg gttgcggtac
101 acggttaacca ggctcgtgcc ttcgatggcg acgttgtagg tacggtattt
151 gccgccgctt tggtaggtgg taaagtccat attgacgggc ttctgaccgg
201 ggatgccgac ttcggcacgg acgacgattt ctttgccgcc cttattgacg
251 atgggattgt ctttgacgtt gacggtcgcg tttttgaatt tcagcatcgt
301 gccggaatag gtgcggatca gcagggtttg aaattctttg gccaacgctt
351 gtttttgccg gtccggacgc gtacgccaag ggttgccgac cgccaatgcg
401 gtcatacgtt ggaatcgaa atagggaacc gcataggctt cggcttttgg
451 gcgtgcagaa gccgcgtcgc cgcttttgag gatggcaca acctgtgtgg
501 cgcttttgcg gatttgtccc actgcgtcgg ccggggaggc aaatgccatg
551 ccgatgctca aaataccgat gcccaatgcg ctgatgaagg aggatttttt
601 cacgatgtct ttcctgaaaa tggatgtgta tgtttattct gcggcttttt
651 ccgcattgcc gccctcagcg tttttctcgg cgaagctggt catgaattta
701 ccgatcaggt tttccagaac cattgcagaa ctggttacgg agatggtgtc
751 gccggcagca aggttttccg taccgcccgc ctgctgcagc ccgatgtact
801 gttcgcccaa aagtcgccaa gtcaggattt gcgcggaaac gtcactgctg
851 aactgatact tgccgtccaa atcaaggcgc accctgcct gataggattt
901 cgggtcaagc ccgatagcgc cgacgcgcc gaccaatacg cctgcggatt
951 tgacgggggc attgaccttc aaaccgccga tgcgccgaa atcggcataa
1001 accggtgtaag tttgtccga accgccgaac ccgcgcgc ccgccacgcg
1051 gaaagcgaga aaggcaaccg ccgccgcgc gatcaagacg aacagtcgga
1101 cccaaaattc caatatgttc tttttcatta a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

```

g543.pep
1  MVCRLFAAVF GFOLGNQPVDF AFGFDDFAEL VAVHGNQARA FDGDVVGTVF

```

821

```

m543.pep      VGRGAPRVADRQCGHT1 EIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
               |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543          VGRGT130PRVADRQCGHTLEIEIGNRIGFGFWACRSRVA140AFEDGQNL150CGVLADLSHC160VGRGG170
               190      200      210      220      230      239

m543.pep      KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIA190AVGIFLGKTRHEFADK200V
               |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543          KCHADAQNTDAQCADEGGFFHDV---FPENGCVCLFCGFFRIA210ALSVFLGEAGHEFTDQV220
               190      200      210      220      230

m543.pep      FQNHCR240TGYDGVAGSKVFRVAALLQPDVLLAQKSR250SQDLRGNVAAELILAVQIEAHPRL260
               |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543          FQNHCR240TGYDGVAGSKVFRIAALLQPDVLLFAQKSR250SQDLRGNVTAEILILAVQIKAH260PRL270
               240      250      260      270      280      290

m543.pep      IGFRVKSDSADAPDQYACGFDGGIDLQ300TADVAEIGINGVSVFRTAERRTAGHAESEKGNR310
               |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543          IGFRVKPDSADAPDQYACGFDGGIDLQ300TADVAEIGINGVSVFRTAERRAARHAESEKGNR310
               300      310      320      330      340      350

m543.pep      RRANQDEQSDPKFQYVLLHX360
               |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543          RRADQDEQSDPKFQYVLFHX360
               360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543.seq
1   ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTTCCAC GCCTTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGCGCGCG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTT251TAAAT TCAGCATCGT
301 GCCGAATAG GTGCGGATCA GCAGGGTTTG AAAT301TCTTG GCCAACGCTT
351 GTTTT351TGCGC GTCGGACGCG GTGCGCCAAG GGT351TGCCAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTT401TG
451 GCGGGCGGTG TTGGCATCAC CGCTTTT451TAA GATGCTCAAT ACTT451GAGTGG
501 CGTTT501TGACG GATTG501GTTT ACCCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATT551TTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTT651TCCGC ATTGCCGCCG TCGGCATT651T TCTCGGCAAA ACTCGTCATG
701 AATT701TGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATT801TGCGC GGAAACGTCG
851 CTGCTGAACT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATT901TCGGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
951 CGGATT951TGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT1001T GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1   MAYGLLA1AVX SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGG51EVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQ101QGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITA151F* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCR201TGYD
251 GVAGSKVFRV AALLQPDVLL AQKSR251SQDLR GNVA251AEILIL VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQ301TADV AEIGINGVSF VRTAERRTAG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1587>:

MS	1	ATGAWAAAAA	TACTACCCGC	CGCCGTCGTC	GCACCTGATCG	GCATCCTCCT
	51	TGCCATCGTC	CTCmTCCCG	ACAGCAAAC	CGCGCCCGCC	TTCTCCmTGC
	101	CGGACCTGCA	CGGAAAAAC	GTTTCCAAC	CCGACCTGCA	AGGCAAAGTA
	151	ACCCTGATTA	ATTTTGTGTT	TCCCTCCTGT	CGCGGTTGTC	TGAGCGAGAT
	201	GCCCAAATC	ATTAACACGG	CAATGACTA	TAAAAWCAAA	AACTTCCAAG
	251	TACTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
	301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
	351	TGTCGGACAG	CGGTTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCCCTTATCG
	401	GCAAATAAGG	CGAAATCTTC	AAAACCTACG	TCGGCAATAC	CGATTTCCGC
	451	AAACTCTACC	AAGAAATCGA	TACGCGCGTG	CGGCAATAG	

MS44:pcp

1	<u>MXKILTA</u> AVV	<u>ALIGILLA</u> IV	<u>LXPDSK</u> TAPA	FSXPDLHGKT	VSNADLQGV
51	TLINFWFPSC	PGCVSXMPKI	IKTANDYKXK	NFQVLAVAQP	IDPIESVRQY
101	VKDYGLPFTV	MYDADKAVGQ	AFGTQVYPTS	VLIQ*GE_L	KTYVGEPDFG
151	KLYOEIDTRV	AO*			

ORF 544 shows 90.7% identity over a 162 aa overlap with a predicted ORF (ORF 544.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m544.pep	MXKILTAAVVALIGILLAIVLXPDSKTAPAFSXPDLHGKTVSNADLQGKVTLINFWFPSC					
	:					
g544	MKKILTAAAVALIGILLATVLIPDSKTAPAFSLPDLHGKTVSNADLQGKVTLINFWFPSC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVSXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
	:					
g544	PGCVSEMPKVTKTANDYKNKDFQVLAVAQPIDPIESVRQYVKDYGLPFTVIYDADKAVGQ					
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQVYPTSVLIGKKGEIFKTYVGEPDFGKLYQEIDTRVAQX					
	:					
g544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

1	ATGAAAAAAA	TACTCACCGC	CGCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCATCCCGC	ACAGCAAAAC	CGCGCCCGCT	TTCTCCCTGT
101	CCGANCTGCA	CGGAAAAANC	GTTTNCAACG	CCGACCTGCA	AGGCNAAGT
151	ANCTTGATTA	ANTTTTGTT	TCCCTCCTGT	CCGGGTTGTG	TGAGCGAAGAT
201	NCCANAATC	ATTAAAACGG	CAATGACTA	TAAAAACAAA	AAGCTTCAAG
251	TCCTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	CGGTTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCTTTATCG
401	GCAAAAAAAG	CGAAATCCTC	AAAACCTATG	TCGGCGAACC	CGATTTCCGC
451	AAACTCTACC	AAGAAATCGA	TACCGCGCTG	GCACAATAG	

```

1  MKKILTAADV ALIGILLAIV LIPDSKTAPA FLSXLHGKX VKNADLQGXV
51  XLIXFWFPSC PGCVMEMXI IKTANDYKNK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGO AFGTOVYPTS VLIQKKGEIL KTYVGFDFEG

```

825

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFLLRKYLFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFLLRKYLFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
g547	ELLTILVKNLSPNGKKRFVFCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547.seq
1  ATGTTCTAG  ATAACGGATT  TAATAAACG  GTAGCGAGTT  TTGCCCAAAT
51  CGTCGAAACT  TTCGACGTAT  TCTTCTTTAG  GAACAATTGC  ACCTTTTSTA
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGGT  ATATCTCGTT
151 GATATCTTTC  CAAGATGCGG  CTTGAGATT  CCGAACCGCT  CCTTTAAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAATG
251 CCGAAGTCGA  GATAGATGCT  CATTACTCC  CCTTACTCAG  AAAATATTTA
301 AAATTTATAA  TGTACATAT  ATTTACAAAT  ATTAAAGTTT  TTTT.TGTGT
351 GTGCGTCAAG  GAATTGTTGA  CAATTTTAGT  T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547.pep
1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNNC  TFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSFKELGL  LIQISLSERF  RTNAEVEIDA  HYFLLRKYLV
101 KFIHLHIFTN  IKVFXCVCVK  ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFLLRKYLFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFLLRKYLFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548.seq
1  atgttttccg  taccgcgttc  ctttttgccg  ggcgttttcg  taacttgccg
51  gcttgccgcc  tgcaaacctc  aagacaacag  tgcggcgcaa  gccgcttctt
101 caagtgcac  cgcgcggct  gcggaataat  cggcaaacgc  gcaaacgcgc
151 ggtacggata  tgcgtaagg  agacatcggc  ggcgatttca  cactgaccga
201 cggcgaaagg  aagcctttca  gcctgagcga  tttgaaaggc  aaggctcgtg
251 ttctgtcttt  cggctttacg  cactgtcccg  atgtctgccc  gacagggttc
```

827

```

                190      200      210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                |||
g548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTC CG TACCGCGTTC CTTTTTGCCG GCGCTTTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGGATTTCG CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTACGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCAATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTCTCTCG
601 CCTTACGGA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSLP GVFLAALAA CKPDNSAAQ VASSSASASA AENAARKPQTR
51  GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

```

                10      20      30      40      50      60
m548.pep      MFSVPRSLPGVFLAALAAACKPDNSAAQVASSSASASAENAARKQXTRGTDMRKEDIG
                |||
a548          MFSVPRSLPGVFLAALAAACKPDNSAAQVASSSASASAENAARKPQTRGTDMRKEDIG
                10      20      30      40      50      60

                70      80      90      100     110     120
m548.pep      GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTLTYSDTLKQLGGQAKDVKVV
                |||
a548          GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTLTYSDTLKQLGGQAKDVKVV
                70      80      90      100     110     120

                130     140     150     160     170     180
m548.pep      FVSIDPERDTP EIIGKYAKQFNPDFIXLTATGGQNLPIKQQYRVVSAKVNQXDDSENYL
                |||
a548          FVSIDPERDTP EIIGKYAKQFNPDFIGLTATGDQNLPIKQQYRVVSAKVNQKDDSENYL
                130     140     150     160     170     180

                190     200     210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                |||
a548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaaatgc cgcctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1   CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTGTTCAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTCGC
451 CAGCGGCGGC AGGATTTCGG GATTCGGGTT GGCCATAGCG AACACGATGG
501 GTTTTTCGTT CATGGTGTTT AGTATTTCAG GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGAGATC GCAAACGGTC
701 ACGTTTTCGC GTTTCAGGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGCGCGT AATGATGGCC
851 GTGCCGTGCT GGTCTGCTG GAATACGGGG ATTTTGCAGC GTTTCGCTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1   LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FCGSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQTAE DEREQYIVH LVREVGAAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGVEL FGLVHTVFVF AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYSGG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```

                                     10      20      30
m550.pep                               DGIGKHALAVVFNGVELFGLVHTVFVFAGL
                                     |||
a550      EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVFVFAGL
               170      180      190      200      210      220

               40      50      60      70      80      90
m550.pep      VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTGQVQYGGGGNDG
               |||
a550      VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYSGGGNDG
               230      240      250      260      270      280

               100
m550.pep      RAVLVVVEYGDFAAFAX
               |||
a550      RAVLVVVEYGDFAAFAX
               290      300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1   atgaagctga aaaccttgtt attgcccttc gccgcactg9 catttgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttggca cgttggctg9
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgcg9 aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcgttat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgtga aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcggta gtcgctcgtt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcggatc ttggactgca
```

831

```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCCTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGT GCGAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLLPF ATLALCTNAF AAPPDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTTELRLI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

```

              10      20      30      40      50      60
m552.pep      IKLKTLLLPFATLALCTNAFAAPPDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK
              |||
a552           IKLKTLLLPFATLALCTNAFAAPPDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK
              10      20      30      40      50      60

              70      80      90     100     110     120
m552.pep      ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
              |||
a552           ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
              70      80      90     100     110     120

              130     140     150     160     170     180
m552.pep      YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTTELRLIICGGKNPDAG
              |||
a552           YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTTELRLIICGGKNPDAG
              130     140     150     160     170     180

              190
m552.pep      CKQAGQVGKRHQKX
              |||
a552           CKQAGQVGKRHQKX
              190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
 51 GTGCACCAAT GCTTTTGCCG CCCCGCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTTG ATTACGCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CCGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAAGCCG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 LNIKLTLLL PFATLALCTN AFAAPPDAS LARWLDTQNF DRDIEKNMIE
 51 GFNAGFKPYA DKALAEMPEA KKDQAAEFN RYRENVKDL ITPEVKQAVR
101 NTLKNAREI YTQEEIDGMI AFYGSVPGQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTTELRL IICGGKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

m553.seq (partial)

1	ATGGATTATT	TATCAAGACT	GTCCTTTGGA	TTTAACAAA	AGCTACCTGT
51	CATTCTGCAA	ACAGAAGTTG	CTGAATGTGG	TTTAGCATGC	CTGACATCCA
101	TCTTGTCTTA	TTATGGCTTT	CACACTGATT	TAAGAACGTT	ACGCCAAAAA
151	TACACCTGT	CATTAAAGGG	CGCAAATCTT	GCAGACATCA	TGAGATTTGG
201	CAATGAAATG	AAATTAAACG	CAGCAGCTTT	CGGTTTAGAG	TTAGATGAGC
251	TGTCAAATTT	ACAATTACCC	TGCATTCTCC	ATTGGAACAT	AAACCAATTT
301	GTTGTACTTT	GTTCCATTTC	CAAAGACAGT	ATCGTCATTA	TGGACCTTGC
351	TGTCGGTATG	CGAAAAATCA	AAATGGACGA	AGTTTCACAA	AAATTCACAG
401	GGATTGCCCT	AGAATTATTC	CCCAATACCC	ATTTTGAAGA	GAAAAAAGAA
451	ACAAAGAAAA	TCAAAATATT	ATCTCTATTA	AGGGGGGG. T	CAGGCTTAAA
501	ACGCTCTTTA	ATTCAAATGC	TTTATTAGC	TATTTCTTTG	GAAGTCTTTG
551	ACATG				

m553.pep (partial)

1 MDYLSRLSFG FNKKLPVILQ TEVAECLGAC LTSILSYGYF HTDLRTLRLQK
51 YTSLSKGANL ADIMRFGNEM NLTPRALRL LDELSNLQLP CILHWNLNHF
101 VVLCSISKDS IVIMDPAVGM RKIKMDEVSQ KFTGIALELF PNTHFEKKE
151 TKKIKILSLR RGXSGLKRSI IOMLILAISS EVFAL...

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

m553/q553

	10	20	30	40	50	60
g553.pep	MDYLQNLSLGLTKKLPVILQTEVAECGLACLAAGFYGYFTDLRALRSKYCLSLKG	ENL				
	: ::			::: :	: :	
m553	MDYLSRLSFGFNKKLPVILQTEVAECGLACLT	SILSYYGPH	TDLR	TLRQKY	TL	SLKGANL
	10	20	30	40	50	60
	70	80	90	100	110	120
g553.pep	ADIVRFADDMGLTGRALRLDLDELGSLRLPCILHWDLNHFV	LVESVSDGAAVMDPASGR				
	: :: :	: ::		:	: : :	
m553	ADIMRFGNEMNLT	PRALRL	ELDEL	SNLQLPCILHWN	LNHFVVLCSISK	DSIVIMDPAVGM
	70	80	90	100	110	120
	130	140	150	160	170	180
g553.pep	RKVKTEEISRKFTGIALELWPNT	RFEAGEEKQEI	RILPMLRGISGLGR	TLFQ	LALLAAAM	
	: : :		: :	: : :	:	: : : ::
m553	RKIKMDEV	SQKFTGIALEL	FPNTHFE	EKKETKKIKI	LSLLRGXSG	LKRSLIQMLILAI
	130	140	150	160	170	180
	190	200	210	220	230	240
g553.pep	EVFAFLQNVSFKIGRGESLALIGRSGCGKSTLLDILSGNLP	PPESGKVMINGHDI	YSLPPP			
	:					
m553	EVFAL					

a553.seq

```

1   ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAAA AGCTGCCTGT
51  TATCTGCGAA ACAGAAATAT CAGAAATGCGG CTGGCATGTG CTGGCGGCTG
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
151 TAC

```

```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TCGCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAAACCGT CGCGCAGGCT TCTCTAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AACCGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1 MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTQPT PETLTAAHIV
51 IDLQSKQILS AKNINTPVEP AALTQMLTAY LVFKNMKSGN IQSEENLKIP
101 ESAWASEGSR MFVRPGDVS TDKLLKGMIA LSANDAALTL AGRLNGSIE
151 NFVQOMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFNIEQNN RNILLYRDNV VNLKAGHTE SGGYNLAVSY
251 SGNRHLVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRONGY TIAEKEIVAL ENVKRSRWQ RLWACLGTQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554 . pep	MTAHKILPVL LSIILGVSHATAASPAPNRP TVHAAPTQPT PETLTAAHIV IDLQSKQILS					
g554	MTAHKILPVL LPIILGVSHATAASPAPNRP TVHAAPTQPT PETLTAAHIV IDLQSRQTL					
	70	80	90	100	110	120
m554 . pep	AKNINTPVEP AALTQMLTAY LVFKNMKSGN IQSEENLKIP ESAWASEGSR MFVRPGDVS					
g554	AKNINTPVEP AALTQMLTAY LVFKNMKSGN IQSEENLKIP ESAWASEGSR MFVRPGDVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m554 . pep	TDKLLKGMIAL SANDAAL TLAGRLNGSIE NFVQOMNKEA RRLGMKNTVF KNPTGLSREG					
g554	TDKLLKGMIAL CANDAAAL TLADRLNGSIE NFVQOMNKEA RRLGMKNTVF KNPTGLGREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m554 . pep	QVSTAKDLALL SEALMRDFPEYYPLFSIKS FKFNIEQNN RNILLYRDNV VNLKAGHTE					
g554	QVSTAKDLSLL SEALMRDFPEYYPLFSIKS FKFNIEQNN RNILLYRDNV VNLKAGHTE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m554 . pep	SGGYNLAVSY SGNRHLVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI					

837

	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
a554	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
a554	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
a554	250	260	270	280	290	300
m554.pep	310	320	330	340	350	360
a554	310	320	330	340	350	360
m554.pep	370	380	390			
a554	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcttgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccatacctgct tgcgcgcgtc atcgtcgcgc cgctgcccgg cggttttgtt
151 tggacatccc gccgacagca acgccagttt atcgaacgtc tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcggacaa caccagaaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cacgctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKRPTR QEINQMAAQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC TCGCTTGGGC GGCCTGATT TACTGACCAC
51  CGCCGTTT TA AGCCTCATT TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAaaaaatt
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTCGCAAA AATGTTCCGT GGACGAGGCG CACGCTATGT TCAaaaaacg
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

1	atgaacaaaa	tatttccttac	tgcgcgagcc	ttggtgctgg	gcgcgtgcgg
51	tttcacctg	aaaggtgcag	acggcatttc	tccgccgtg	acctaccgga
101	gctggcacat	cgaagcgcgga	caggcatgtc	aatttccttt	ggaaacccgcg
151	ctgtatcagg	cttcgggcag	ggtggacatg	gctgccgcgcg	cgcagatgac
201	ctctgctata	gacagcgctt	cccaaaaaca	ggaaccttat	accgttacc
251	gtgcggcagt	catcaacgaa	tatcttttga	tattgacggt	tgaagcgcag
301	gtattgaaac	gcggcgagcc	ggtcggcaaa	ccgatgaccg	tgtccgtccg
351	ccgcattttg	gattatgccg	acaacgaatt	tttgggcata	caggaagaag
401	aagaaaacct	gtgggcggaa	atgcggcagg	atgttgccta	acagattgtc
451	caccgcctga	ctctttctga	qqcqaatga		

q557.pap..

1 MNKIFLTAA LVLGACGFHL KGADGISPP L TYRSHWIEGG QALQFPLETA
51 LYQASGRVDD AAG~~AQ~~MTLRI DSVSQNKETY TVTRA~~AV~~INE YLLILTVEAQ
101 VLKRGE~~PF~~VGK PMT~~SV~~RRIL DYADNEILGK QEEEE~~TL~~WAE MRQDVAEQIV
151 RRLTELKAE*

m557.seq..

1	ATGAACAAAC	TGTTTCTTAC	TGCCGCAGTG	CTGATGCTGG	GCGCGTGCGG
51	TTTCCACCTG	AAAGGTGCAG	ACGGCATTTC	TCCGCCGTG	ACCTACCGGA
101	GCTGGCATTAC	CGAAGGCGGA	CAGGCATTGC	GGTTTCCTTT	GGAAACCCGG
151	CTGTATCAGG	CTTCGGGCAG	GCTGGACGAT	GCTGCCGGCG	CGCAGATGAC
201	CCTCGGTATA	GACACGCTTT	CCCAAAACAA	GGAAACCTAC	ACCGTTACCC
251	GTGCGGCAGT	CATCAACGAA	TATCTTTTGA	TATTGACGGT	TGAAGCGCAG
301	GTATTGAAAC	GCGGCGAGCC	GGTCGGTAAA	CCGATGACCG	TGTCCGTCGG
351	CCGCGTCCTT	GCTTATGCCG	ACAACGAGAT	CTTGGGCAAA	CAGGAAGAGG
401	AAGCGGCATT	GTGGGCGGAA	ATGCGGCAGG	ATGCCGCCGA	ACAGATTGTC
451	CGCCCGCTGA	CCTTTCTGAA	GGCGGAATGA		

m557.pep..

```

1  MNKFLTAAV LMLGACGFHL KGADGISPP L TYRSHWIEGG QALRFPLETA
51 LYQASGRVDD AAGAQM LTRI DSVSQNKETY TVTRA AVINE YLLILTVEAQ
101 VLKRGE PVGK PMT VSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
151 RRLTFLKAE*

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

	10	20	30	40	50	60
m557.pep	MNKLFLTA	AVLMLGACG	FHLKGADG	ISPLTYRS	WHIEGGQAL	RFPLETALYQASGRVDD
	:	: :				
g557	MNKIFLTA	AALVLGACG	FHLKGADG	ISPLTYRS	WHIEGGQAL	QFPLETALYQASGRVDD
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQM	TLRIDSV	SQNKETY	TVTRA	AVINEY	LLILTVEAQVLKRGE
g557	AAGAQM	TLRIDSV	SQNKETY	TVTRA	AVINEY	LLILTVEAQVLKRGE
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNE	ILGKQEE	EAAALW	AEMRQD	AAEQIV	RRRLTFLKAEX
			:	:	:	:
g557	DYADNE	ILGKQEE	EETLW	AEMRQD	VAEQIV	RRRLTFLKAEX
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 164>:

841

m558.pep..
 1 MNACFFVIPT QAGIRRFIV FKRSGRILAG AGMMPLYTFSELYMFQQGTA
 51 HQAPHCVLPE RDYPPIRFYR HKQTGFNRKG MGIKSISDIX RAMPSENQSP
 101 LSDGIV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

m558/g558

	10	20	30	40	50	60
m558.pep	MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPLYTFSELYMFQQGTAHQAPHCVLPE					
	:	:	:	:	:	:
g558	MDACFFVIPAQAGIRRFIVFKRSGRILAGAGMMPLYTFSELYMLQQGTAHQAPHCVLPE					
	10	20	30	40	50	60
	70	80	90	100		
m558.pep	RDYPPIRFYRHKQTGFNRKGMGIKSISDIXRAMPSENQSPLSDGIVX					
	:	:	:	:	:	:
g558	RGCPPIRFYRYKQTGFNRKGMGIKSISDTSRAMPSENQSPLSDGIVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

a558.seq
 1 ATGAATGCTT GTTTTTTCGT CATTCCCACA CAGGCGGGAA TTCGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
 101 TGCCCTTATA TATAGTGGAT TAAATTAAAT TCAGGACAAG GCGACGAAGC
 151 CGCAGACAGT ACAATAGTA CGGCAAGGCG AGGCAACGCC GTACTGGTTT
 201 AAATTTAATC CACTATACTT TCTCCGAGCT TTATATGTTT CAACAGAGGA
 251 CGGCACATCA AGCACCGCAC TCGGTGTTGC CCGAACGAGA CTGCCCTCCG
 301 ATTAGATTCT ATCGCTATAA ACAGACGGGT TTCAACCGAA AAGGAATGGG
 351 AATGAAGTCC GTTCCGACCT CCTCTCGGCT GATGCCGTCT GAAAACCAAT
 401 CTCCACTTTC AGACGGCATT GTTTAG

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

a558.pep
 1 MNACFFVIPT QAGIRRFIV FKRSGRILAG AGMMPLYIVD *I*IRTRRRS
 51 RRQYK*YGKA RQRTGTLNLI HYTFSELYMF QORTAHQAPH CVLPERDCPP
 101 IRFYRYKQTG FNRKGMGMKS VSDTSRAMPS ENQSPLSDGI V*

m558/a558 70.2% identity in 141 aa overlap

	10	20	30			
m558.pep	MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPLY-----					
	:	:	:	:	:	:
a558	MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPLYIVDXIXIRTRRRSRQYKXYGKA					
	10	20	30	40	50	60
	40	50	60	70	80	
m558.pep	-----TFSELYMFQQGTAHQAPHCVLPERDYPPIRFYRHKQTGFNRKGMGIKS					
	:	:	:	:	:	:
a558	RQRTGTLNLIHYTFSELYMFQQRTAHQAPHCVLPERDCPPIRFYRYKQTGFNRKGMGMKS					
	70	80	90	100	110	120
	90	100				
m558.pep	ISDIXRAMPSENQSPLSDGIVX					
	: :	:	:	:	:	:
a558	VSDTSRAMPSSENQSPLSDGIVX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1649>:

g560.seq
 1 atgctcatca tccgcaacct gatttactgg ctgatactct gttccagcct

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEKCEHLIETQQPLISGAGPFAA					
g560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```

a560.seq
1  ATGCTCATCA  TCCGCAACCT  GATTTACTGG  CTGATACTCT  GTTCCACCCT
51  GATTTTCCTC  TTCCCTTA  TGCTGCTCGC  CTCGCCTTTC  CGAGACGGGG
101 CGCACAAAGAT  GCGCGGGGTC  TGGGTCAAAA  TCCTCAACCT  CTCGCTCAAA
151 CACATCGTCG  GGCTCAAATA  CCGCATCATC  GGCGCGGAAA  ACATCCCGGA
201 CCGCCCCGCC  GTCATCTGCG  CCAAACACCA  AAGCGGCTGG  GAAACGCTCG
251 CCCTTCAGGA  CATTTTCCG  CCGCAGGTTT  ACGTTGCCAA  ACGCGAGTTG
301 TTCAAAATCC  CCTTTTCGG  CTGGGGCTTG  AAACCTGGTCA  AAACCATAGG
351 CATAGACCGC  AACAAACGCC  GCGAAGCCAA  CGAGCAGCTC  ATAAACAGG
401 GGTGCGCGC  CAAAAACGAA  GGCTATTGGA  TTACCATTTT  CCCCAGAGGC
451 ACACGCCITG  CGCCCGGAAA  ACGCGGCAAA  TACAACTCG  GCGCGCGCGC
501 CATGGCGAAA  ATGTTTGAGA  TGGACATCGT  CCCCCTCGCC  CTCACAGCG
551 GCGAATTTTG  GCGAAAAAC  TCCTTTCTGA  AATATCGGG  GGAAATCACC
601 GTCGTCATCT  GTCCGACCAT  CCGCACGCA  AGCGGCAGCG  AAGCCGAATT
651 GATGGGAAA  TGCGAACACC  TCATCGAAAC  GCAGCAGCCG  CTCATTTCCG
701 GCGCAGGCC  GTTGCCGCC  AAAATGCCGT  CTGAAACCGC  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```

a560.pep
1  MLIIRNLIYW  LILCSTLIFL  FPFMLLASPF  RDGAHKMARV  WVKILNLSLK
51  HIVGLKYRII  GAENIPDRPA  VICAKHQSGW  ETLALQDIFP  PQVYVAKREL
101 FKIPFFGWGL  KLVKTIGIDR  NNRREANEQL  IKQGLARKNE  GYWITIFPEG
151 TRLAPGKRGK  YKLGARMAM  MFEMDIVPVA  LNSGEFWPKN  SFLKYPGEIT
201 VVICPTIPHA  SGSEAELEMG  CEHLIETQQP  LISGAGPFAA  KMPSETA*

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m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
a560	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVKILNLSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
a560	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

845

501 QESLSNIRKH ARATHVKFTL SEHGGRTMT IQDNGQGFDT EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQQGTTVS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRL	ENAASVIEEAGNLRMQAY				
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALSVVLTLLLSR	LENAASVIEEAGNLRMQAY				
	10	20	30	40	50	60
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAE	FEKSLKRIAQSDAIHPLIPSDT	PLAYDLIQSMLIIDWQA			
g561	RLAYMAGEGSPRAQIDNQIAE	FEKSLKRISQSDAIHPLIPSDN	PLAYDLIQSMLIIDWQA			
	70	80	90	100	110	120
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGN	IELFLQALENANEKNTWWLRR	FQWAIMLMTLVSSVLM			
g561	NILPPLQAYRRPTQIELYRFAGN	IELFLQALENAGEKNTWWLRR	FQWVIMLMTLVSSVLM			
	130	140	150	160	170	180
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIG	RRCFDIPVPEGGTPEFKQVGR	CFNQMGGRCLKIYDDL			
g561	LFWHQIWVIRPLQALREGAERIG	RHRFDIPVPEDVRPNSNRSG	VSTKWRSGX			
	190	200	210	220	230	
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQNQNLTLLY	QTTTDLHQSYIPQAAEHFLNR	ILPAVGADSGRVC	LDG		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTTGCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCCCT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCCTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	CCCGGAAACA	TCGAACTGTT	TTTGACGGCA
451	TTGGAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCAATG
501	GGCAATTATG	TTGATGACGC	TGGTGTGCTC	TGTAATGATG	CTGTTTTGGC
551	ACCAGATTTG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAATTCAAA	CAGGTCGGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCCCTG	CTGTACCAAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGACCGGC
901	GGATCCGATG	TTTATGTTTC	CATTTCATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCGGATTTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCATTT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCCTG	CTTGCAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCCTTTGC
1251	CGAAACAAA	CGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTTCCGT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCCGAA	GCCGTTGCCG	ACCTATTCTC

847

	370	380	390	400	410	420
m561.pep	430	440	450	460	470	480
	REEAAENISFIKTGVQECYEDVRELLLNFR	TKISNKEFPEAVADLFARFTQQTGITVETA				
a561	430	440	450	460	470	480
	REEAAENIGFIKTGVQECYEDVRELLLNFR	TKISNKEFPEAVADLFSRFTQQTGTTVETA				
m561.pep	490	500	510	520	530	540
	WENGSLPPEAQLOMIFILQESLSNIRKHARATHV	KFTLSEHGGRFTMTIQDNGQGFD				
a561	490	500	510	520	530	540
	WENGTHLPTQDEQLQMIFILQESLSNIRKHARATHV	KFTLSEHGGRFTMTIQDNGQGFD				
m561.pep	550	560	570	580	590	
	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSQAQ	QGTTVSLTVASEESLKX				
a561	550	560	570	580	590	
	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSQAQ	QGTTVSLTVASEESLKX				

The following partial DNA sequence was identified in *N. glaucochromae* <SEQ ID 1659>:

g562.seq..

1	atggcaagcc	cgctcagatct	gcctttcaat	tcgggcaaga	ccaaaccgac
51	ggcttttgcc	gcgccggttt	tggtcggaat	catgttttcc	acgccgctgc
101	ggcgcgcgcg	caggtctttg	tggcgcacgt	cggtaacggt	ttggtcggtg
151	gtcagtgctg	ggatggtggt	cattgcgcct	ttgacgatgc	cgacgctttc
201	gctcaacact	ttggcaaccg	gcgagaggca	gttgggtggtg	caggaaagcgt
251	tggaacgac	ggtcatgtcg	gcggtcagga	cgctgtcgtt	cacgccgtac
301	acgacggttg	catcgacatc	gtcgccgccc	ggtgcgga	tgaggacttt
351	tttcgcgccg	ctttcgaggt	ggattttggc	tttttctttg	ctggtgaacg
401	cgccgggtgca	ttccatgacc	aaatcgacac	cgagttcttt	ccacggcagt
451	tcggcagggg	tgccgggtcga	gaagaagggg	attttgtcgc	cgttgacgat
501	gaggttgccg	ccgtcgtggg	atacgtcggc	ttcaaagcgt	ccgtgtacgg
551	tgtcgaattt	ggtcagatgg	gcgttggttt	caaggctgcc	gctggcggtg
601	acggcgacga	tttgaggttg	gtcttga		

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

1	MASPSLFPN	SGTKPTAFA	APVLVGIMFS	TPLRARRRSL	WRTSVTVWSL
51	VSAWMVVIAP	LTMP TSLNT	LATGERQLVV	QEALETTVMS	AVRTLSFTPY
101	TTVASTSSPP	GAEMRTFFAP	LSRWILAFSL	LVNAPVHSM	KSTPSSFHGS
151	SAGLRVEKKG	ILSPLTMLRL	PSWDTSASKR	PCTVSNLVRW	ALVSRPLPAL
201	TATIWSWS*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

1	ATGGCAAGCC	CGTCGAGCCT	GCCTTTCAAT	TCGGGCAGTA	CCAAACCGAC
51	GGCTTTTGCC	GCGCCGTTT	TGCTCGGAAT	CATGTTTTC	ACGCCGCTGC
101	GGCGCGGCG	CAGGTCTTTG	TGGCGCACGT	CGGTAACGGT	TTGGTCGTTG
151	GTCAGCGCGT	GGATGGTGGT	CATCGCGCCT	TTGACGATGC	CGACGCTTTC
201	GCTCAACACT	TTGGCAACCG	GCAGAGAGCA	GTTGGTGGTG	CAGGAAGCGT
251	TGGAACGAC	GGTCATGTCG	GCGGTCAGGA	CGCTGTCGTT	CACGCCGTAC
301	ACGACGGTTG	CATCGACATC	GTCGCCGCC	GGTGCGGAAA	TGAGGACTTT
351	TTTCGCGCCG	CTTTCGAGGT	GGATTTTGGC	TTTTTCTTTG	CTGGTGAACG
401	CGCCGGTGCA	TTCCATGACC	AAATCGACAC	CGAGTTCTTT	CCACGGCAGT
451	TCGGCAGGGT	TGCGGGTCGA	GAAGAAGGGG	ATTTTGTGCG	CGTTGACCAT
501	GAGGTTGCCG	CCGTCGTGGG	ATACGTCGGC	TTCAAAGCGT	CCGTGCACGG
551	TGTCGAATTT	GGTCAGATGG	GCGTTGGTTT	CAAGGCTGCC	GCTGGCGTTG
601	ACGGCGACGA	GTTGGAGTTG	GTCTTGA		

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

1	MASPSLFPN	SGSTKPTAFA	APVLVGIMFS	TPLRARRRSL	WRTSVTVWSL
51	VSAWMVVIAP	LTMP TSLNT	LATGERQLVV	QEALETTVMS	AVRTLSFTPY

849

	70	80	90	100	110	120
m562.pep	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R T L S F T P Y T T V A S T S S P P G A E M R T F F A P					
a562	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R M L S F T P Y T T V A S T S S P P G A E M R T F F A P					
	70	80	90	100	110	120
m562.pep	L S R W I L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V E K K G I L S P L T M R L P P S W D T S A S K R					
a562	L S R X T L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V X K X G I L S P L T M R L P P S W D T S A S K R					
	130	140	150	160	170	180
m562.pep	P C T V S N L V R W A L V S R L P L A L T A T S W S W S X					
a562	P C T V S N L V R W A L V S R L P L A L T A T I W S W S X					
	190	200	209			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563.seq

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1  ATGAACAAAA CCCTCTATCG TGTGATTTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGGTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTTCTTTAT GTTTGGCTTT
201 GGGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCTAAAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCCc tACTTCGGCa ggGGTTCTG TTAATCAATA
351 TGCCCAAGTT GATGTGGGTA ATcgCGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GCGGTTGGA TTCAAGGCAA TCCTTGCTTG
451 ACAAGGGGCG AAGCACGTGT GGTGTAAAC CAAATCAACA GCAGCCATCC
501 TTCACAAC TGATCAGTAC GGCCGAACAA GCAGGCATTG GTAATCAAGG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCCTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTTAAGATAA GGCAAGGCAA TGCTGTAATC GCCGACACG
701 GTTTGGATGC CCGTGATACC GATTTACAC GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTG GTAATCAAGG
801 GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCAGCATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAGTCAA TATCCGCAGT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 AACTGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTACAG CAAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAAACTGGAT ATTGCGTTAC AAGATGATT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACTTGC AAGCAGGAAA ACGCATTCGG
1351 ATTAAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CCGTACGACA GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAAACAAA ATCCAAGCCG GGCAAATGAA TAATATCGGT
1501 ACAGGTCCGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTTAGG CATTGAACAA TTAAATAACC GTGAAAACAG TCTGATTTAC
1651 AGCGGTAACG ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCCAAAGGA TACACAATGC CGGCGCAATC ATTGAAGCTG
1751 CAGGCAAAAT GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT
1801 TTGAAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATG TTGATTACGA
1851 AGCATTTGGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
1901 GCTGGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAAC TGCGCTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

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851

5201 TAGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC
 5251 GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CCAAAAACAT
 5301 TCAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCGG
 5351 CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA
 5401 CGACATTCGG GCAGCCTGAA AAACATATTT GACAAAGATA GAGTGCAAAG
 5451 TGAACCTGGAT TTACAAAgaa CCGTCAGCCA AGATTTTAGT AAAAATGTTT
 5501 AACAAACCAA TACCGAGATT AACCAACATT TAGACAAACT CAAAGCAGAC
 5551 AAAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT
 5601 GGAAACTGCC AAACGCAAAG CCCATGAAGC TCAAGATGCG GCAGCAAAAG
 5651 CAGATAATTG GCAACAAGGC AAAGTCATTC TCAACATGTT AGCCTCAGGT
 5701 TTAGCTGAGC CGACCCAAAG CGGAGCgggc ATCGCTGCGG CTACCGCATC
 5751 GCCAgCGTA TCGTATGCGA TTGGACAGCA CTTTAAagaT TTAGCCGGTC
 5801 AAAACGCGAA TGGCAAACCTA ACCGCCAGTC AagaAACCCG TCACGTTCTT
 5851 GCCCAGCGCG TATTAGGAGC AGCGGTTGCC GCAGCATGAG GCAACAATGC
 5901 CCCGGCAGGA GCATTGGGTG CGGGCGGGTc ggAagcggCC GCCCAATCA
 5951 TCGGCAAATG GCTGTACGGC AAAGGAGAcg gcggcagccT GAATgcgga
 6001 gaaaAAGaga CCGTTTCGGC GATTACAAGG ATGCTGggtta cGgctGCCGG
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 6101 cggtTCaga TTTCGCTTCC TCTTTTTCAT ATCCTATAAA CATGTGA

This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pep..

1 MNKTLYRVIF NRKRGAUVAV AETTKREGKS CADSGSGSVY VKSVSFIPTH
 51 SKAFCFSALG FSLCLALGTV NIAFADGIIT DKAAPKTQQA TILQTGNIP
 101 QVNIQTPTSA GVSVNQYAQF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL
 151 TRGEARVVVN QINSSHPSQL NGYIEVGRR AEVVIANPAG IAVNGGGFIN
 201 ASRATLTGQ PQYQAGDFSG FKIRQGNVAV AGHGLDARDT DFTRILLYAN
 251 KITLISTAEQ AGIRNQQLF ASSGNVAIDA NGRLVNSGTM AAANVQDMNN
 301 TAEHKVNIRS QAFENSGTAV SQQGTQIHSQ SIQNTGKLLS AGTEDLAVSG
 351 SLNNQNGEIA TNQQLIIHDG QQSTVVIDNT NGTIQSGRDV AIQAKSLSN
 401 GTLAADNKLD IALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLQAGKRIR
 451 IKANNLDNAV QGNIQSGGTT DIGTQHNLTN RGLIDGQQTQ IQAGQMNNIG
 501 TGRIYGDNIA IAATRLDNQD ENGTGAALAA RENLNLGIEQ LNNRENSLIY
 551 SGNDMAVGGA LDTNDQATGK AQRIHNAGAI IEAAGKMRIG VEKLHNTNEH
 601 LKTQLVETGR ERIVDYEAFG RHELLREGTQ HELGWVFNYN ESDHLRTPDG
 651 VAHENWHKYD YEKVTQETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA
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 751 NYTLPEEITR DISLGSFAYE SHSKALSRHA PSQGTLPQS NRDNIRTAKS
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 2001 EKETVSAITR MLGTAAAGAE GNSSADAVWG CFQTASDFAS SFSYPINM*

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3001  GAAAAGAAAG TATTCAGTGA AAATGGCAAA TTACACAGCT ATTGGCGTGA
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3101  TGCCGGAGGA AATCACACGC AACATTTTAC TGGGTTTCATT TGCCTATGAA
3151  TCGCATCGCA AAGCATTAAAG CCATCATGCG CCCAGCCAAG GCACTGAGTT
3201  GCCGCAAAGC AACGGTATTT CGCTACCCTA TACGTCCAAT TCTTTTACCC
3251  CATTACCCAG CAGCAGCTTA TACATTATCA ATCCTGTCAA TAAAGGCTAT
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3351  TGACTATATG CTGGACAGCC TCAAACCTAGA CCCAAACAAT TTACATAAAC
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6051  CGACAGCGAC AGTCAAAGCA GCATCACAAA AAGCGGCATC AACACCCGCA

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563_{rig})

from *N. gonorrhoeae*:

m563/q563

[illegible]

857

g563.pep	GSDLIIDSKAVFNSDSRIIAGGQLLVQTEKDGLHNEQTFGEKKVFSSENGKLHNYWRARRK
m563.pep	GNDLTIDGKEVPNTDSQIIAGGNLIVQTEKDGLHNEQTFGEKKVFSSENGKLHSYWREKHK
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g563.pep	750 760 770 780 790 800
	GHDETGHREQNYTLPEEITRDISLGSFAYESHKALSRHAPSQGTLPQSNRDNIRTAKS
m563.pep	GRDSTGHSEQNYTLPEEITRNISLGSFAYESHKALSHHAPSQGTLPQSN-----
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m563.pep	-GISLPYTSNSFTPLPSSSLYIINPVNKG YLVETDPRFANYRQWLGS DYMLDSLKLDPNN
	1080 1090 1100 1110 1120 1130
g563.pep	870 880 890 900 910 920
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m563.pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEQFKALMDNGATAARSMNLSVGIAL
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g563.pep	1050 1060 1070 1080 1090 1100
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	1500 1510 1520 1530 1540 1550
g563.pep	1290 1300 1310 1320 1330 1340
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m564.seq
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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

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751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
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865

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          1310      1320      1330      1340      1350      1360

1460      1470      1480      1490      1500
m564 .pep  Q T S G N E R N G N T A I - D R M A G I N V V - G S H T E Q V D N R T S D - G I L S L H A S N D I N L N A A T V S N Q V
          | | : | : : : | : | : : : : | : | : | : | : : : : : : | : : : | |
fhab_borpe T T S A N K L S V D V A S W D N A G S L D I K K G G A Q V T V A G R Y A E H G E V S I Q G D Y T V S A D A I A L A A Q V
          1370      1380      1390      1400      1410      1420

1510      1520      1530      1540      1550
m564 .pep  --K D G T T Q I T A G N N L N L G T - I R T E ---H R E A Y G T L D D E N H R H V R Q S T -----E V G S
          : | : : : : : : : : : | : : : | : : : : : | : : : : : | : :
fhab_borpe T Q R G G A A N L T S R H D T R F S N K I R L M G P L Q V N A G G P V S N T G N L K V R E G V T V T A A S F D N E T G A
          1430      1440      1450      1460      1470      1480

1560      1570      1580      1590      1600
m564 .pep  S I R T Q N G A L L R A G N D L K I R Q G E L E A E E G K T V L A A G R D V --T I S E G R Q I T E L D T S ---V S G
          : : : : : | : | : : : : | : : : : | : : : : | : : : : | : :
fhab_borpe E V M A K S A T L T T S G A A R N --A G K M Q V K E A A T I V A A S V S N P G T F T A G K D I T V T S R G G F D N E G
          1490      1500      1510      1520      1530

1610      1620      1630      1640      1650      1660
m564 .pep  K ---S K G I L S S T K T H D R Y R F ---S H D E A V - G S N I G G G K M I V A A G Q D I N V R G S N L I S D K G I
          | : | : : | : : : | : | : | : | : : : : : | : | : : : : : : :
fhab_borpe K M E S N K D I V I K T E Q F S N G R V L D A K H D L T V T A S G Q A D N R G S L K A G H D F T V Q A Q R I --D N S G
          1540      1550      1560      1570      1580      1590

1670      1680      1690      1700      1710
m564 .pep  V L K A G H D I D I S T A H N R Y T G -----N E Y H E S K K S G V M G T G G L G F T I G N R K T D D T D R T N I V
          : : | | | | : : : | | | | : : | : : : : | : : : : | : : | : |
fhab_borpe T M A A G H D A T L K A P H L R N T G Q V V A G H D I H I I N S A K L E N T G R V --D A R N D I A L D V A D F T N --
          1600      1610      1620      1630      1640      1650

1720      1730      1740      1750      1760      1770
m564 .pep  H T G S I I G S L N G D T V T V A G N R Y R Q T ----G S T V S S P E G R N T V T A K S I D V E F A N N R Y A T D Y A
          | | | : : : | : | : | : : | : : : : | : | | | | : : : : : |
fhab_borpe -T G S L Y A E H D A -T L T L A Q G T Q R D L V V D Q D H I L P V A E G T L R V K A K S L T T E I E T G N P G S L I A
          1660      1670      1680      1690      1700      1710

1780      1790      1800      1810      1820      1830
m564 .pep  H T Q E Q K G L T V A L N V P V V Q A A Q N F I Q A A Q N V G K S K N K R V N A M A A A N A A -W Q S Y Q A T Q Q M Q Q
          : : | | : : | : | | : : : : : | : : : | : | | : : | : | :
fhab_borpe E V Q E -----N I D N K Q A ----I V V G K D L T L S -S A H G N V A N E A N A L L W A A G E L T V K A Q N
          1720      1730      1740      1750

1840      1850      1860      1870      1880      1890
m564 .pep  F A P S S A G Q G Q N N N Q S P S I S V S I T Y G E Q K S R N E Q K R H Y T E A A A S Q I I G K G Q T T L A A T G S G
          : : : : | : : | : : : : : | : : | : : | : : : : | :
fhab_borpe I T N K R A A L I E A G G N A R L T A A V A L L N K L G R I R A G E D M H L D ---A P R I ----E N T A K L S G E V
          1760      1770      1780      1790      1800      1810

1900      1910      1920      1930      1940      1950
m564 .pep  E Q S N I N I T G S D V I G H A G T A L I A D ---H I R L Q S A K Q D G S E Q S K N K S S G W N A G V A V K I G N G I R F
          : : : : : | : : : : : | : : | : | : : | : : : : | : : | :
fhab_borpe Q R K G V Q D V G G E H G R W S G I G Y V N Y W L R A G N G K K A G T ----I A A P W Y G G D L T A E Q S L I E V
          1820      1830      1840      1850      1860

```

867

```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAACTCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCCGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRATAVAACS HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTCEFIL KAMANTTSFA NTSSSIANSIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
               |||||||
g565          MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
               10      20      30      40      50      60

                70      80      90      100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
               |||||
g565          AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51 CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA
251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAACTCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRATAVAACS HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTCEFIL KAMANTTSFA NTSSSIANSIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
               |||||||

```

869

```

q566      MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60
           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
q566      AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```
a566.seq
  1  ATGCCGCTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTGTTAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTTACCG
101 TTTACCCAAA CTGCGGCGCG GACGGCGCCG CGCGCAAAAG TCATCGCGGT
151 GCTTGCCCTTG TGGGTGATTT CCACGCGCTC GCCGTGCGTG GCGAAGAGGG
201 CGGTGTGGTC GCCAGCATG TCGCCCGCGC GGACGGTGGC AAAGCCGATG
251 TTGGACGGAT CGCGCGGGCC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TGTGTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A
```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```
a566.ppep
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFTVYPNCGA DGAGGKGHAA
51  ACLVGDFHAL AVGGEEGGVV ADDVARADGG KADGGRIARA GVFAAVNGA
101 LFEVSAERAG DDFAHA*
```

m566/a566 94.0% identity in 116 aa overlap

	10	20	30	40	50	60
m566.pep	MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL					
a566	MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL					
	10	20	30	40	50	60
	70	80	90	100	110	
m566.pep	AVGGEEGGVVADDVACADGGKADGRRIRARTGVAFAAVNGALFEVSAERAGDDFAHAX					
a566	AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

g567.seq..

1	atcgacgacg	gggcagcggc	atcgacacgtg	cgggttttgc	gtccggcgctt
51	tatcaggctct	tatttggcg	tgcgacgtg	cagtcgcgg	cggtagcgag
101	cacgaaggcg	ggatacggcg	tgttgggtgc	gaacgcgcgc	gcttgcggcg
151	gcggaatacg	agctggtgca	ggaatacgcc	cgggaagtgc	gtttgaaaaa
201	cgcgcctaac	gcagtgggcg	aagattacga	ctttattctg	atcgactgtc
251	cgccttcgct	gacgctgttg	acgcttaacg	gcttggtggc	ggcgggcgcg
301	gtgattgtgc	cgatgttgtg	cgaatattac	gcgctggaag	ggatttccga
351	tttgattgcg	accgtgcgca	aaatccgtca	gcgggtcaat	cccgatctgg
401	acatcacggg	catcgtgcgt	acgatgtacg	acagccgacg	caggcttggt
451	gcggaagtcg	gcgaagacgt	gcgcagccat	ttccgggat	tgctttttga
501	aaccgccatc	ccgcgcaata	tccgccttgc	ggaagcgccg	agccacggta
551	tgcccgtgat	cgcttacgac	tcgcaggcaa	aggggtccaa	ggcggtatctt
601	gccttgccqg	acqaactgqc	ggcgagggtg	tcggggaagt	ag

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

g567.pep

1	MRRRAAASTR	RVCSPAFIRS	YWAMRTCSR	RYAAKRADTA	CWVRTRALAG
51	AEIELVQEIA	REVRLKNALK	AVAEDYDFIL	IDCPPSLTLL	TLNGLVAAGG
101	<u>VIVPMLCEYY</u>	ALEGISDLIA	TVRKIRQAVN	PDLDITGIVR	TMYSRSRLV
151	AEVSEQLRSH	SGDLLFETAI	PRNIRLAEAP	SHGMPVMAYD	AQAKGAKAYL
201	ALADELAARV	FGK*			

871

```

251 GCGTGTGGG TCGGAACCGC GCGCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TCGGAATATT ACGCGCTGGA AGGGATTTCC GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGATATCAGG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTGCGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TGTCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
  1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
 51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GGYGVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLDT GIVRTMYDSR SRLVAEVSEQ
201 LRSHEFDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

m567/a567 97.7% identity in 257 aa overlap

              10      20      30      40      50      60
m567.pep      MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              |||
a567           MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              10      20      30      40      50      60

              70      80      90      100     110     120
m567.pep      VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
              |||
a567           VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
              70      80      90      100     110     120

              130     140     150     160     170     180
m567.pep      DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT
              |||
a567           DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT
              130     140     150     160     170     180

              190     200     210     220     230     240
m567.pep      GIVRTMYDSRSRLVAEVSEQLRSHEFDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
              |||
a567           GIVRTMYDSRSRLVAEVSEQLRSHEFDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
              190     200     210     220     230     240

              250
m567.pep      KAYLALADELAARVSGKX
              |||
a567           KAYLALADELMARVSGKX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
  1 atgctcaggg tcagaccggt attatttgcc gtcaaggcct ccgcctcttc
 51 gataccttgc agaatctgcc gattaaagcg ttcgcggctg cccaatatct
101 tcaggcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaagcc
151 tgtaaaaaca gccccatcag gaacgaaact tcgtcttcgg ggcgacgcca
201 gttttcggtt gaaaaggcaa acacggtcag atattgcacg ccagatttgg
251 cgcaatgctt caccatatct tccaacgcgt ccaagccgcg tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggcgcg tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg

```

873

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1   ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTTGAC GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTAATAACA GCCCATCAG GAACGAACT TCGTCTTCG GCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTGCGGTT CGGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGCAGGT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCG CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1   MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCTIF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFEDVVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVKASASSMPFRIXRLKRSRLPSIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m568.pep	ICLGMAVCSKTACVLLFMSAFRGSAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLGMAVCSKTACVLLFMSAFRGSAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADRDAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADGDAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
	250					
m568.pep	HRHADQVADSCRVSQVX					
a568	HRHADQVADSCRVSQVX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1   atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgcgggc
101 tgattgcctt gaccgccttg tgggagtatg cccgatggc cggtttctgc
```

875

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGCTTT TCGGCGTGGT
201 TGCCTATGCG GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCCTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGGGCGTGT TCGACCGCAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

a569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGIC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRDTSL
251 IAVISVYAAM MSVLN*

```

m569/a569 99.6% identity in 265 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGICKIKTNHYLAA					
a569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGICKIKTNHYLAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
a569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m569.pep	ALVSLRPHFDDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEAIGGAVC					
a569	ALVSLRPHFDDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEAIGGAVC					
	130	140	150	160	170	180
	190	200	210	220	230	240
m569.pep	VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLSWLKRAAGIKDSSKLLPGH					
a569	VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLSWLKRAAGIKDSSNLLPGH					
	190	200	210	220	230	240
	250	260				
m569.pep	GGVFDRDTSLIAVISVYAAMMSVLNX					
a569	GGVFDRDTSLIAVISVYAAMMSVLNX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

g570.seq..

```

1 atgatccgtt tgaccgcgc gtttgccgcc gccctgatcg gtttatgctg
51 caccacaggc gcgcacgcg acacctcca aaaaatcggc tttatcaaca
101 ccgagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc ccgtcaggac gaattgcaaa aactgcaacg
201 cgaaggcttg gatttggaag ggcagctcgc cggcgggcaa ctttaaggacg
251 caaaaaaggc gcaagccgaa gaaaaatggc gcgggctggt cgaagcgctt
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaacgccaa ccgcgtcatc gtcaaaatcg

```

877

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
  1  MTRLTRFAAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
  51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
 101  RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
 151  TQYDVTDSVI KEMNAR*

m570/a570  97.6% identity in 166 aa overlap

                10      20      30      40      50      60
m570.pep      MTRLTRFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTL DSEFSARQD
                |||||
a570           MTRLTRFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTL DSEFSARQD
                10      20      30      40      50      60

                70      80      90     100     110     120
m570.pep      ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
                |||||
a570           ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
                70      80      90     100     110     120

                130     140     150     160
m570.pep      SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX
                |||||
a570           SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX
                130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
  1  atgcgcgttt tccgagtaaa ccgatttggt gttaccgttt tggcgccgg
  51  tataggttct gccgtcccaac acgctgcctg cgtcggaaca caggctcagg
 101  cggacgggtgc gtgcgtcttt cgcaccgggc atcggaaga gcagctcggc
 151  ggagacgttg gctttttgtg tgcgcgcgta gctgattttt tgcgcgtatt
 201  cgtcatacac ttcggggccg agcgtgccgc ttcgtagcc gcgcaccgaa
 251  cccaggccgc cgcgcgtaga gttttcaag aaggggattt ctttggttct
 301  gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
 351  ttttgc...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
  1  MRVFRVNRV VTVFGGGIGS AVPHAACVGK QAQADGACVF RTGHREEQLG
  51  GDVGFFVAAV ADFFAVFVIH FRAERAAFVA AHRTQAAAVE VFKEGDFFGS
 101  AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCGG CCGGTCGCGG
  51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACAGCT GCCTGCGTCG
 101  GCAAAACAGG TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGCATCGG
 151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
 201  TTTTTCGCCC GTATTCGTCA TAGACTTTTC GACCGAGCGT GCCGCTTTCG
 251  TATCCGCGCA CCGAACCAG CCGCGCGCCG TAGAAGTTT CAAAGAAGGG
 301  GATTTCCTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
 351  GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACCAGGT TTGGTTGTGG
 401  GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTGGCGGTT
 451  CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
  1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
  51  EEQLGGDVGF FVAAVADFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
 101  DFFGSAVAAR NADFAAEHQE EGFAQGEE?G LVVGGGVVLQ FAARQGDFFGV
 151  HARQVAARRP *

```

879

```

1  atgtgcgccca tcgtcggggc gccggggctg ccttcgcgcg tcgcagcggc
51  gcaaaaaggc aaaaccattt atctggcaca caaagaaacg ctggtggttt
101 ccggcgcggtt gtttatggaa accgccgcg caaacggcgc ggcaagtgtg
151 cccgtcgaca gcgaacacaa cgccattttc caagttttgc cgcgcgatta
201 cacagaccgt ctgaacgaac acggcatcga ttcgattatc ctgaccgctt
251 ccggcgggccc gtttttaaca accgatttaa gcacgttcga cagcattacg
301 ccgagcgagg cggtcaaaca cccaattgg cgtatggggc gcaaaatctc
351 cgtcgattca gccactatgg caaacaaggg cttggaactg attgaagcgc
401 attggctgtt caactgtccg cccgacaaac tcgaagtcgt catccatccc
451 caatccgtga tacacagtat ggtgcgctac cgcgacggct ccgtgctggc
501 gcaactgggc aatcccgata tgcgaacgcc catcgccat tgtttgggct
551 tgcgcgagcg catcgattcg ggtgtcggca aactcgattt cggcgcatcg
601 tccgcgctga ccttcacaaa gcccgacttc ggccgcttcc cctgcctgaa
651 gttcgccctat gaaaccataa acgcaggcgg agccgcgccc tgcgtattga
701 acgcgcgcaa cgaaaccgcc gtccgcgcct ttttggacgg acagattaag
751 tttaccgaca ttgccaaaac cgtcgccac tgcttgcac aagacttttc
801 aaacggcatg ggcgatatag aaggactgtt ggcgcaagat gcccgacac
851 gcgcacaagc gcgggcattt atcggcacac tgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1714; ORF 572.ng>:

```

g572.pep.
1  MCAIVGAAGL PSALAAQKG KTIYLANKET LUVSGALFME TARANGAAVL
51  PVDSEHNAIF QVLPRDYTDR LNEHGIDSII LTASGGPFLT TDLSTFDSIT
101 PEQAVKHPNW RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGKLDGAL
201 SALTFQKPDF GRFPCLKFAY ETINAGGAAP CVLNAANETA VAAFLDGQIK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1715>:

```

m572.seq.
1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCGCGCG TCGCAGCGGC
51  GCAAAAAGGC AAAACCATT TATCTGGCAA CAAAGAAACG CTGGTGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCGTG CAAACGGCGC GGCAGTGTG
151 CCGGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTCG CGCGCGATTA
201 CGCCGGCCGT CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCCC GTTCTGACC GCCGATTTAA ACACGTTTGA CCGCATTACG
301 CCGCCCAAAG CGGTCAAACA CCCCATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCCGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGCTGGC
501 GCAACTGGGC AATCCCGATA TCGGAACGCC CATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCC GGTGTCGGCG ACCTGGATT TCGACGATTG
601 TCCGCGCTGA CTTTCAAAA GCCCGACTTT GACCGCTTCC CCTGCCTGAG
651 GCTCGCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCCGCGCCT TTTGGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCAC TGTCTTGAC AAGACTTTTC
801 AGACGCATA GCGATATAG GGGGGCTCTT GCGCAAGAT GCCCGACAC
851 GCGACAAGC GCGAGCATTT ATCGGCACAC TGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1716; ORF 572>:

```

m572.pep.
1  MCAIVGAVGL PSALAAQKG KTIYLANKET LUVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPRDYAGR LNEHGIASII LTASGGPFLT ADLNTFDRIT
101 PAQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFQKPDF DRFPCLRLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIAKTVAH CLAQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*

```

m572/g572 92.9% identity in 295 aa overlap

```

          10      20      30      40      50      60
m572.pep  MCAIVGAVGLPSALAAQKGKTIYLANKETLUVSGALFMETARANGAAVLPVDSEHNAVF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572       MCAIVGAAGLPSALAAQKGKTIYLANKETLUVSGALFMETARANGAAVLPVDSEHNAIF
          10      20      30      40      50      60

          70      80      90     100     110     120
m572.pep  QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g572       QVLPRDYTDRLNEHGIDSII LTASGGPFLTDLSTFDSITPEQAVKHPNWRMGRKISVDS

```


881

	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSVMVRYRDGSVLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSVMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDLFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAAANEAA					
a572	CLGLPERIDSGVGDLDLFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGGQIKFTLIAKTVAHCLAQDFSDGIGDIGSLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGGQIKFTDIAKTVAHCLSQDFSDGIGDIGSLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1   atgccctggt tgtgccgcct taatcgcaat atcggcagtt tccaaatcac
51  gaatctcacc gaccataatg atg.ccgggt cctgacgcag gaaagacttc
101 aaagcagcgg caaaagtcag accctgctta tcattgacgt taacctgatt
151 gatgcccgcc aggttaaatct cggcagggtc ttccgccgtt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga caccgtctta
251 cccgaaccgg tcggaccggg taccagcacc atcccgtaa gacgggtgaat
301 cgcttccaac acaaattttt tctggaacgg ctcaaaaccg agctgggtcga
351 tgttcaaga cgcgcatcg gaattcaaaa tccgcatcac gaccttttcg
401 ccaaacagcg tcggcaatgt gctgacacgg aaatcgacag gcttgccgcc
451 cttttgaaag gtcagctgca tcctaccgtc ctgcggtatc cgtttttcgg
501 aaatgtccaa acgcgacatt accttaatcc gggaagcaag ctgccccctt
551 accgcaatgg gcggctgaac cacctcgagg agctgcccgt ccacacggaa
601 acggatacgc gcattgtgtt cgtaaaactc gaaatggatg tcggatgccc
651 cgctacgcaa ggcacccgac aaagttttat ggataaacct cggaacaggg
701 ccgtcttctg cctcctcgtc gtcgatatac aggggtgtgc tttcctcttc
751 ctcttgcccc tccccaaagt cctgaagcag cgatgtcgaa cgcgaaacca
801 cccaatcgag caaacccgcc aactggtcat cctcgacaat gaccaactca
851 accgcaatcc ctgcggcaga aaccgttttc tgaatttgcg gcattctgggt
901 cggatcgga accgcaaaaa atactttgtc gcccccacgg aaaaccggca
951 cacagtggaa ctccaccatc tgctcctccg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgataaac tgaacacctt
1051 cgcaatcaat gccgcaagcg acttgggcga aatgacacgg tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1   MPCLRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51  DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHPVVRTVN
101 RFQQQFFLER LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPTV LRYPFPGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTRIVFVKL EMDVGCPATQ GIRQSFMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNRNPGCR NRFLNLRHLG
301 RIGNRKRYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1   ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTAAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACCGTGAAT
301 CGCTACCAAC aCaw.TTTTT TCTGAAACGG CTCA.ACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT

```

883

a573.seq

```

1  ATGCCCTGTT TGTGCCCTCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAACAGG TATAGAGCGA CACCGTCTTA
251 CCGGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAATTTTT TCTGAAACGG CTCAAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGTAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGGAAGCAAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCCGACGG AAAACCGGCA
951 CACAGTGGA TCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```

1  MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51  DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNFCGR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQTLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573.pep	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHFFLKR LKTELVDVQR					
a573	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFFGNVQTRHYLNPKSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAQGIQSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAQGIQSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	VDIQGVAFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNFCGRNGFLNLRHLC					
a573	VDIQGVAFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNFCGRNGFLNLRHLC					
	250	260	270	280	290	300

885

```
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCTG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AAACCTCAGC ATATGAATCC GGCTTGAAAA
1051 GCCGATGCCG ACATGATGCG TTCGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCT
1151 GGCACTGCCC CGCCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```
1  MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GKPEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDMNPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

m573/g573 97.8% identity in 402 aa overlap

m574.pep	10	20	30	40	50	60
	MRPNLPNSLK	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA	KSIPSGFYKS
g574	MLPNLPNSLK	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA	KSIPSGFYKS
	10	20	30	40	50	60
m574.pep	70	80	90	100	110	120
	LDALVDRNSG	RAARELAEV	DGRPQSYDLN	LTLGKLYRQR	GENDKAINIH	RTMLDSPDTV
g574	LDALVDRNSG	RAARELAEV	DGRPQSYDLN	LTLGKLYRQR	GENDKAINIH	RTMLDSPDTV
	70	80	90	100	110	120
m574.pep	130	140	150	160	170	180
	GEKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	LQDGKMAREA	RQHLLNIYQQ	DRDWEKAVET
g574	GEKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	LQDGKMAREA	RQHLLNIYQQ	DRDWEKAVET
	130	140	150	160	170	180
m574.pep	190	200	210	220	230	240
	ARLLSHDDQT	YQFEIAQFYC	ELAQALFKS	NFDVARFNVG	KALEANKKCT	RANMILGDIE
g574	AQLLSHDDQT	YQFEIAQFYC	ELAQALFKS	NFDVARFNVG	KALEANKKCT	RANMILGDIE
	190	200	210	220	230	240
m574.pep	250	260	270	280	290	300
	HRQGNFPAAV	EAYAAIEQQN	HAYLSMVGEK	LYEAYAAQ GK	PEEGLNRLTG	YMQTFPELDL
g574	HRQGNFPAAV	EAYAAIEQQN	HAYLSMVGEK	LYEAYAAQ GK	PEEGLNRLTG	YMQTFPELDL
	250	260	270	280	290	300
m574.pep	310	320	330	340	350	360
	INVVEKSL LK	CEKEAAQT AVEL	VRRKPD LNGV	YRLGL KLSDMN	PAWKADADMM	RSVI
g574	INVVEKSL LK	CEKEAAQT AVEL	VRRKPD LNGV	YRLGL KLSDMN	PAWKADADMM	RSVI
	310	320	330	340	350	360
m574.pep	370	380	390	400		
	GRQLQRSVMY	RCRNCHFKS	QVFFWHCPACN	KWQTFTPNKI	EVX	
g574	GRQLQRSVMY	RCRNCHFKS	QVFFWHCPACN	KWQTFTPNKI	EVX	
	370	380	390	400		

887

	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGKPEEGLNRLTGYMQTFPELDDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGKPEEGLNRLTGYMQTFPELDDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDMNPAWKADADMMRSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDLDPWKADADMMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

g575.seq (partial)

```

1 ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51 ccgtaaaaca gtccgcttcc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggaacttc actggctgtt tccgaacag
151 gttcggaaac ggtgttacgg gtttcgtcgg tcggcggtgc gatggcagaa
201 gcggcggtct cttggggggg cggattcggc agcgggttcc gatgcggcag
251 tatttcagc gggtacaggt cgggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggggttcgggt cgaacggcgg gtttttcgc
351 ttttgcctcg ggcgcggcaa cttttgtctc aggtttttca accggttttt
401 cgacaggttt ctctatcggt ttctccacag ttgcctgttt ggacggttca
451 gacggcatgg atgcagtttc ggccttgggt ttgcgcgttt gcggtttggg
501 ttgttcgct ttgatttttt tgggtgctgc cgctttgatc ctgttcagat
551 tcggaatgtg a*
```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

g575.pep (partial)

```

1 ..MPCLRRQAAR CTNRRTRQT VRFRLLRQK PVRQVRQVR RQLHLWFPQ
51 VRKRCYRFR SACRWQKRRL LGGADSAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGS RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDGS
151 DGMDAVSALG FAVCGLGCSA LIFLGAALI LFRFGM*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

m575.seq

```

1 ATGGTTTCGG GCGAGGAAGC CTTAGGAAG CCTGCCAGTC CGGAGGGTGA
51 GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TIGTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTGACAGG
201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGTGTCT GTGGATTCTGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTGCGCG GCTGCCAGGC TGTGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCCGATAA CTCTTCTTCA GATCCCCAT CTAAGGCAAG TGTGTCGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGGG TGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATTAATGCC GCGCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCCGA ACAGACCGTC AAACAGTCCG CTTTCGGTTT
701 CTTCTTCGGC AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGGTCG GCGTGTCTAT GGCAGAAGCG GCGGCTTCTT GGGGGCGGGA
801 TTCGGCAGCG GTTTCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTTCG
851 VSDTAGLGS CGGTTTTCG GCTTTTGCTT CGGGCGCGGC AACTTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTCGGGTT
1001 GTTCCGCTTT GATCCTGTTT AGATTCGGA TGTGA
```

889

m575/a575 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
m575.pep	MVSGEEAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
a575	MVSGEEAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m575.pep	SMTISTGLYGLKVGSGSYTLSDVSMFQASARFWVSSSCVSPDKMPFCAAARLSKSKSM					
a575	SMTISTGLYGLKVGSGSYTLSDVSMFQASARFWVSSSCVSPDKMPFCAAARLSKSKSM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m575.pep	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR					
a575	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m575.pep	SGSSSGTDSSVRRARLDWARRKSSSRINAAPPPASSKVYEPNRPNSPLSVSSSAETC					
a575	SGSSSGTDSSVRRARLDWARRKSSSRINAAPPPASSKVYEPN----SPLSVSSSAETC					
	190	200	210	220	230	
	250	260	270	280	290	300
m575.pep	STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTGSGRTAGFSAFASGAATFA					
a575	STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTGSGRTAGFSAFASGAATFA					
	240	250	260	270	280	290
	310	320	330	340		
m575.pep	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
a575	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1  ..atgggctgacg acatcgagcgt ctcctgaaa caaatgaagg aacagggcgc
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttcctgcagg agcagcagcg taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgcccgcg
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 cagggtgaaq gcaaacagcc gacaaaagac gacatcgtaa ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc cactttccct ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgggtc aaatcggcgc acccgaaaac
601 gcgcccggca agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1  ..MGVDIGRLK QMKEQGAIEID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

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891

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601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
  1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKQKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

                                10      20      30
m576.pep                                MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                                |||
a576      CGKKEAAPAS ASEPAAASSA QGDTSSIGSTM MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m576.pep      FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
                                |||
a576      FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
                                90     100     110     120     130     140

                                100     110     120     130     140     150
m576.pep      KDGVKTTASGLQYKQKQEGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ
                                |||
a576      KDGVKTTASGLQYKQKQEGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m576.pep      VIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA
                                ||
a576      VILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA
                                210     220     230     240     250     260

                                220
m576.pep      KQPAQVDIKKVN
                                |||
a576      KQPAQVDIKKVN
                                270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

```

g576-1.seq
  1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
 51 ACTTTCCGCC TCGGCGAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTTCAAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGCGC CGGAAATCGA TTTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCCTGCAG GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCAGTACA AAATCACCAA ACAGGGTGAA GGCAAACAGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG CCACCTTCCC TTTAGCCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCGCC AAGCAGCCGG ATCAAGTCGA
801 CATCAAAAA GTAAATTAA

```

893

```

1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCGCGCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGCGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGGCG
701 GCGACAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGCGC CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKOPTKDDIV TVEYEGRLID GTVFDSEKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISAL	TLSAALALSA	CGKKEAAPAS	ASEPAASSA	QGDTSSIGST	MQQASYAMGV
m576-1	MNTIFKISAL	TLSAALALSA	CGKKEAAPAS	ASEPAASSA	QGDTSSIGST	MQQASYAMGV
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLQMK	EQGAEIDLKV	FTAMQAVYD	GKEIKMTEE	QAQEVMMKFL	QEQQAKAVEKH
m576-1	DIGRSLQMK	EQGAEIDLKV	FTAMQAVYD	GKEIKMTEE	QAQEVMMKFL	QEQQAKAVEKH
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKE	KGEAFLENAA	KDGVKTAS	GLQYKITKQ	GEGKOPTKDD	IVTVEYEGRLID
m576-1	KADAKANKE	KGEAFLENAA	KDGVKTAS	GLQYKITKQ	GEGKOPTKDD	IVTVEYEGRLID
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKAN	GGPVTFPLSQ	VILGWTEGV	QLLKEGGEAT	FYIPSNLAYR	EQGAGDKIGPN
m576-1	GTVFDSSKAN	GGPVTFPLSQ	VILGWTEGV	QLLKEGGEAT	FYIPSNLAYR	EQGAGDKIGPN
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLV	KIGAPENAPA	KQPAQVDIKK	VNX		
m576-1	ATLVFDVKLV	KIGAPENAPA	KQPAQVDIKK	VNX		
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

895

```

|||||
g577      YTVIKIIILLFLLLAVINMDAVTFSYLPQSVNLP L I V V L F G A F V V G I V F G M F A L F G R L
              70      80      90      100      110      120

              130      140      150      160
m577.pep   LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPES TKQ P X
              |||||:|||||:|||||:|||||:|||||:|||||
g577      LSLRGENSRRLRAEVKK SARLSGQKLTAPPIQNAAESAKQ P X
              130      140      150      160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1  ATGGAAAGGA  ACGGTGTATT  TGGTAAATTT  GTCGGCAATC  GCATACTCCG
51  TATGTCGTCC  GAACACGCTG  CCGCATCCTA  TCCGAAACCG  TGCAAATCGT
101 TTAAGTAGC   GCAATCTTGG  TTCAGAGTGC  GAAGCTGTCC  GGGCGGCGTT
151 TTTATTTACG  GAGCAAACAT  GAAACTTATC  TATACCGTCA  TCAAAATCAT
201 TATCCTGCTG  CTCTTCCTGC  TGCTTGCTGT  CATTAATACG  GATGCCGTTA
251 CCTTTTCCTA  CCTGCCGGGG  CAAAAATTCG  ATTTGCCGCT  GATTGTCGTA
301 TTGTTGGGCG  CGTTTGTCTG  CGGCATCGTG  TTCGGAATGT  TTGCCTTGTT
351 CGGACGGTTG  TTGTCGTTAC  GTGGCGAGAA  CGGCAGGTTG  CGTGCCGAAG
401 TAAAGAAAAA  TGCGGTTTGG  ACGGGGAAGG  AGCTGACCGC  ACCACCGGCG
451 CAAAATGCGC  CCGAATCTGC  CAAACAGCCT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.pep
1  MERNGVFGKI  VGNRILRMSS  EHAAASYPKP  CKSEFKLAQSW  FRVRS CPGGV
51  FIYGANMKLI  YTVIKIIILL  L F L L L A V I N T  D A V T F S Y L P G  Q K F D L P L I V V
101 L F G A F V V G I V  F G M F A L F G R L  L S L R G E N G R L  R A E V K K N A R L  T G K E L T A P P A
151 Q N A P E S A K Q P  *

```

m577/a577 98.1% identity in 160 aa overlap

```

              10      20      30      40      50      60
m577.pep   MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSEFKLAQSWFRVRSCLGGVFIYGANMKLI
              |||||
a577      MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSEFKLAQSWFRVRS CPGGVFIYGANMKLI
              10      20      30      40      50      60

              70      80      90      100      110      120
m577.pep   YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLF G A F V V G I I F G M F A L F G R L
              |||||
a577      YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLF G A F V V G I V F G M F A L F G R L
              70      80      90      100      110      120

              130      140      150      160
m577.pep   LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPES TKQ P X
              |||||
a577      LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESAKQ P X
              130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq
1  atgggaaagc  tcgacatcgg  gatattgttt  gccgatttct  tcaaagattt
51  cgcgccacag  ttcggtggtt  tccaaaacgt  tggctttgcc  tacggagcag
101 acttttttgc  tgcgtttttg  ggcggattgg  aaggccacgt  gggcgatgcg
151 gcggatttcg  ctttcgctgt  atttcattgt  gttgtagcct  tcgtgttcgc
201 cgttttccaa  aacacggatg  ccgcgcgggt  cgccgaaata  aatatcgccg
251 gtaagttcgc  gcacaatcaa  aatatccaaa  ccggcaacga  tttcaggctt
301 gagcgtggag  gcgttggtta  a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.pep
1  MGKLDIGILF  ADFFKDFAPQ  FGGFQNVGFA  YGADFFAAFL  GGLEGHVGDA
51  ADFAFV F H G  V V A F V F A V F Q  N T D A A R F A E I  N I A G K F A H N Q  N I Q T G N D F R L

```


897

```

51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCCCTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCT CCGGTTCAAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

```

g579.pep..
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

```

m579.seq..
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCCT CCGGTTCAAA GTCGGCGACT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

```

m579.pep..
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
g579	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
g579	KDQLSNFAAGALIIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120

899

```

1   ATGGACTTCA AACAAATTTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGGGCATCTG GCTGAAAAGG CGTGGCGGTT CGGGCTGAAC CTGCGCGCGG
101 CGCTGCTTAT TTTCTTGGTC GGAATATGGG CGGCGAAACG CATTGTCGCC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGGG ACGGTTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGTT GCGGTTGTCC TAAAAGACC AGCTGTCCAA
351 TTTTCCCGCC GCGCGCTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ACTTTATCCG TGTCGGCGGT TTTGAAGGAT ATGTCGGGA AATCAAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCAGC CTGCGCGCTT
551 GCGCGCGCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAGAGG CGGTGTTGAA AGCGCGCGCC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGCCCG CCGCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAATCAA
801 TATCAACATC CCGTCCCCGC AACCGGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1   MDFKQDFDLH LISVSGWHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVLPNSV V MGNSIVNRSS LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAE EHPLSVQNEE ROPAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1   ATGGACTTCA AACAAATTTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGAGCATCTG GCTGAAAAGG CGTGGCGGTT CGGGCTGAAC CTGCGCGCGG
101 CGCTGCTTAT TTTTCTTGGTC GGAATATGGG CGGCGAAACG CATTGTCGCT
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGTT GCGGTTGTCC CTGAAAGACC AGCTGTCCAA
351 TTTTCCCGCC GCGCGACTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCGGAGA GATTAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCACA CTGCCGCTGT
551 GCGCGCGCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAGAGG CGGTGTTGAA AGCGCGCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCTG CCGCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCCGC AACCGGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1   MDFKQDFDLH LISVSGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVLPNSV V MGNSIVNRST LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
g579-1	MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
	10	20	30	40	50	60
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	70	80	90	100	110	120
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	70	80	90	100	110	120
m579-1.pep	GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVLPNSVVMGNSIVNRST					
	130	140	150	160	170	180

901

```

|||||
m579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

```

g580.seq
1   atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
51  cgcgtcgcag cccatttcga tggcaaggca gacttcgccg atcatgtcgc
101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
151 tcgaaaaatca gcttggtaaa gccgttgctg caaccgttgg caatcgcacg
201 accggaagcc gcccatggga agttggcttt ggtaatattg cggcctgatg
251 ctttggcaga caattcgggt tcaccgaccc atgccacttc cggggaagtg
301 tag

```

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

```

g580.pep..
1   MDSPKVGCGW MVLPSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
101 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

```

m580.seq..
1   ATGGATTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCGGCA
151 TCAAAAATCA GCTTGGTAAA GCCGTTGTCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCC GCCCAGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCGGA CAGTTCGGTT TCGCCACCCC ACGCCACTTC GGGGAAGTG
301 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

```

m580.pep..
1   MDSPKVGCGW MVLPSAASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
101 *

```

m580/g580 97.0% identity in 100 aa overlap

```

          10      20      30      40      50      60
m580.pep  MDSPKVGCGWMVLPSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS
          |||||
g580       MDSPKVGCGWMVLPSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS
          10      20      30      40      50      60

          70      80      90     100
m580.pep  QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX
          |||||
g580       QPLAIARPEAAHGKLALVILRPDALADNSVSPHATSGEVX
          70      80      90     100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

```

a580.seq
1   ATGGATTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCTGC
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCAGCA
151 TCAAAAATCA GCTTGGTGAA ACCATTGTCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCAGA CAATTCGGTT TCGCCACCCC ATGCCACTTC AGGAGAAGTG
301 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

```

a580.pep
1   MDSPKVGCGW MVLPSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

```

903

```

a581.seq
  1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
 51  CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101  CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151  TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201  CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCTTCGGA CGCATCAATC
251  AATTCGCCTG CCAAACG CAG GTCCATGGAT TTCTACCAC GTTTCGGGC
301  CGCATCGCA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
  1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTQADRG LSHFISLSK
 51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101  RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGF	TRVNMGGNTDVTQADRG	LSHFISLSK	LETEVRECFV		
a581	MHFAQLVGQTGIEQNTFCRRGF	TRIDMGGNTDVTQADRG	LSHFISLSK	LETEVRECFV		
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFG	RINQFACQTQVHGFLLTF	AGRIANPAHCQS	QTAX		
a581	GFSHTVYFFTFFQRTATAFG	RINQFACQTQVHGFLLTF	AGRIANPAHCQS	QTAX		
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
  1  atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
 51  agagaccgcg ctgcaatgcg ccgcttttgc ggaacatggt acgcgttttg
101  cgtgttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151  gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201  cagcttggaat aagggcgagg cggtcattgt tgttgaaaaa ggcggggatg
251  cgcttcctgc cgacagtgcg ggcgaaacgg ccgatatact tacgcctttg
301  agcctgatgt acgacttgga caaaaacgat ttgcgcgggc tgttgggcgt
351  acgcgaacac aatccgatgt acctatgcc gttttggtat aacaattcgc
401  ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451  ttccggacagc agaaacgtgc ggaacccaaa ttgcagggtt cgttcaaaag
501  caaaaattgcc gaaaatttgt ttaaaacccg ccgagatctg tggttcggct
551  acaccctaaag atccgatttg cagatttaca accaaggcag gaaatccgcg
601  ccgttccgca atacggatta caaacctgaa attttcctga cccagcctgt
651  gaagggcggt ttgccgttcg gcggcaggct gcgtatgctc ggtgcgggtt
701  ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttcttggaac
751  aggatttatg ccatggcagg catggaatgg ggcgaattga cggtgattcc
801  gcgcgtgttg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851  ccgatattgc cgactatatg gggatggcg acgtgaagct gcagtaccgc
901  ctgaacgaca ggcagaatgt gtattccgta ttgcgttaca accccaaaac
951  gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc gggttgatgt tcaacgactg
1101 ggacgcgcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
  1  MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAQO
 51  EQQESKAVLN LTETVRSLLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101  SLMYDLKND LRGLLGVREH NPMYLMPPFW NNSPNYAPSS PTRGTTVQEK
151  FGQKRAETK LQVSFKSKIA ENLFKTRADL WFGYTRSDW QIYNQGRKSA
201  PFRNTDYKPE IFLTQPVKAD LPFGRLRLML GAGFVHQSNQ QSRPESRSWN
251  RIYAMAGMEW GKLTVI PRVW VRAFDQSGDK NDNPDADYM CYGDVKLYR
301  LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKVVVRG FHGYGESLID
351  YNHKQNGIGI GLMFNDWDGI *

```

905

```

m582.pep  LNDQRNVYSVLRYPKTYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
          |||||
g582      LNDQRNVYSVLRYPKTYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          |||||
g582      GLMFNDLDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTACGA CAGGATT:..T GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GCGGGGGATG
251 CGCTTCCTGC CGACAGTGCG GGCGAAACCG CCGACATCTA TACGCCTTTC
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCG
401 CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACACC AGAAACGTGC GGAAACCAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TAAAAACCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAATGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ATCCCAAAAC
951 GGGCTACGCG GCGATTGAAG CCGCCTACAC GTTTCGATT AAGGGCAAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVRH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQOKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDIDYD GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

m582/a582  100.0% identity in 370 aa overlap

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||||
a582      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPSLMYDLKNDLRGLLGVRH
          |||||
a582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPSLMYDLKNDLRGLLGVRH
          70      80      90      100     110     120

          130     140     150     160     170     180

```

551 CCCAATTICA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFCAFCCI GAVTAGNRLH NRMYNAAAAA GIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIHR RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 QQRPSRLRDP VGYGQCQNOG AQYCGNGEGY RFETQFHHD LKKDRPEKS
201 EK*

m583 / g583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT HLAFCAFCCI GAVTAGNRLH NRMYNAAAAA GIGRNGSQQ QFGKSETVTD					
g583	MIVDQSQIFT HLAFCAFCCI GAVTAGNRLH NRMYNAAAAA GIGRNGSQQ QFGKSETVTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m583.pep	AQRFSKNGDK QISDTHPQPCFEQTARNHNC DGNQPNQRI GERTQRI HRARFVGGYAG					
g583	AQRFSKNGDK QISDTHPQPCFEQTARNHNC DGNQPNQRI GERTQRI HRARFVGGYAG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m583.pep	YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG QQRPSRLRDP VGYGQCQNOG AQYCGNGEGY					
g583	YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG QQRPSRLRDP VGYGQCQNOG AQYCGNGEGY					
	130	140	150	160	170	180
	190	200				
m583.pep	RFETQFHHD LKKDRPEKSEKX					
g583	RFETQFHHD LKKDRPEKSEKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTGCCTT TCTGTGCCTT
51 TTGCGGGATT GGAGCCGTAA CTGCCGCGCA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGCGCAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACGCGCGC AAATCATAAC TCGCATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTCGGCGG
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAAGGC GCACAATACT GCGCAATGG CGAGGGGTAT CGGTTTGAAA
551 CCCAATTICA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFCAFCCI GAVTAGNRLH NRMYNAAAAA GIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIHR RARFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
151 QQRPSRLRDP VGYGQCQNOG AQYCGNGEGY RFETQFHHD LKKDRPEKS
201 EK*

m583/a583 99.0% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT HLAFCAFCCI GAVTAGNRLH NRMYNAAAAA GIGRNGSQQ QFGKSETVTD					

909

m584.pep..

```

1 MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51 EGRDKNVNA EFVKKFNKFI RSKNKSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep      MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTA EGRDKNVNA
              ||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           MLRSILAASLLAVSFPAAAEALNYNIVEFS ESAGIEVAQDTMSARFQVA EGRDKNVNA
              10      20      30      40      50      60

              70      80      90     100     110     120
m584.pep      EFVKKFNKFI RSKNKSFKTELVSRSAMPRYQYTNRRRIQTGWEERAEFK VEGRDFDELN
              ||||| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
g584           EFVKKFNNTK RSKNKSFKTELVSRSAMPRYQYTNRRRIQTGWEERAEFK A EGRDFDALN
              70      80      90     100     110     120

              130     140     150     160     170     180
m584.pep      RFIADIQADAALXYTDFHVS RERRNEVIXQVSKDAV' RFKARA EKLAVLGASGYKIVKL
              ||||| :||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
g584           RFIADVQTDASLEDTF SVSRERRNEVIDQVSKDAVLRFKARAE' LAGVLGASGYKIVKL
              130     140     150     160     170     180

              190     200     210     220     230
m584.pep      NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVEEISISVNGTVQFX
              ||:||||| ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
g584           NFGQIGSHIAGDGAVRAKMLRAMPMAASVNMKGTD SAAPGVEEISISINGTVQFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

```

a584.seq
1 ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51 .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTCAAC AGAAAATCAA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TGCGTTGAAC CGTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTGG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCGCG
651 CGCGCCTGGT GTGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

```

a584.pep
1 MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51 EGRDKNVNA EFVKKFNFT RSKNKSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep      MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTA EGRDKNVNA
              ||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
a584           MLRSILAASL----- IVEFS ESAGVEAVQDTMSARFQVTA EGRDKNVNA
              10      20      30      40

```

```

1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTACC GACAACGGCC CCGCGGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGAATGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAAATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

```

m585.pep..
  1 MKLFQIRIFAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
  51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGEKKD ILNRYIDSYT
 101 IERARLFAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLI
 151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
 201 LETRISQQVD DRDDELSHLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS
 251 PLARMQAIIV LIQAQPKQKE QYLRLEGELE TRMDTLAGEL LTLSRLETSN
 301 MALEKESLKL LPFLGNLVED NQSIQKNGQ TVTLSADGKI PENTTILANE
 351 SYLYRAFDNV IRNAVNSPE GSTILINIQ DHKHWIIDVT DNGPGVDEMQ
 401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
 451 RFILPKKKTG SKTEKSAN*

```

m585 / g585 88.3% identity in 231 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG					
g585	MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFKTRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGEKKDILNRYIDSYTIERARLFAAGHPHNSNLVHIE					
g585	DNGAREILTEWKNPSSAVYVIQGEKKDILNRYIDNYTIERARLFAANNPHNSNLVRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGEEYLFFTKDWDLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGGLMAYILAG					
g585	YDRFGEEYLFPIKWDNHQAQRLPSPLFIPGLPLAPIWHEFIILSFIIIVGGLMAYILAG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAKPIRILGNMMDRVANGELETRISQQVDDRDELSHLAIQFDKMVEKLEKLVAKERHL					
g585	NIAKPIRILGNMMDRVAERELEDRVCQVVRDRDELADVAMQFDTMVEKLEX					
	190	200	210	220	230	
	250	260	270	280	290	300
m585.pep	LHHVSHEMRSPLARMQAIIVGLIQAQPKQKEQYLRLEGELETRMDTLAGELELTLSRLETSN					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

```

a585.seq
  1 ATGAAACTGT TCCAACGCAT CTTGCCACA TTTGCGCGG TTATCGTCTG
  51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCTTG
 101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
 151 AGCATCATTT CCGCATTCG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
 201 CCTGACGGAA TGGAAAGACA GCCCGTCTC ATCGGGCGTG TACGTTATAC
 251 AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC
 301 ATCGAACGCG CCCGCTTTT CGCGCGCGGA CACCCGCATT CCAACCTCGT
 351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAG
 401 ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC
 451 GGCTTGCCGC TCGCCCCGAT TTGGCACGAA CTCATCATAT TGTCTTCAT
 501 CATCATCGTG GGAATGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
 551 AACCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
 601 CTTGAAACCC GTATCTCCA ACAGGTCGAC GACCGCGACG ACGAATTGTC

```


913

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1 atggcgagccc atctcgaaga acaacaagag ttagacaact ttaaatatatt
51 ttggaaaacc acgggcaaatt ggctgtttgc cctgctgatt ttggcggcac
101 tcggctactt gggatacacg gtttaccaaa accgtgcggc ttcccaaaat
151 caggaagcgg cggcgggtgct ggcaaacatc gtggaaaagg cgcaaaacaa
201 agccccgcaa agcgaaatca atgccgaact gtccaaactc caacaaagct
251 acccccattc catttccgcc gccaagcca cgctgatggc ggcggaacc
301 gaatttgacg cgcagcgta cgaatgttgc gaaggtcatt tgaatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttggcg gcgcagcgtc
401 tggcggtgtt gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451 ctgcacacgc cggttgaggg ggacttcgcc cccctgctga tggaaactaa
501 aggcgatgtt tatgccgcac aggaaaaaag ccaggaagcc ttaaaaaact
551 acggacaggg tttggaaaaa atgcctcaag attctgtcgg tcgcgaattg
601 cttcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1 MAAHLEEQQE LDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNRASQN
51 QEAAAVLANI VEKAQNKAPQ SEINAEISKL QQSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHLKWVLSN QKDSLQALA AQLRGVLLQ QKKYDAALAA
151 LDTPEADFA PLLMETKGDV YAAQKSQEA LKNYGQALEK MPQDSVGRRL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1 ATGGCAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAAC TTAATATATT
51 TTGGA AAAACC ACGGGCAAAT GGCTGTTTGC CTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTAAAGT TTCCCAAAT
151 CAGGAAGCGG CGCGGTTGCT GGCAAAATC GTAGAAAAGG CGCAAAGCAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAAT GACCAAATC CAACAAAGCT
251 ACCCGCATTC CATTTCCGCC GCCCAAGCCA CACTGATGGC GGCGGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 GTTGTCCAAC CAAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAAT ACGATGCCGC GCTTGCCGCG
451 CTCGATACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGA AAAAG CCAGGAAGCC TTA AAAA ACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCAATTG
601 GTTCAATGA AACTTGATT GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1 MAAHLEEQQE LDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNRKVSQN
51 QEAAAVLANI VEKAQSKAPQ SEINAEITKL QQSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHLKWVLSN QKDSLQALA AQLRGVLLQ QKKYDAALAA
151 LDTPEADFA PLLMETKGDV YAAQKSQEA LKNYGQALEK MPQDSVGRRL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAAHLEEQQELDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNRKVSQN QEAAAVLANI					

915

```

                190      200      210
m586.pep      LKNYGQALEKMPQDSVGRELVMKLDLKK
               |||||
a586          LKNYGQALEKMPQDSVGRELVMKLDLKK
                190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
1   atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 gccgcacttg ccgcaccggg ttacattcaa accggcgcaa cctcgtttat
201 cccatttccg accgaaattc aagaaaacgg cagc?atacc gatatgctcg
251 ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301 ggcagcggca gctatctgtg gcacgaagaa cgcaaaactc acggcaacgg
351 caaaacccgc aacaaacgga tgtccgacat atccgccggc atcagccaca
401 ctttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501 gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
1   MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSNSR
51  AALAAPVYIQ TGATSFIPIP TEIQENGST DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151 TVYEKSRNKA SLIKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
1   ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCCG
151 GCCGAACTTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCTGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCCTA CCGCATCAAC GGCAGCAAAA CCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCACTACCT GCTGCTCAAC CCCAACATCT CATTTGCTGC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTCC GCGCAGGTTT CGGTTTCACC AAAACACCGC CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
1   MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGST DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTILSDGIR
201 YKSGNYLLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60

917

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGH					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGH					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
1  atgcttaaac atctcgcat cctactgccc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaagaagac gggcttcctt caggcaagg catatggcgt
151 tgcgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgccgg ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaacaag ccttggcaca cggcaggttc gccgcctcgc aaaacggcga
351 aacctctttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
1  MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMLSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCGTCTCTGA CTTCCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTCG TTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAAC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
1  MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAKGKTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FLEPFNSDST KFRNMLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENMIK EVKLPKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

```

301 atcgggatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
351 ttggatgatt ccgcctgtat ggcatgtttg actggcaagc atagtgcac
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaaggg
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgcgattta
501 cctgtattcc gtttatatgc tgttttcag ttcgcatgcy gcgcacggt
551 tggcgcatgt gtattttgaa gcgggcgtga tggatgatcg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcaccaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cggcaccaca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttatc
751 cgcaccaacc acggcgaacg catcgctgcc gacggcatta tcgaaagcgg
801 cagcggttgg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggg gggcggcaaa gtgttggcgg gcgcgctgat gaccgaaggg
901 agcgtggtgt accgcgcgcg gcagctcggc agccaaaccc tgcctcggcg
951 catgatgaac gcgctctctg aagcacaagg cagtaaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaaactgt cgtgggcac
1051 gcgcttctga cttttatcgt tgcctggctg attaagggcg attggacggg
1101 cgcaatgatg cagcgcgttg ccgttttggg gattgcctgc ccgtgcgcg
1151 tcggctctggc gacccctgcc qcgattatgg tcggcatggg caaagcgggtg
1201 aaacacggca tttggtttaa agcgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtatttg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgaggttgc cgcgctttat tacgttcccg acagcggctt tgacgaagac
1351 gctttgtacc gcatcgccgc cgcgctcgag caaaacggcg cccaccgct
1401 cgcgcgcgcc atcgtctcgc ccgcacaagg gcgcggtttg gagattcccg
1451 ctgcacaaaa tgcgcaaaac gttgtcggag caggcattac cgcgcaagtg
1501 gaaggcgtgg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcgtttggga aatcgccagt gcggttcgca
1601 tatctgtaaa cggcaaacgg atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccgaagg cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggctcga tacgtcgcca
1751 aacaactggg catcgcacac gccttcggtg atatgagtcc gtgcgacaaa
1801 gccgcggaag tgcagaaact caaagccgcc ggcaaaacgg tggcgatgg
1851 cggcgacggc atcaacgacg cgcgcgcgct tgccgcgcgc aacgtcagct
1901 tcgccatgaa aggcggtgcg gacggttgcc aacacaccgc ctccgccacg
1951 ctgatgcagc attcgttaa acagtcgccc gatgcctgc tgatatcgaa
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttcttctaca
2051 atatattggg cattccgctc gccgcgctcg gctttttaa tcccgtcata
2101 gcaggcgcg caatggcggc aagctcggtt tcggtatttg gcaatgccct
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIARI IEKTGYGAKE KTEDTLPOPE AEHHIGWRLW LLTINIPFL
101 IGMVGMMLKG LNWTRHDWMI PPVWQFVLAS IVQLWLAIPI YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHYFFE AGVMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESHLTGES NPEEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPQVAAYV YVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFALTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIGR LKKHNIIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGG DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFILNPVI
701 AGAAMAASSV SVLGNALRLK WKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAATCGAA GGCATGACCT GCCAGGCCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTCGCCAGC GAAGAGGCGC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCGGTTCTTT

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921

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g589      MQQKIRFQIEAMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADIAKI
           10      20      30      40      50      60

           70      80      90      100     1      110
m589.pep   IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLLTINIPFLIGMVGMMLKGLNWTNRHDWMI
           70      80      90      100     110     120

           120     130     140     150     160     170
m589.pep   PPLWQFALASVVQLWLAIIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
           ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      PPVWQFVLASIVQLWLAIIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA
           130     140     150     160     170     180

           180     190     200     210     220     230
m589.pep   AYGMAHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           |:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      AHGMAHVYFEAGVMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           190     200     210     220     230     240

           240     250     260     270     280     290
m589.pep   IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           250     260     270     280     290     300

           300     310     320     330     340     350
m589.pep   SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFFIVTWL
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVGIALLTFFIVAWL
           310     320     330     340     350     360
```

923

```

1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAAACGCCG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CGCCCGAGGC GCGCGTTTG GAGATTCCCA
1451 CCGCACAAAA TGCCCAAACC ATTGTCGGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTTGGTAAA AGCAGGCAAA GCCGAATTTG CCGAACTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGTTGCCG
1601 TATCTGTAAG CGGCAAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCCGCCGAAG TGCAGAACT CAAAGCCGCC GGCAAACCG TGCGCATGGT
1851 CGGCGACGGC ATCAACGACG CGCCGCGCT CGCCGCCGCC AACGTCAGT
1901 TCGCCATGAA AGGCGGTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGTTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCCGCTC GCCGCGCTCG GCTTTTAAA CCCGTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCTGAAA CGGGTAAAAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

```

a589.pep
1  MQQKVRFOIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIAMI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLAINIPFL
101 IGMVGMMLKG LNWTRHDWML SPLQFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201 LGKFEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251 RANHGERIAA DGIIESGSGW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWEKDAA AMEEAAHVDA VVLDKTGTLT EGKPCQVAAY CVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501 KGAGLVKAGK AEFALTLPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551 KADTAEAIGR LKKHNDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGA DVAHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*

m589/a589 94.9% identity in 725 aa overlap

10 20 30 40 50 60
m589.pep MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIAMI
||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
a589 MQQKVRFOIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIAMI
10 20 30 40 50 60

70 80 90 100 1 110
m589.pep IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG----RHDWMI
||||||||||||||||||||||||||||||||:||||:||||:||||: |||||
a589 IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLAINIPFLIGMGMMLKGLNWTRHDWML
70 80 90 100 110 120

120 130 140 150 160 170
m589.pep PPLWQFALASVVQLWLAIIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
|| |||||||||||||||||||||||||||||||||||||||||||||||||||
a589 SPLQFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
130 140 150 160 170 180

180 190 200 210 220 230
m589.pep AYGMHVYFEVGVVIGFVSLGKFEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
|||||||||||||||||||||||||||||||||||||||||||||||||||||
a589 AYGMHVYFEVGIMVIGFVSLGKFEHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
190 200 210 220 230 240

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925

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501 ctgggaaggc ctgacggggg aaacgggtta tcaaaaaggc ttcaaaagct
551 accgcaacag ctatgatgcg cctttgttca aaatcaagct ggcagacaaa
601 ggcgatgccg cgtttgaaaa agcgcatttc gattcggaag cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggt gtcgattaca acgtcaaatt gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccgggga atcggggcgcg ttatcgaca gcgaaggcg gttccgtttc
901 gatacgttgg tgtacggcga tgaataatc ggcgcctgg acatccatat
951 cgctgccgaa cactcgatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgcaaaa aaaatgactg aggaacaaat cgcgaatgat
1051 ttgattgcgg cagtcaaaag cgaatgcttc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag ggaaaaattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tcctcaaaaa atgttggaag atttgccggt aagtcaggct ggaaatatat
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 ltaaatgaaa cattgcgcct gatggtggac agtacggctc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccctaaaaa caacgccctg aagttaaacg ggaaaacgct gcaaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttccggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

```

g590.pep.
1 MKKPLISVAA VLLGVALGTP YYLGVKAES LTQQQKILQK TG.LLVESHQ
51 YDRGWFTSTE TTVIRLKPEL LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 FAGGFQTQAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGKKEDLN
401 QLGLMLKkte ANIRMSIPQK MLEDLAVSQA GNIFSVNAED EAERASIASD
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

```

m590.seq (partial) ..
1 ..TGGTTTACCT CTATGGAAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAAAATACC TGCCGGATAA CCTGAAAACA GTGTTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGCGCGA
151 TTCGCGACGC AGGCGTACAT TGAACCCGAG TTCAAATACG CGCCTGAAAC
201 GGAAAAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCC GCTTCCCTTG
251 CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG.CTGCACT GGAAGGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTTGTTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAAG TGCATTTCGA TTCGAAACT TCAGACGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGA AAAATTCTCC CTAGAATGGA
551 AAGAGGTGTG CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTTGTI
601 ACCGATTTCG AGATTGGCGC GTTTATCAAT CCAACGGCA GCATCGCACC
651 TTCCAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGCGAGT TCCGTTTCGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATTT GATTGCCGCC
901 GTCAAAAGGAG AGGCTTCCGG ACTGTTCAAC AACAATCCC TATTGGACAT
951 TAAAACTTTC CGATTACGC TGCCATCGGG AAAAATCGAT GTGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTTGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCAAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTT AGCGTCAATG
1151 CCGAAGATGA GCGGAAGGC AGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTC AACGGCGACC AGATTGATAC TGCCATTCT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGGT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1   ATGAAAAAAC CTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCTGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGTGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCCT
301 TTTGCCGGCG GATTGCGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAAATGGAA
451 GTCAGTGTTT CCGCCTTCGA TTATGAAGAG CTGTGCGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCCG CGTTTGAAAA AGTGCATTTT GATTGCGAAA CTTACAGCGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGCTG
751 GTCAATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAAACTT TCCGATTCAC GCTGCCATCG GGAATAATCG
1151 ATGTGGGCGG AAAATCATG TTTAAAGACA TGAAGAAGGA AGATTTGAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1   MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE AGFLTVESHQ
51  YERGWFTSTE TTVIRLKP EL LHNQKYL PD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLT L EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDKEY GPLDIHIAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTRFTLPS GKIDVGKIM FKDMKKEDLN
401 QLGLMLKKE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTLNGDQID TAISLKNQL KLNKGTQLQNE
501 PEPDFDEGGM VSEPPQ*
```

m590/a590 97.8% identity in 462 aa overlap

```
m590.pep                                10      20      30
                                WFTSMETT VIRLKP ELLNNA RKYLPD NLKT
a590                                VKAESLTQQQKILQEAGFLTVESHQYERGWFTSTETT VIRLKP ELLNNA RKYLPD NLKT
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m590.pep VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
a590 VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
                                90     100     110     120     130     140

                                100     110     120     130     140     150
m590.pep GSGKMEVSVPAFDYEE LSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
```



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1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGGCGCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A

```

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

```

1 MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE TGFLTVESHO
51 YERGWFTSME TTVIRLKP EL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PAFDYELSG
201 GDAAFEKVHF DSETSDGINP L LGSSNLTL EKFSLEWKEG VDYVVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSYEVGKLA FSTKTGESGA FINSEGQFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGEAS GLFTNNPVL D IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTNGDQID TAISLKNQQL KLNGKTLQNE
501 PEPDFDEGGM VSEPQQ*

```

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQETGFLTVESHOYERGWFTSME					
g590	MKKPLISVAAVLLGVALGTPYYLGVKAESLTQQQKILQKTGFLTVESHOYDRGWFTSTE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m590-1.pep	TTVIRLKPPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE					
g590	TTVIRLKPPELLHNAQKYLDPNLKIVLEQPVTLVNHITHGPFAGGFGTQAHIEEFKYAPE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKG					
g590	TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLKFSLEWKEG					
g590	FKSYRNSYDAPLFKIKLADKGDAAFEKAHFDSETSDGINPLALGSSNLTLKFSLEWKEG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m590-1.pep	VDYVVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFTSTKTGESGAFINSEGQFRF					
g590	VDYVVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFTSTKTGESGAFIDSEGRFRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKYGPLDIHIAAEHLDASALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEAS					
g590	DTLVYGDEKYGPLDIHIAAEHLDASALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGDAS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m590-1.pep	GLFTNNPVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK					
g590	GLFTHDPVLNLIKIFRFTLPQGKIDVGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPQK					
	370	380	390	400	410	420
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTLNGDQID					
g590	MLEDLAVSQAGNIFSVNAEDEAEARASIADINE.LRLMVDSTVQSMAREKYLTLNGDQID					
	430	440	450	460	470	480
	490	500	510			
m590-1.pep	TAISLKNQQLKLNGKTLQNEPEPDFDEGGMVS-EPQQX					

931

```

401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCATCGc cteaTGGCAG
751 GAATGygcaa acctgACccg cCAA3CCCG ggcAAAAAAA Tcacctgac
801 ctacgAaCGC GCcggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAacagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AACTAATCA GCGGCAACGC CTCTGTcAGC
1051 CATATTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACCGGT
1251 CCAAACATC GGTTCGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

m591.pep..

```

1  LQTLIAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRK
51  DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSFAEKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWAQIR RSYRPSVVR AFGMWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTVIEWIR KPLGERVQNI GLRFLALMM LMMAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1  TTGCACACCC TTCTAGCTTT TATCTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CTAAGTCGG CACAGTCGAA CCCGACCA
401 TTGCCGCCCC CGCCGCTTC CAAAGCGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AACTAATCA GCGGCAACGC CTCCGTcAGC
1051 CATATTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACCGGT
1251 CCAAACATC GGTTCGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTCGCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..

933

```

1   TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TCGGTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGACACACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCGG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CTTTTTAAAA TCACACCGT
651 TGCCGGCGGC GTGAAAAAAG GCAGCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACGT
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGCTCTT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCCTCAA ATTTTTCGGC AAATAATCA _JGGCAACGC CTCGCTCAGC
1051 CATATTTCCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTTT GGCCTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACCGCT
1251 CCAAAACATC GGTTCGCTG TCGGGCTTGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```

a591.pep
1   LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFETRKR
51  DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTIAAPAGF QSGDKIQSVN
151 GTPVADWGS A QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFLGLALM LMMVAFFND VTRL LG*

```

m591/a591 99.6% identity in 446 aa overlap

```

          10      20      30      40      50      60
m591.pep  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFETRKR DTEWCLAPIP
          |||
a591      LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFETRKR DTEWCLAPIP
          10      20      30      40      50      60

          70      80      90     100     110     120
m591.pep  LGGYVKMVD TREGEVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT
          |||
a591      LGGYVKMVD TREGEVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT
          70      80      90     100     110     120

          130     140     150     160     170     180
m591.pep  ELRPYVGTVE PDTIAARAGF QSGDKIQSVNGT PVADWGS AQTEIVLNLEAGKVAVGVQTA
          |||
a591      ELRPYVGTVE PDTIAARAGF QSGDKIQSVNGT PVADWGS AQTEIVLNLEAGKVAVGVQTA
          130     140     150     160     170     180

          190     200     210     220     230     240
m591.pep  SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA
          |||
a591      SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA
          190     200     210     220     230     240

```

935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGTTC AAACTTCCG AACATCCGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQQPYGDL SG
 101 AALTQAAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSA PNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSA PNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQQPYGDL SGAALTQAAIVSQVGQWAGFL					
g592	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQQPYGDL SGAALTQAAIVSQVGQWAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVWX					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTT TCGGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTGCAA ACATGATGA
 101 TGGGCATCAA ACGCGGCTG TATCCAACG AGCGGGTAT GGGTCCGCG
 151 CCGAACGCGC CCGCGCCGC CGAAGTGAAA CACCCTGTT CGCAAGGTAT
 201 GATTCAAATG CTGGGCGTGT TTGTCGATC CATCATCGTT TGTCTTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGCGCA TTTGAGCGGT
 301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGCGC
 351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTTCG TATGCTGGTT TTGGCGTGG TCTATTTCCG
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTGTGCGCCA TCCTGTGCT CTCGCCCTTG
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGTTC AAACTTCCG AACATCCGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQQPYGDL SG
 101 AALTQAAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

937

```

201 TATGCCGCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGCG CTGGAAAATG CGGCATTCCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AAACCTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTCC AGTTTGGACA CGCATTTGCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GCGGCATCC
551 CTGCCGTTT GGTAACGCAT TCGCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTGCGCCGA CTGATGGGTT
701 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTTCAGC CTGTCCGTCC TCCATCCGGA ACAAGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCG TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
      1 MLELNLCKR FGKNTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
      51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
     101 QKMPKAEAEER LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
     151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
     201 EIAVMHKGRI LQYGTPELV KTPSCVQVAR LMGLPNTDDN RHIPQHAVRF
     251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWNLDMRHA GAVSGKDTVR
     301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGKNTVADNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGEIWL					
	: : : : : : :					
g593	MLELNLCKCFGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPEKRRISLMFQDYALFPHMSALENAAGFLKMQKMPKAEAEERLAMAALAEVG					
	: : : : : : :					
g593	NGENITCMPEKRRISLMFQDYALFPHMSALENTAFGLKMQKMPKAEAEERLALSALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
	: : : : : : :					
g593	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAMVHKGRI LQYGTPELVKTPSCVQVARLMGLPNTDDN					
	: : : : : : :					
g593	GGIPAVLVTHSPEEACTAADEIAMVHEGKILQCGTPETLIQTAGVQVARLMGLPNTDDD					
	190	200	210	220	230	240

939

```

|||||:|||||:|:|:| |||||:|:| ||||:|||||:|
a593      GGIPAVLVTHSP EEACTAADEIAVMHEGKILQCGTPETLVQTPAGVQVAHLMGLPNTDDD
          190      200      210      220      230      240

          250      260      270      280      290      300
m593.pep  RHIPQHAVRFDQDGM ECRVLSRTCLPESFSLSVLHPEHGILWLNLD MRHAGAVSGKDTVR
          |||||:|||||:|:|:| |||||:|:| ||||:|||||:|
a593      RHIPQHAVRFDQDGM ECRVLSRTCLPESFSLSVLHPEHGILWLNLD MPHAGEISGNDTVR
          250      260      270      280      290      300

          310
m593.pep  IHIEEREIVRFRX
          ||||:|||||:|
a593      IHIEDREIVRFRX
          310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

```

g594.seq..
1  atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51  tctcgTTTT agcatactcc ggctgctggt ccgcacCGGA attgggatcg
101 gtaagtTCGc cgttcaggcc ttTCAGGTCT ttaagctgct gatctGTACg
151 gttgagcacc caaatCGGTT TGCCTTGCCA CTCGCGGTC agcagCTGac
201 ccgctTCGat tttactgaca tccacctCGa cggcagcacc ggaggccttg
251 gctTTTTCCg aagggAAAAA actggCCaCa aacggCGTtG ccacacCCAA
301 tgctGCCact ccgcccCGcGc cgcaggTCGc aagtgtcAGg aaacggCGGc
351 ggccGTtGtT gatTTCTTga ttatccatta ttcagTCGtc ctaatatTTT
401 gggaatgCCg agccattAAA cattGCAatt ttaccCAGtT tgcagTGata
451 ctcaaagcat tatttAAAat aagGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

```

g594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR KCQETAAAVV DFLIIHYSV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

```

m594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGCGGTC AGCAGCTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CCGCAGCACC GCGCGCCTTG
251 GCTTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCC CGC GCAGGTGCG GAGTGTcAGG AAACGGCGGC
351 GGCCGTtGtT gatTTCTTga ttatccatta ttcagTCGtc ctaatatTTT
401 GGGAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTtAAAAT AAGGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

```

m594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgatgat ggtggtggac gaacgcqaaa atatcgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgga aaactgcccc accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cggcaccgcg gtccattacg aacgcacgac accgattgcc
601 gagcttttca gcgaactcga ccccgtcac gatgcgtgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggcttccac cgtatcgaa
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gtccctccg ggcaaatggg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaaacagc ggcaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg ccaaaaacaa agccttggtg gaaaaaacgg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcaccaa
```

943

m595.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT'
g595	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMNRNLLPGEYEMTCGLLT
	70 80 90 100 110 120
m595.pep	130 140 150 160 170 180
	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
g595	NPRGKLVVTD SGFKDTANEADLEKLQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE
	130 140 150 160 170 180
m595.pep	190 200 210 220 230 240
	KAKSLFADTRVHYERIEPIAE L FSELD PVIDAREDDFKDGA KDAGFTGFHRIEYALWVEK
g595	KAKSLFAATR VHYERIEPIAE L FSELD PVIDACEDDFKDGA KDAGFTGFHRIEHALWVEK
	190 200 210 220 230 240
m595.pep	250 260 270 280 290 300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGA SELIEEVAGSKISGEEDRYSHTD
g595	DVSGVKETA AKLMTDVEALQKEIDALAFPPGKVVGGA SELIEEAAGSKISGEEDRYSHTD
	250 260 270 280 290 300
m595.pep	310 320 330 340 350 360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTD TNFQVNEILAKYRTK DGFETYDKLG
g595	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTD TNFQVNEILAKYRTK DGFETYDKLS
	310 320 330 340 350 360
m595.pep	370 380 389
	EADRKALQASINALAEDLAQLRGILGLKX
g595	EADRKALQAPINALAEDLAQLRGILGLKX
	370 380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

```

a595.seq
1  ATGAGAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATAT TAAAAACA CAACGCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTGCA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCGTTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATCGAGA CAAAAACAA AGCCTTGTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGCGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

```

a595.pep
1  MRKFNL TALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVVD ERENIA PGLS

```


945

```

451   ttccggcgata aagtgtgat tgacggtttg agcttcaaag tgcggcgagg
501   cgcgattgtc ggcatcatcg gcccgaacgg cgcgggtaaa tcgacgctgt
551   tcaaaatgat tgcgggcaaa gagcagcccg attcgggcca agtgaaaatc
601   gggcaaacgg tgaatatgag cttgattgac caaagccgag aaggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701   aggtcggaca gtttgaaatc cccgcccggc aatatattggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt cggcgggcga
801   acgcggccgt ctgcacttgg caaaaacctt gttgggcggc ggcaatgtgt
851   tgctgtgtga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgcg
901   ttggaagacg cattgtttga atttgccggc agcgtgatgg tgatttcgca
951   cgaccgctgg ttctcgcacc gcatagccac gcatatcttg gcgtgtgaag
1001  gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaaac gccgactcgg caaagaagcg gcgaaaccga aacgcacaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKG NYSSWLEQKE KRLNEAKSE AARVKAMQKE LEWVRQNAKG
101 RQAKPKARLA RFEEMSNEYE QKRNETQEIF IPVAERLGNV VIEFVNVSKS
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GOTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
251 FKGSQSKIA RQLSGGERGR LHLAKTLLGG GNVLLLEDEPS NDLDEVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF PDGNYQEYEA
351 DKKRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATT AAGATATTTT CCTTCTTTTC TTCCCCGGCG
101 CGAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGG TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 CGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 CGGCAGGTTC GTCCACGGGC GGCGGTGCGG AACACGAATT GGAAATCGCC
451 GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTGTTC
501 CGGCGGTGAA AAACGCCGCG TTGCCTTTGT CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGGCA CAGTCGTGTC
651 GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCGGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAACG GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTGTGA AATGTTTCCA
1001 AATCGTTTCG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTTCG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
1151 AAATCGGACA AACCGTGAAA ATGAGCTTGA TTGACCAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAA GCGCGACAT
1251 TTGTCAGGTT GGTCAAGTTG AAATCCCCGC CCGCCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1351 GGCGAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTTGA GCGGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCTGTC
1451 GCGCGTTGGA AGACGCATTG TTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GTTGGTTCCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGGCGAC TCTAAATGGG TGTTCTTCGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAATACA AACCGGTAAC GCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

947

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLD	EPSNDLDVETLRALED	ALLEFAGSVMVISHDRWFLDRIATHIL			
g596	LHLAKTLLSGGNVLLLD	EPSNDLDVETLRALED	ALLEFAGSVMVISHDRWFLDRIATHIL			
	280	290	300	310	320	330

	520	530	540	550	559
m596.pep	ACEGDSKWVFFDGN	QYEYADKKRPLGEEGAKPKRIKYKPVTRX			
g596	ACEGDSKWVFFDGN	QYEYADKKRRLGKEGAKPKRIKYKPVTRX			
	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTA AAGATATTTT CCTTCTTTT TTCCCCGGCG
101 CGAAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAAGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 GCGATTGAC GCGTTGGCGG AAGAGCAGGG GCGTTTGAA GCGATTATTG
401 CGGCGGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCT
451 GCCGACGCGC TGCGCTGCC GGAATGGGAT GCCAAATCG ATAATTGTG
501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCGGTA CAGTCGTTGC
651 CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA CTCGCTTGG
751 TTGGAGCAGA AAGAAAAACG TTTGAAACG GAGGCGAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAATGCCA
851 AAGGCGTCA AGCCAAGTCC AAAGCGCGTT TGGCGCGTTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCGGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTCGG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGCGCGA TTGTGCGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCGTGAAG ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAA ACCTGCGAAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCCGC CCGCCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCCGGC
1351 GGCGAACGCG GACGTTTGCA CTTGGCAAAA ACCTTGTGTG GCGGTGGCAA
1401 TGTGTGTGCT CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCTGC
1451 GCGCGTTGGA AGACGCATTG CTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GCTGTTTCTT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGGCGAC TCAAATGGG TGTTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.pep
1  MSQQYVYSML RVSKVVPQK TIIDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEP LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADFD ALAEEQGRLE AIIAAGSSTG GGAHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAEE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAARVK AMKQELWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSTFKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKITGQLSG
451 GERGRLHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNQ QEYADKKRR LGEEGTPKPKR
551 IKYKPVTR*

```

m596/a596 99.3% identity in 558 aa overlap

g597 . pep

1	MLLHVSNSL	QLOERIQRE	RIRQERIROA	RGNSLASVNRK	QREAWDFKFO
51	LNTELNRLKT	EVAATKIQE	RFQSVNGYKNS	RPNVALFLK	NAEPGQKNRF
101	LRYYTRYVNS	NEVVTKLEK	QKALAVQEQ	KINNELARLK	KIQANVQSL
151	KKQGVTDAAE	QTESRRQNAK	ISKDAKLE	QKQNEQOLNK	LLSNLEKKKA
201	EHRIQDAEAE	RKLEAKALAA	AEKARKAEAA	QKAEARRAE	SNLTAEADNR
251	QAPSVMGIGS	ADGFSRMQGR	LKKPVDGVPT	GLFGQNRSGG	DVWKGVFYST
301	APATVYESAP	GTVSVADELD	GYGKVNVVDH	GENYISYAG	LSEISAGKGY
351	TVAAGSKITG	SGSPDGEED	LYLQTYRRQG	VLPNSGWR	

m597.seq

1	ATGCTGCTTC	ATGTCAGCAA	TTCCTTCAA	CAGCTTCAGG	AAGAGCGTAT
51	CCGCCAAGAG	CGTATCCGTC	AGGCGCGCGG	CAACCTTGTG	TCCGCTCAACC
101	GC AAAACAGCG	CAGGGCTTGG	GACAAGTTCT	AAAAACTCAA	TACCGAGCTG
151	AACCGTTTGA	AAACGGAAGT	CGCCGCTACG	AAAGCGCAGA	TTTCCCGTTT
201	CGTATCCGGG	AACTATAAAA	ACAGCGCAGC	GAATCGGGTT	GCCCTTTTCC
251	TGAAAACAGC	CGAACCCGGT	CAGAAAACAC	GCTTTTTCGG	TATACGCGGT
301	TATGTAAACG	CCTCCAATCG	GGAAGTTGTC	AAGGATTTGG	AAAAACAGCA
351	GAAAGGCTTG	CGCGTACAAG	ACGACAAAAA	ACAACATGAG	CTTGGCCGTT
401	TGAAGAAAAA	TACGGAACAC	GTGCAATCTC	TGCTGAAAAA	ACAGGGTGTA
451	ACCGATGCGG	CGGAACAGAC	GGAAGCCGCG	AGACAGAATG	CCAAAAATCGC
501	CAAAAGATCG	GCCAAAACGT	TGGACACAGAA	AGGGAACGAG	CAGCAGCTGAG
551	ACAAGCTCTT	GAGCAATTTG	GAGAAGAAAA	AGGCCGACAA	CCGCATTGCA
601	GATGCGGAAG	CAAAAAGAAA	ATTGGCTGAA	GCCAGACTGG	CGGCAGCCGA
651	AAAGAGCCGA	AAAGAAGCGG	CGCAGCAGAA	GGCTGAAGCA	CGAGCTGCGG
701	AAATGTCFCA	CTCGACCGCC	GAAAGCAGGA	ACATCCAAGC	GACCTTCGGT
751	ATGGGTATCG	GCAGTGCCGA	CGGTTTCAGC	CGCATGCAAG	GACGTTTGAA
801	AAAAACCGGT	GCGAGTTGTC	AGCCCGGACT	TTTCGGGACG	AACCGACGCT
851	CGGGCGATAT	TTGGAAGATG	GTGTTCTATT	CCACTGCACC	GGCAACGGTT
901	GAAAGCATTG	CGCCGGGAAC	GGTAAGCTAT	GCGGACGAGT	TGGAACGGCTA
951	CGGCAAACTG	GTCGTGGTGC	ATPACCGCGA	GAACTACATC	AGCATCTATG
1001	CCGGTTTGTG	GCAAAATTTCC	GTCCGCAAGG	GTTATATGCT	GCGGCGAGGA
1051	AGCAAAATCG	GCTCGAGCGG	GTCGCTGCCG	GACCGGGGAG	AGGGGCTTTA
1101	CTCTGCAATA	CGTTATCAAG	GTCAGGTATT	GAACCCCTCG	AGCTGGATAC
1151	TTTGA				

m597 . pep

1	MLLHVSNSLR	QLQEEIRIQE	RIRQARGNLA	SVNRKQREAW	DKFQKLNTEL
51	NRLKTEVAAT	KAQISRFSVG	NYKNSQPNAV	ALFLKNAEPG	QKNEFLRYTR
101	YVNASNREVV	KDLKEQQKAL	AVQEKQINNE	LARLKKIQAQ	VOSLLKKQGV
151	TDAAEQKTES	RONAKIAKDA	RKLLKQKNEE	QQLNKLLENL	EKKKAEHRIQ
201	DAEAKRKLEA	ARLAAAEKAR	KEAAQQKAGE	NRAGMSNLTA	EDRNIQAPSV
251	MGIGSADGFS	RMQGRLLKPV	DGVPDTGLFG	RRAEDDIWKG	VFYSTATPATV
301	ESIAPGPTVSY	AEDLDGYGKV	VVDVGHENYI	SIYAGLSEIS	VGKGVMVAAG
351	SKIGSGSGLP	DGEEGLYLOI	RYOGVONLPS	SWIR*	

951

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951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGTCGC TGCCCGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTCGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

a597.pep

```

1 MLLHVSNSLK QLQEEIRQE RIRQERIROA RGNLASVNRK QREAWDKFQK
51 LNTLNLRLKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QOKALAVQEQ KINNELARLK KIQANVQSLL
151 KKGQVTDAAE QTESRRONAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKTGFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISIIYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGG VLNPSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

	10	20	30	40	50	60
a597.pep	MLLHVSNSLKQLQEEIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNLRLKT					
m597	MLLHVSNSLKQLQEEIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNLRLKT					
	10	20	30	40	50	
	70	80	90	100	110	120
a597.pep	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
a597.pep	QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRONAKIAKDARKLLE					
m597	QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRONAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
a597.pep	QKGNEQQLNKLLSNLEKKKAHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLLSNLEKKKAHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
a597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
a597.pep	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
a597.pep	SGSLPDGEEGLYLQIRYQGGVLNPSWIRX					
m597	SGSLPDGEEGLYLQIRYQGGVLNPSWIRX					
	360	370	380			

953

```

      |||
g601  TIRAYGALKMGLISDVSEAAARARTPKPAFVAPAADYTASSGKTVNAADIDLPRALSMG
      70      80      90      100     110     120

      130     140     150     160     170
m601.pep KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHGHPSGTLRVGAAAECQDGQWT
      |||
g601  KLHHAMMGIA SVAI--AAAVLGTLVNLAAGGGTRKEVRFHGHPSGTLRVGAAAECQDGQWT
      130     140     150     160     170

      190     200
m601.pep ATKAVMSRSARVMMEGWVRVPEDCFX
      |||
g601  AAKAVMSRSARVIMESWVRVPDDCFX
      180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCGCGCGCG
251 ACACGCC3AA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAATGC CGCGACATC GATTTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTG CCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCGG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGGAAAGGTG GGTGAGGGTG
601 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTKEVRFHG HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

      10      20      30      40      50      60
m601.pep MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
      |||
a601  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
      10      20      30      40      50      60

      70      80      90      100     110     120
m601.pep KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
      |||
a601  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
      70      80      90      100     110     120

      130     140     150     160     170     180
m601.pep KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHGHPSGTLRVGAAAECQDGQWT
      |||
a601  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHGHPSGTLRVGAAAECQDGQWT
      130     140     150     160     170     180

      190     200
m601.pep ATKAVMSRSARVMMEGWVRVPEDCFX
      |||
a601  ATKAVMSRSARVMMEGWVRVPEDCFX
      190     200

```

955

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
a602	MLLHQCDKARHMRPLLLGRQVNRHGQTGNGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHV CNSVHELFFLN I H V I V E M C A W Y G V S A G E Y T V N L Q M R D Y I T R F X Q L H X					
a602	AGLHV CNSVHELFFLN I H V I V E M C A W Y G V S T G E Y T V N L Q M R D Y I T R F X Q L H X					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603.seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTT
101 CAGACGGCCC CGCACAAAAA AAACAACCAC AAATAACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCTGAAC TGCCTCAGTT CATCGCTCAA
201 AGGCGCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCTTA AGCTGCCTCG
251 GGGAAACGCT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCCCT GAGCGGCCGC AACTGCCACG CCGGCGCGGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCAGGCG GCGAAAAATA TCACGAGTCC
451 GTCCTCATCG ACCAAGACGT CTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCGC GCGAATTGCG
651 CAAAAAATAC GCCTTCCGCC GCTACGGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTCt ggaaGACATC
751 CGCATGATTA TTGCCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCG ATCGAAGGTT
851 TGGTAATGGG TACACGTTCG GCGACACCG ATCCGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTTCCCG GTATTTCCga actTCCCAAC GACTGCCGCA
1001 CCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGGCGCGCG CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCCT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTTAC CGGCGGTATC GGCAGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCCT ATCTTGATT CTGGGTCTG
1201 CACATCGACA CCAAAGCCAA TATGAAAAA CGTACGGCA ATTCCGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCGG CATCTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603.pep

```

1  MDSRLRGNDA RYKIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTRRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTTP EAVITFNKDG
101 NKROVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLEDE LKACIPFAPL HNPANISGIL AAQEHFPGLP NVGVMDTSFH
201 QTMPERAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISELPN DCRTLEIAAD EGREGARLAL
351 EVMTCRLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDPLGL
401 HIDTKANMEK RYNGSGIISP TDSSPAVLVV PTNEELMIAC DTAELAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603.seq

```

1  CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TGCGCCTGAT GTCTGC.CTT
101 TTTCAGACGA CCCACACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAmAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCACG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

957

```

g603      LAAQEHFGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLNGASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISELSND CRTLEIAA DEGHEGARLAL EVM TYRLAK
          |||||:|||||:|||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGIS ELPND CRTLEIAA DEGREGARLAL EVM TCRLAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVGC GVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          |||||:|||||:|||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          |||||:|||||:|||||:|||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1   CTGTCTCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
101 TTTTCAGACGA CCCACACACC. AAAAAACAAC CACAAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGCG CGGAACTGCC ACGCCGCGCG
351 GGTGGGTATG CTGTTGAACG AACTGGAAAA ACACGAACTG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGAC
551 AGGAACATTT CCCCCTCTG CCCAATGTCG GCGTGATGGA TACTTCGTTC
601 CACCAAAACCA TGCCGAGCGC TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCTGAAGCC GCATGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACGCGC TGCGCGGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTC CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCGGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGTTGACG CACTCGTGTT CACCGCGGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCTGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TGCGACACTG CCGAACTTGT CCGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1   LSSRRRGRNN DRKCGIRFAQ RGRLKHTPPN AHPFSDPTX KKQPQTTRRN
51  IMSDQILILVL NCGSSSLKGA VIDRKSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHNPNANISGI LAAQEHFGL PNVGVMDTSF

```

g604 . pep

m604.seq

m604 . pep

m604 / g604

a604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
51 CCAGCGTACC GGGCACGGCG GCGGCGGTGC CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCAA TTTGCCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTGC GCGGCATTCA CGGTTTTGCC ACTGGAGGCG GTGTAATCGG

961

```

951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCCAGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTACAG AGCTATGTCG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNNTKLKE IFTAIESSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIEEGFF
251 GQEINHHTYN LARMNMF LHN VNYNKFHIEL GDTLTNP KKLK DSKPFDVVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNLYSGRG
351 RAAIVSFPGI FYRGGAEQK ROYLVEGNYV ETVIALAPNL FYGTCLAVNI
401 LVL SKHKDNT DIQFIDASGF FKKETNN NVL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQT V KDNGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTGGA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCCGAC
151 TATATGACAG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCTC CAAAGGCGTG GCGGAACTCG ATTTCCGCAA
501 TTTTGAAAA CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGTGCCAAC GCAGGCAAAT CCGGCGCGCA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCGCGA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GCGCACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAA CTTTGATGTC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCAGCATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCGG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTACAG AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

```

```

                                963
                                430      440      450      460      470      480
                                490      500      510
m605.pep    IIDIKQLNAEIGETVAKIERLRREIDEIVIAEIEAX
              :|||:|||||:|||||||||||||||||:
g605         VIDIRQLNAEISETVAKIERLRREIDEIVAIETX
              490      500      510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1911>:

```

a605.seq
1   ATGATGACCG  AAATACAACA  ACGCGCCCAA  CTGCACCGCC  AAATTTGGAA
51  AATTGCCGAC  GAAGTAGCGG  GCGCGGTGGA  TGGCTGGGAC  TTTCAACAAT
101 ACGTTCTCGG  CACACTTTTC  TACCGCTTTA  TCACGCAAAA  TTTACCGAC
151 TATATGCAGG  CAGGCGACAG  CAGTATTGAT  TACGCCGCTA  TGCCGGACAG
201 CATCATCACG  CCCGAAATCA  AAGACGATGC  CGTCAAAGCT  AAAGGCTATT
251 TCATCTACCC  CGGCCAGCTT  TTTTGCAATA  TTGCGCCGCA  AGCCCCATAA
301 AACGAAGAGC  TCAACACCAA  GTTGAAAGAA  ATTTTACCG  CGATTGAAG
351 CTCCGCCTCC  GGCTATCCGT  CCGAACAAAG  CATTAAAGGC  CTGTTTGACG
401 ACTTCGACAC  CACCGACGAG  CGGCTCGGCA  GCACCGTTGC  CGACAAGAAC
451 AAACGCCTTG  CCGCCGTCTT  AAAAGCGGTG  CGGGAATCTG  ATTTCCGCGC
501 TTTTGAAGAC  CACCACATCG  ACCTTTTCGG  CGATGCCTAC  GAATACCTGA
551 TTTCCAACTA  CGCTGCCAAC  GCAGGCAAA  CCGGCGGCGA  ATTTTTTACC
601 CCGCAAAGCG  TATCCAAGCT  GATTGCGCGG  CTGGCGGTGC  ACGGGCAGGA
651 GAAAGTAAAC  AAAATCTACG  ACCCAGCTTG  CGGCTCGGCG  AGCCTGCTCT
701 TCGAGCGAAA  AAAACAGTTT  GACGAGCACA  TCATCGAAGA  AGGCTTCTTC
751 GGGCAGGAAA  TCAACCACAC  CACCTACAAC  CTCGCCCGCA  TGAATATGTT
801 TCTGCACAAC  GTCAATTACA  ACAAAATCCA  CATCGAATTG  GCGCAGACAC
851 TGACCAATCC  CAAACTCAAA  GACAGCAAA  CCTTTGATGC  CGTCGTTTCC
901 AATCCGCCCT  ATTCATCAA  CTGTGATAGC  AGCGGCGACC  CACCTTAAT
951 CAACGACGAC  CGCTTTGCCC  CTGCAGGCGT  ACTCGCCCCG  AAATCCAAAG
1001 CCGATTTTGC  CTTCATTCTG  CACCGACTCA  ACTACCTTTC  CGGCAGCAGC
1051 CGCGCCGCCA  TCGTCTCATT  CCCCGCATT  TTCTA1CGCG  CGGGCGGCGA
1101 GCAGAAAATC  CGCCAATATC  TGGTGGAGGG  CAACTACGTG  GAAACCGTCA
1151 TCGCCCTTGC  GCCCAATCTC  TTTTACGGCA  CCGGCATCGC  CGTCAATATA
1201 CTGGTTTGTG  CCAAACACAA  AGACAATACC  GACATCCAAT  TCATCGAGAC
1251 AGGCGGCTTC  TTTAAAAAAG  AAACCAACAA  CAACGCTCTA  ACCGAAGAAC
1301 ACATTGCCGA  AATCGTCAAA  CTCTTCGCGG  ATAAAGCCGA  TGTGCCGCAT
1351 ATCGCCCAAA  ACGCCGCCCA  GCAAACCGTC  AAAGACAACG  GCTACAACCT
1401 CGCCGTGAGC  AGCTATGTTG  AACCCGAAGA  CACCCGCGAA  ATTATCGACA
1451 TCAAACAGCT  TAACGCCGAA  ATCAGCGAAA  CCGTTGCCAA  AATCGAACGG
1501 CTGCGGCGTG  AAATTGACGA  AGTGATTGCA  GAGATTGAAG  CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

```
a605.pep
  1  MMTEIQQRAQ  LHRQIWKIAD  EVRGAVDGDW  FKQYVLGTLF  YRFISENFTD
51  YMQAGDSSID  YAAMPDSIIT  PEIKDDAVKV  KGFIYFPQGL  FCNIAAEAHQ
101 NEELNTKLKE  IFTAIESSAS  GYPSEQDIKG  LFDFFDPTTS  RLGSTVAADK
151 KRLAAVLKGV  AELDFGSFED  HHIDLFGBAY  EYLISNYAAN  AGKSGGEFFT
201 PQSVSKLIAR  LAVHGEQKVN  KIYDPACGSG  SLLLQAKKQF  DEHIEEGFF
251 GQEINHNTY  LARMNMFNLN  VYNYNKFHIE  L GDTLTNPKL  DSKPFDVAVS
301 NPPYSINWIG  SGDPTLTND  RFAPAGVLAP  KSKADFAFIL  HALNYLSGRG
351 RAAIVSFPGI  FYRGGAEQKI  RQYLVEGNYV  ETVIALAPNL  FYGTGIAVNI
401 LVLSKHKDNT  DIQFIDAGGF  FKKETNNNV  L TEEHIAEIVK  LFDADKADVP
451 IAQNAAQQT  V KDNQYNLAVS  SYVEPEDTRE  IIDIKQLNAE  ISETVAKIER
501 LRREIDVIA  EIEA*
```

m605/a605 98.1% identity in 514 aa overlap

	10	20	30	40	50	60
m605.pep	MMTEMQQR	QLHRQIW	KIAD	EV	RG	AVD
	GG	WDF	KQ	YV	LG	TL
	FY	RF	ISE	N	FT	DY
	MQ	AG	D	S	S	I
	:	:	:	:	:	:
a605	MMTE	IQ	QR	QL	HR	QI
	W	KI	AD	EV	RG	AV
	D	GG	WDF	KQ	YV	LG
	TL	FY	RF	ISE	N	FT
	DY	MQ	AG	D	S	S
	I					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMP	DSI	IT	PE	IK	DD
	AV	KV	KGY	FI	YP	GP
	OLF	CN	IA	EA	EH	ON
	EEL	NT	KL	KE	IF	TA
	IE	SS	AS			

965

g606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTGTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGCGGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTTCT GGTACGATG GTATTCCAAA TCCTGTTTCG CTTCCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCCGAA AATGATTTCC GCCTGCAAA
551 GGCTCAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCTGCTC AGCACCCACC CTTCGCTGGA
651 CAACCGTATC GCCCGCCTCA AATCGCTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

	10	20	30	40	50	60
m606.pep	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
g606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

```

601  GGTTCGCGCG TGGCGACAAT GCGGTGTTT TGGTTCAGCG CGCTGGCATT
651  GTGGATTTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGACTGACAG
701  CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751  gGcgcgCCCA TCGGGCTGTC TTATTTTGTG GAAgccaGcg cGTTTTCGTT
801  TATCGTGTTC TTGATTGCGC CTttcggCGA GGATTATGTG GCGGCGCAGC
851  AGGTGCGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901  GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951  TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTCT GGCTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTC GCCGCTGGCA
1051 AGCATGTACA ACGATGaTCC GGCAGTTTTA AGCATCGCCT CCACCGTCCT
1101 GCTGTTTCGCC GGCCTGTtcc aACCGGCAGA CTTACCCAA TGTATCGCGT
1151 CCTATGCCCT GCGCGGCTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TCTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTT ATTGCCTCGC
1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGGAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1  MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFGILIGIF GMILMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRALHAYA SSLNRPRIM LVSPAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMPIQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFRRSPLA
351 SMYNDPAVL SIASTVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMTIH
401 AAAFWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT CCGCTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCACTCTTC CCTTCCCTT GCTGTTGGCG CAGGTGCGCG
101 AGGTGGGCAT CGGTTTTGTC GATACTGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CCGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAAGTG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GCGGATTACG CCGTCCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCGCTGCA CGCTACACT TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GCGGATTCGAC TGGCGACGAT GCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGACTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAATC
751 GGCGACCCA TCGGGCTGTC TTATTTTGTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTC GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GGCGGTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTC AACCAGCAGA CTTACCCAA TGTATCGCCT
1151 CTTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGGAAAT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1  MLLDLNRFSF PVFLKEVRLT TTLALPMLLA QVAQVGIGFV DTMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGGTGTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCC TTAGCCTGA ACCGCCCSCG
501 CCTGATTATG TTGGTCAGCT TTGGCGCGTT TGTGTGAAC GTGCCGTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGAATGACGG
701 CGAAATTCGG CAAACCCGAT TGGCGGCGTG TCAAACAGAT TTGAAAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCTGT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGGC CATCGGCTTT TCGCTTGGGC GGCAGCAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GGCGGTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTCCGC GGCTTGTTC AACCGGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATT ACGGCTTCTG GACGGCATTG ATGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1  MLLDLNRFSF SVFLKEVRLL TALALPMLLA QVAQVGIGFV DTMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFGFLFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMFAA
151 MVHRALHAYA SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVEFKQIWKI
251 GAPIGLSYFL EASAFSFIWF LIAPFGEDYV AAQQVGISLS GILYMIPOSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFRRSLV
351 SMYNNDAVL SIAATVLLFA GLFQPAFTQ CIASYALRGY KVTKVPFMFIH
401 AAATFWCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCRS
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFVPFLKEVRLLTTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
a607	MLLDLNRFSFVPFLKEVRLLTTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLFLGVFGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLFLGVFGMVLMWAAIT					
	70	80	90	100	110	120
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYTSSLNRPRILMLVSFAAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYTSSLNRPRILMLVSFAAFVLN					
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYTSSLNRPRILMLVSFAAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYTSSLNRPRILMLVSFAAFVLN					
	190	200	210	220	230	240

971

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
 551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep
 1 MSALLPIINR LILQSPDSRS ELAFAAGKTL TLNIAGLKLA GRITEDGLLS
 51 AGNGFADTEI TFRNSAVQKI LQGGEPPAGD IGLEGDLILG IAVLSLLGSL
 101 RSRASDELAR IFGTQADIGS RAADIGHGK QIGRNIAEQI GGFSRESESA
 151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng)

from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRSELAFAAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
g608	MSALLPIINRLILQSPDSRSELTSEAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEPPAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS					
	70	80	90	100	110	120
g608	TFRNSAIRKILQGGEPPAGDIRLEGDLILGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	130	140	150	160	170	180
m608.pep	RAADIGHGKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
g608	RATDIGHGKQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	189					
m608.pep	LERDIWIDX					
	189					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq
 1 ATGTCCGCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
 51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA
 101 TTGCCGGGTT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
 151 GCGGGAAACG GCTTTGCAGA CACCGAAATC ACCTTCGCA ACAGCGCGGT
 201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GCGGGGCGAC ATCGGCTCTG
 251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
 301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
 351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAAA CAAATCGGCA
 401 GGAACATCGC CGAACAAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
 451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
 501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
 551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep
 1 MSALLPIINR LILQSPDSRS ELAFAAGKTL TLNIAGLKLA GRITEDGLLS
 51 AGNGFADTEI TFRNSAVQKI LQGGEPPAGD IGLEGDLILG IAVLSLLGSL
 101 RSRASDELAR IFGTQADIGS RAADIGHGK QIGRNIAEQI GRFSREPESA
 151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

```
a609.seq
  1  ATGGTTGTGG  ATAGACTCGA  AATTCTCGCT  CTCGACGACG  AAACTCTTGA
51  TGCAGTTTGC  GGCAATCAGC  GAAGTAGCAG  CATCGCGCAC  CATATCTTCG
101 ACGAATTTCT  GGTATTCGTA  GGCPTTTTCC  GTAACGTATT  TTTCATCTGG
151 GCGTTTGAGC  AGGCCGTAGA  GTTGGCAGCT  CGCCTGCGCC  TCCACATAAT
201 CGATGACTTC  CTCGATACCG  ACTTCGGCAT  CGGCAGTCAG  GCTGACGGTA
251 ACGTGCGAAC  GCTGTTGTG  CGGCCATAT  TGGGAAATTT  CTTTGGAAAC
301 CGGGCAAAGC  GAGGTTACGG  GAATCATGAC  CTTCATACTG  TGGCCGTATG
351 CACCGTCTTT  CATTTTCGCC  GTGAGGCTGA  CATCATAATC  CAGTAA
```

a609.pep

1	MVVDRLLEILA	LDDETLDAFV	GNQRSSDIAH	HIFHEFRVTV	GFFGNVFFIG
51	AFEQAVELAA	RLRLHIIDDF	LDTDFGIGSQ	ADGNVRTLTV	RAILGNFFGT
101	BAKRGYGNHD	LHTVAVCTVF	HFAREADIII	O*	

		10	20	30	40	50	60
m609.pep		MVVDRL	EILALD	DETLD	AFVGNQ	RSSDIA	HHIHFH
a609		MVVDRL	EILALD	DETLD	AFVGNQ	RSSDIA	HHIHFH
		10	20	30	40	50	60
		70	80	90	100	110	120
m609.pep		RLRLHI	IDDFLD	TDFGIG	SQADGN	VRTLVV	RAVLGN
a609		RLRLHI	IDDFLD	TDFGIG	SQADGN	VRTLVV	RAILGN
		70	80	90	100	110	120
		130					
m609.pep		DFARETD	IIIIQX				
		:					
a609		HFAREAD	IIIIQX				
		130					

g610.seq

1	ATGATTGGAG	GGCTTATGCA	ATTTCCTTAC	CGCAATGTTC	CGGCTTCGCG
51	TATGCGCCGT	ATGCGCAGGG	ATGATTTTTC	ACGCCGCCTG	ATTGCGGAGC
101	ATATGCTGAC	CGCGATGAT	TTGATTTATC	CGGTGTTCGT	ATTGGAGGGG
151	CGCGGCGCGC	AGGAGGATGT	GCCTTCTATG	CCGGGCGTGA	AGCGCTCAGAG
201	TTTGGACAGG	TCGCTGTTTA	CGCCGAAGA	GCGCGTGAGC	TCGCGATTTC
251	CGATGTTGGC	ACTCATTCCC	GTGGTTACGG	CAAAACAAAAC	CGGGGCGTCG
301	CAGGAGCGCT	CAAAATCCCA	AGGACTCGTG	CCGTCAACTG	tccgagcctt
351	GCGCGAGAGG	TttcCggaac	tggggattat	gacgagtgtc	gcgtctcgAtc
401	cttatacggt	gcacGGTGAC	GACGGCATGA	CGGACGaaaa	cggttaCGTG
451	ATGaagtATg	aaaCCGTAGA	AGTCTTGGTG	AAACAGGCTT	TATGTCATGC
501	AGAGGCGGGC	ACGAGGTCG	TTGCTCCTTC	CGATATGATG	GACGGGCGTA
551	TCGCGCCCAT	CCGCGAGGCT	TTGGAGGATG	CCGACATATC	CCATACCGGG
601	ATTATGGCAT	ATTCCGCCAA	ATATGCTTCT	GCATTCTACG	GCCCTTTCCG
651	TGATGCGGTA	GGCAGTTCGG	GCAATTTGGG	AAAGGCAGAT	AAAAAGACCT
701	ATCATAGTGA	TCCTGCAAA	ACCGATGAGG	CGCTGCTAGA	AGTGCGCTGA
751	GATATTACGA	AAGGTGCGGA	TATGGTATG	GTGAAGCCCG	GTGTGGCGTA

975

```

g610      DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240

           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTTYAYQVSGEYAMLQAAIAN
           |||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300

           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           |||
g610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCGTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTTATC CGGTGTTCGT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGC
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTCCCGAAC TGGGCATTAT GACGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1  MIGGLMQFPY RNVASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KPTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSGE YAMLQAAVAN
301 GWLDGGKVVV LESLLAFKRAG ADGILTYYAI EAAKMLKR*

m610/a610  99.4% identity in 338 aa overlap

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           |||
a610      MIGGLMQFPYRNVASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60

           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120

           130     140     150     160     170     180

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977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               |||||
g611          MPSENGMGKRQLAGCRLFGKLSLVFRLLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
               10      20      30      40      50      60

               70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIAVDGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               |||||
g611          LAQVVAVILGRAGLFARHNFQYLIAVYGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
               |||||
g611          ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
               130     140     150     160     170     180

m611.pep      X
               |
g611          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1  ATGCCGCTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCTGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAATCCG GCGGATTTCC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCG AACGGGTTAC GTCGCTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GTCATGCCG TAGCGCGTTA
501 CCATTTGCG CGCCATTTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1  MPSENRMGKR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIAVDGF PHQGFARHFL
101 LVAVFIEDFV GNILLVQNP ADFRIDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

m611/a611    98.9% identity in 180 aa overlap

               10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               |||||
a611          MPSENRMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               10      20      30      40      50      60

               70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIAVDGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               |||||
a611          LAQVVAVIFGRAGLFARHDFQYLIAVDGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
               |||||
a611          ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
               130     140     150     160     170     180

m611.pep      X

```

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
 51  GKVVFADKAVE KCAENVLFEEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101  NPYXKLNKSK SPDIFRRFFX GHSN*

m612/a612  96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep    MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
              |||||
a612        MGFGGNIAKKLAGVDEIAFDGIVDFDGRDDAVRHSGVINTAVACLHIVGKVVFADKAVE
              10      20      30      40      50      60

              70      80      90      100     110     120
m612.pep    KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFX
              |||||
a612        KCAENVLFEEVPAIHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRRFFX
              70      80      90      100     110     120

m612.pep    GHSNX
              ||||
a612        GHSNX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCTG CGAGGCAGTC GGCAAGGGCT TCGTTGCCGG
101  TGTtTGcGGA CTCGGGTTTCG CGGGAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTgtttGAT GCCGTGTCCG ATGTCGGTGG CACGgctgcc
201  gatgcCTGCC TGCCTGCCGA AAATCCGTGC CAATTCgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCG
301  CCTTCGAGCC TGATGTGCCC AGCCCCGGGT TCGCCGCTT GGAGGATTTT
351  CCGTATCGCG CTGTTGCCGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501  GCTGTCCGGG CTTTCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT
601  ATTTTACAGG CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
 51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFPASFKPS SVMRPASFSP
151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
201  ILQA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCTG CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101  TGTtTGcGGA CTCGGGTTTCG CGGGAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTGTtTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201  GATGTCTGCC TGCCTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301  CCTTCGAGCC CGATGTGCCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351  CTGTACCGCG CTGTTGCCGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
501  GCTGTCCGGG CTTTCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT

```

981

```

                130      140      150      160      170      180
m613.pep      LLRKVISVSAKPFPAESKPSSVMPASFSFSPAMFRVSVLPAPAKAASSERLSGLCRIRRLMMG
                |||||
g613          LLRKVISVSAKPFPAESKPSSVMPASFSFSPAMFRVSVLPAPAKAASSERLSGLCRIRRLMMG
                130      140      150      160      170      180

                190      200
m613.pep      RRADIFSDRGGECLLLLLPLILQAX
                |||||
g613          RRADIFSDWGGECLLLLLPLILQAX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1   ATGTCGCGTT  CGAGCCGGTC  GAGGCGTTCG  TTGAGGCGTT  CCACGCCGTC
51  GCGCAGTCTG  CTTATTTCGT  CGAGGCAGTC  GGCAAGGGCT  TCGTTGCCGA
101 TGTTTGCGGA  CTCGGGTTCG  CGGGAAAATC  TGCCGATTTC  TTCGGCGATG
151 TTCCTGCCGA  TTTGTTTGAT  GCCGTGTCCG  ATGTCGGCGG  CACGGCTGCC
201 GATGTCTGCC  TGCCTGCCGA  AAATCCGTGC  CAATTCGTCC  GATGCGCGGG
251 AACGCAGGCT  GCCGAGCAGG  GACAGTACCG  CGATGCCGAG  GATGAGGTCG
301 CCTTCGAGCC  CGATGTCGCC  CGCCCCGGGT  TCGCCGCCTT  GGAGGATTTT
351 CTGTACCGCG  CTGTTGCCGA  AGGTGATTTC  GGTGTCTGCA  AAGCCGTTTC
401 CCGCCGAGAG  CAAACCGTCT  TCCGTGATGC  GTCCCGCCAG  TTCAACCCG
451 GCAATGTTCA  GGGTCAGTGT  TTTGCCTGCG  AAGGCGGCAA  GTCCGAGCG
501 GCTGTCCGGG  CTTTGACAG  TCAGGCGGTT  GATGATGGGG  AGGAGGGCGG
551 ACATATTTTC  TGATCGGGGC  GGAGAATGCC  TGTGTGTGCT  GTTGACGCTT
601 ATTTTACAGG  CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```

a613.pep
1   MSRSSRRSLRRSTPSRSL LISSRQSARA SLPMFADSGS RENLPICSAM
51  FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFPAESKPS SVMRPASFNP
151 AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLTL
201 ILQA*

m613/a613    98.0% identity in 204 aa overlap

                10      20      30      40      50      60
m613.pep      MSRSSRRSLRRSTPSRSL LISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP
                |||||
a613          MSRSSRRSLRRSTPSRSL LISSRQSARASLPMFADSGSRENLPICSAMFLPICLMPCP
                10      20      30      40      50      60

                70      80      90      100     110     120
m613.pep      MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPWPWIFCTA
                |||||
a613          MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPWPWIFCTA
                70      80      90      100     110     120

                130     140     150     160     170     180
m613.pep      LLRKVISVSAKPFPAESKPSSVMPASFSFSPAMFRVSVLPAPAKAASSERLSGLCRIRRLMMG
                |||||
a613          LLRKVISVSAKPFPAESKPSSVMPASFSFSPAMFRVSVLPAPAKAASSERLSGLCRIRRLMMG
                130     140     150     160     170     180

                190     200
m613.pep      RRADIFSDRGGECLLLLLPLILQAX
                |||||
a613          RRADIFSDRGGECLLLLLTLILQAX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

983

```

m614.pep
  1  MAAFNALDGK KEDNGQIEYS QFIQVNNGE VSGVNIIEGSV VSGYLIKGER
 51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101  LIGAWFYFMR MQTGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151  KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEGAG
201  VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251  GAGLGGGNDE REQTLNQLLV EMDGFESNOT VIVIAATNRP DVLDPALQRP
301  GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLA RGTGPGFSGAD
351  LANLVNEAAL FAGRRNKVKV QSDLKTPKT KSIWVRNAAV W*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

m614.pep	10	20	30	40	50	60
	MAAFNALDGKKEDNGQIEYSQFIQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFTNA					
g614	MAAFNALDGKKEDNGQIEYSQFIQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFTNA					
	10	20	30	40	50	60
m614.pep	70	80	90	100	110	120
	PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG					
g614	PLDDNLIKTL LDKNVRVKVT PEEKPSALTA LFYSLLPVLL LIGAWFYFMR MQAGGGKGG					
	70	80	90	100	110	120
m614.pep	130	140	150	160	170	180
	AFSFGKSRAR LLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
g614	AFSFGKSRAR LLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
	130	140	150	160	170	180
m614.pep	190	200	210	220	230	240
	AGSPGTGKTL LAKAIAEGAG VPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
g614	AGSPGTGKTL LAKAIAEGAG VPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
m614.pep	250	260	270	280	290	300
	DEIDAVGRQR GAGLGGGNDE REQTLNQLLV EMDGFESNOT VIVIAATNRP DVLDPALQRP					
g614	DEIDAVGRQR GAGLGGGNDE REQTLNQLLV EMDGFESNOT VIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
m614.pep	310	320	330	340	350	360
	GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLA RGTGPGFSGAD LANLVNEAAL					
g614	GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLA RGTGPGFSGAD LAKLVNEAPL					
	310	320	330	340	350	360
m614.pep	370	380	390			
	FAGRRNKVKV QSDLKTPKT KSIWVRNAAVWX					
g614	FAGRRNKVKV QSDLKTPKT KSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

```

a614.seq
  1  ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGCAAAAT
 51  CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101  TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCAGCGC
151  ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTTGGACG ACAACCTGAT
201  TAAAACACTG CTCGACAAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
251  AACCGAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCTGCTG

```

985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAAC  GCGCGCGCGC  CGGTGtcggC  AACTTTgaag  agcagcGaAT
51  agatgCCGCC  GGCAAACCCAC  AATGCGGAAa  gcaggCtgaa  gcGGTTgcgC
101 GGCagcTTca  tGCCGCCTCC  TcGTCCaGCC  ACGtttGgca  gattttggac
151 aggcgcAGGa  ATTTGCcgCc  gcgtgcggCA  agtatgtcgc  gcCAttgtgc
201 cacttcttcg  gcggacggTG  cttcgtcgaT  gctgCATTCG  TACagcagga
251 aatcgagggt  ttcttctatg  acggGgatgg  AttccgTTTG  GataAgCTgc
301 ttgagttcgt  tcatgactGt  TCgGATAcgg  aaatcgggaa  aatgccgtct
351 gAaagggtt  CAGACGGCat  tggATTATTT  GCTGTGCAGG  AAgcgcgttg
401 cctcttccca  tttgcCGGAA  AtgATGTcGg  gtacggcctg  cAGGGATttg
451 gCGACGGcat  cgtcgatttg  ccgGcgggtg  ttCcgcgctc  ggtttGTTca
501 agacgtagcc  gaCGACGagg  ttgcggtcGC  CGGGgtggcC  GATGCCAGG
551 CGCAGGCGGt  aatagtctgC  CGTGCCGAGT  TTTGCctgAA  TGTCTTTCAA
601 GCCGTTCTGT  CgcgCGttgc  cgcCGCCGAG  TTTGAATTtG  ATCCGTCCGC
651 AAGGGATGTC  GAGTTCGTcG  TGGACGACGA  GGATTTCTTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACCGCC  TGTCCGGAAC  GGTTCATGAA
751 CGTGGCCGGT  TTGAGCAGCC  AAACATCGCC  GTCGGGCAGG  GCGGCGCGGG
801 CAACTTCGCC  GAAGAATTTT  TTTTCTTCTT  TAAACGAAGC  CTTCCATTTT
851 CACGCCAGTT  CGTCGAGGAA  CCAAAGCCC  GCATTGTGGC  GGGTCTGTTC
901 GTATTCTTTG  CCCGGGTTCG  CCAAGCCGAC  AACCATTTTG  ATTGTGttcg
951 acatgataTT  TtccgtgTTT  CTgTCGaatg  cggTCtgaAG  GCTTCAGacg
1001 gcatggTtaT  TCTTCTTgaT  TTtgaACgcg  tgtgcggCGC  GCTTCTTTGG
1051 GGTTCGATCAA  CAGCGGCGG  TACACTTCGA  TCGGTCGCC  GTCGCGCAGC
1101 GGCTGTCTGT  CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG  SFEEQRIDAA  GKPQCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101 LSSFMTVRIR  KSGKRLKGL  QTALDYLLCR  KRVASSHLPE  MMSGTACRDL
151 ATASSICRRC  FRARFVQDVA  DDEVAVAGVA  DAEAQAVIVC  RAEFCLNVFQ
201 AVVSAVAAAE  FEFDPsARDV  EFVVDDEDFF  GFDFVELCKR  GNRLSGTVHE
251 RGRFEQPNIA  VGQGAGNFA  EEEFFFFKRS  LPFPRQFVEE  PKARIVAGLF
301 VFFARVAQAD  NHFDCVRHDI  FRVSVECGLK  ASDGMVILLD  FERVCGALLW
351 GRSTAGGTLR  CGRRRAAACR  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq  Length: 1116
1  ATGCGGAAAA  GCGGTGGCGC  CGGTTCGGC  AGCTTTGAAA  AGCAGTGAGT
51  AAATGCTGCC  TGCAAACCCAC  AATGCCGAGA  GCAGGATAAA  GCGGTTCGCT
101 GGCAGATTCA  TGCTTGTTCC  TCTTCAAGCC  ATGTCTGGCA  TAGTTTGAT
151 AGGCGCAGGA  ATTTCCGCC  GCGTGGCGCC  AGCATATCGC  GCCAAACGGC
201 AATTTCTTCG  GCGGAGGGGG  CATCGTCTAT  GCTGCATTCT  TAGAGCAGGA
251 AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTGCGTTTG  GATAAGCTGC
301 TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351 GAAAGGGCTT  CAGACGGCAT  CGGGTCATTT  GCTGTGCAGG  AAGCGGGTTG
401 CTTCTTCCCA  TTTGCGGCA  AGGATGTCGG  GTATGGCTTG  CAGGGATTTG
451 GCGACGGCAT  CGTCAATCTG  TCGGCGGTGT  TCCGTACTG  GGTTTGTTCA
501 GGACATAGCC  GACGACGAGG  TTGCGGTCGC  CCGGGTGGCC  GATGCCGAGG
551 CGCAGGCGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCCTGAA  TGTCTTTCAA
601 GCCGTTGTGT  CCGCGGTTGC  CGCCGCCGAG  TTTGAATTTG  ATCCGTCCGC
651 AGGGAATGTC  GAGTTCGTcG  TGGACGACGA  GGATTTCTTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACTGCC  TGTCCGGAAC  GGTTCATGAA
751 CGTGGCAGGT  TTGAGCAGCC  AAACGTCGCC  GTCGGGCAGG  GCGGCACGGG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1  ATGCGGAAAC GCGCGCGGCG CGGTGTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAACCAC AATGCGGAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCCTCC TCGTCAGCC ACGTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGGGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTGC TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGATTTTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG TTCCGTA CTG GGTTTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTGCTTGA TGTCTTTCAA
601 GCGGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCGCG
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTTCTTC GGGTTTGATT
701 TTATAAACT GCGCAAGGGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGTCGGC TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCACGGG
801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTT
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTCGATCAA CAGCGGCGG TACACTTCGA TCGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1  MRKRRRRGVG SFEEQRIDAA GKPCQCKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCAATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDPGAGNV EFVVDDEDFG GFDFIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQGSTGDFE EEEFFFFK*S LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECRLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHS	LD	RRRNFP	PRAA		
a615	MRKRRRRGVGSFEEQRIDAAAGKPCQCKQAEAVARQLHAASSSSHVWQILD	RRRNLP	PRAA			
	10	20	30	40	50	60
	70	80	90	100	110	120
m615.pep	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
a615	SMSRHCAATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m615.pep	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
a615	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m615.pep	DAEAQAVIVCRAEFCLNVFQAVVSAAAAEFEPDPSAGNVEFVVDDEDFGDFVLCRR					
a615	DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPSAGNVEFVVDDEDFGDFIKLRKG					
	190	200	210	220	230	240
	250	260	270	280	290	300

```

551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCTC
701 GATTTCTGTC TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGCGCGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTGCGCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCGGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

m616.pep

```

1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSQAVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFELG GGNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSTEXX PTDXRRCRQI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
201 FQTACSRFPY PNSHDTQAA YPNRIHPRHR RNPRFPALRM QHRRCPLEPR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPFPFHD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGS LGDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKKASFKEEKKFFGEVARAALPDGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m616.pep	VWLLKPATFMNRSQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFELGGGNGGHNGLK					
g616	VWLLKPATFMNRSQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFELGGGNGGHNGLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m616.pep	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPTDXRRCRQIPASHTRHPCR					
g616	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPTDXRRCRQIPASHTRHPCR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m616.pep	QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHDTQAAYPNRIHPRHRRNPRFPALRM					
g616	QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHDTQAAYPNRIHPRHRRNPRFPALRM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m616.pep	QHRRCPLEPRNCRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS					
g616	QHRRCPLEPRNCRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m616.pep	IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTKAFRTDNRPPIYRSLMVFALCFAL					
g616	IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTKAFRTDNRPPIYRSLMVFALCFAL					
	310	320	330	340	350	360
	370	380	390	400		
m616.pep	FSECAQAWFTATRTGSLGDVLADLTGAALALFTARAACRPDX					
g616	FSECAQAWFTATRTGSLGDVLADLTGAALALFAARSACRPDX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

991

```

m616.pep      QHRRCP LRRRNCRLARYAGRTRRKI PAPIQTMPD MAXRGTS MNLPNR FILL SALLWFAGS
              ||||  :|||:  :||:  ||||:||||:|:|:|  ||  :|:||||  |||||:|:|
a616          QHRRRT IRRRSGT MARHTCRTRRQI PAPVQNL PNVAGRGGG MKLPNRFSLLSALWFAGG
              250      260      270      280      290      300

              310      320      330      340      350      360
m616.pep      IYSLLFKAAETAPPPFP HFDKVAHLALFFAQIWLLTKAFRTDNRPI PYRSLMVFALCFAL
              |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a616          IYSLLFKAA DTAPPPFP HFDKAAHLALFFAQIWLLTKAFKTKGLPI PYRSLMVFALCFAL
              310      320      330      340      350      360

              370      380      390      400
m616.pep      FSECAQAWFTATRTGSLG DVLADLTGAALALFTARAACRPDX
              |||||  |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a616          FSECAQAXFTATRTGSLG DVLADMAGTVLALFAARAADRPDX
              370      380      390      400

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1979>:

```

g619.seq
1  ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCGGTT
51  GCGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
101 TCAACGTC AA AGGAGA TGG GACTTTGTCT TGCACCTGCG CCGTACCAAG
151 CTTGCCCGCG TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACTCAACT
201 CTTCCAAACG CTGACCAACA ACCCGATTCT GACCCCTTCG ATTTTGGGTT
251 TCGATTTCGCT GTATGTGTTT TTGCAGACCT TGCTGgtGTT TACGTtcgGC
301 GCGGTGGGCT ATAcateccct gccgttgacg gGCAAAATTCG GCTTTGAACT
351 GGTGTATTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCCGTC
401 AGGGCGGGCG CGATTTGCCG CACATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTC GCAGCCTTTC CTCGCTGCTT TCGCGCATGA TAGACCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 GCAGCGAGCT TTTAGGCATA GCGCGCTGCG TCCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC ACGAACGCTA CCGCTCGGAC GTACACCTTT TGGGGCGCGA
651 CCAAGCCGTC AATTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCGGT TGTCCGCCCG
751 GTGAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCG
801 gtCCGTGCGC CATTCCTGCC GCCTGCCgat gacggtttGC gtcgGcggCA
851 TCCTCTTGGt cggCggaca ACCGTATTCG AACACTTCTT GGGCATGAag
901 gCggTATTAA GCGTGGTGGt cgaATTGCG ggcggactcG TTTTCTCTTA
951 TCTCGTTTTA AAACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>:

```

g619.pep
1  MPSEKNIGFM AGSSRPLRVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSL YVF LQTLVFTFFG
101 GVGYTSPLPT GKFGFELVVM MGSLLLFYT LIROGGRDLP HMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVRSELLGI GALVLLVSAA
201 VVWHERYRSD VHLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVGP
251 VSFFGLLAAS LANHFSPSVR HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL KHKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1981>:

```

m619.seq
1  ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGCCCGTT
51  GTGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCGTCCTG TTTATGACGC
101 TCAACGTC AA AGGCGATTGG GATTTTGTTC TGCAACTGCG GCTGACCAAA
151 CTTGCCCGCG TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
201 CTTCCAAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
251 TCGATTTCGCT GTATGTGTTT TTGCAGACCT TGCTGgtGTT TACGTTTCGGC
301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAAATTCG GCTTTGAACT
351 GGTGTCATG ATGGGCGGCT CGCTGCTGCT GTTCTACACG CTCATCAAAC
401 AGGGCGGACG CGATTTGTGC CGCATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGATCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 ACAGCGAGCT TTTGGGCATA GCGCGCTGA TTCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTTTACCTTT TGGGGCGTGA
651 CCAAGCCGTC AATTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCGGT GGTCCGCCCG
751 GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCG
801 GTCGGTCAAA CATTCCTGCC GCCTGCCGAT GACGGTTTGT ATCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTGTTTC AACACCTGCT CGGTATGCAG

```


993

```

751 GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTATTCT AACACTTCTT GGGCATGAAG
901 GCGCTATTAA GCGTGGTGGT CGAATTTGCG GCGGACTCG TTTTCCTCTA
951 TCTCGTTTTA AGACACAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
101 GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGGDLPL RMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSA
201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT WILLWIAAL VATATAVVG
251 VSFFGLLAAS LNHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

m619.pep      10      20      30      40      50      60
MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA
|||||
a619          10      20      30      40      50      60
MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
|||||

m619.pep      70      80      90     100     110     120
VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
|||||
a619          70      80      90     100     110     120
VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
|||||

m619.pep     130     140     150     160     170     180
MGSLLLFYTLIKQGGDLRSMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
|||||
a619         130     140     150     160     170     180
MGSLLLFYTLIKQGGDLRSMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
|||||

m619.pep     190     200     210     220     230     240
NTVHSELLGIGALILLVSAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
|||||
a619         190     200     210     220     230     240
NTVHSELLGIGALILLVSAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL
|||||

m619.pep     250     260     270     280     290     300
VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
|||||
a619         250     260     270     280     290     300
VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
|||||

m619.pep     310     320
AVLSVVVEFAGGLVFLYLVLKHKKKX
|||||
a619         310     320
AVLSVVVEFAGGLVFLYLVLKHKKKX
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gttttcgccT TAAGTGCCTG
51  CCGGCagggc gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG CAAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTCA AGTAA

```

995

m620/a620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTL	LAIVAVSALSACRQAE	EGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP			
a620	MKKTL	LAIVAVSALSACRQAE	EGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP			
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQP	VWFSTIKQMF	GYTKLP	EEP	PKGIRVIYV	TDMGNVTDW
a620	DQP	VWFSTIKQMF	GYTKLP	EEP	PKGIRVIYV	TDMGNVTDW
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GF	IGGMGAEDALP	FGNKEQAEKFAKDKGGKVVGFDDMPD	TYIFKX		
a620	GF	IGGMGAEDALP	FGNKEQAEKFAKDKGGKVVGFDDMPD	TYIFKX		
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta cgcgtgtcgg ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAag ctggCGTTTG CCGCCGCCGC CCTGCCAGAA gccgTccgCA
101 ATCTTGCCCC AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGCGAT TCGGAAGaaa TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACACGCTGGA TATGCAGGAA ACCGTGCGCC ACGCCTTCCG CGTTGCCTGC
301 GGCTTGGATT CGATGGTTTT GGGCGAGCCG CAGATTTTGG GGCAGATTAA
351 AGATGCGGTG CGTGCGGCTC AAGAACAGGA AAGTATGGGG GCAAACTCA
401 ATGCCCTGTT CCAAAAACCC TTTTCCGTTG CTAAAGAAAT CCGTACCGAT
451 ACCGCTGTCT GCGAAAATTC GGTTCGATG GCTTCCGCGT CCGTCAAGTT
501 GCGGGAACAG ATTTTCCCGC ACATCGGCGA TTTGAACGTA TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAAT
601 CCCCAGGTGA TGACGGTTGC CAACCGGACG CTGGCGGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTTA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTGGTGG TTTCTTCAAC GCGCAGCCAG
751 CTTCCGATAG TCGGCAAGAG CATGGTCGAA CGCGCATTGA AACAGCGTCA
801 GAGTATGCCG TTGTTTCATG TTAGCTTGGC CGTGCCGCGC GATATTGAAG
851 CGGAAGTCGG CGATTTGAAC GATGCGTATC TTTATACCGT GGACGATATG
901 GTCAACATCG TCCAAAGCGg caaggaggca aggcagaaaag ccgccgcCgc
951 cgcggaacag ctggTGTCGG AAAAGGTTGC CGAATTGTGC AGGCAGCAGC
1001 ACGGCAGGCA GagcgttcCG CTGATTAAAG CCTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AGCAGGTGTT GGAATATGCG ATGAAACAGC TTGCCAAAGG
1101 CGcaacCGCG GAAGaggttt TGgaacggct gtcgcgcCAA CTGACCAACA
1151 AAGTGCTGCA TTCGCCAAT CAAACCTTGA ATAAGCGGGG GGAAGAAGAT
1201 AAAGatttGG TTCATGCCgt cGCGCAGATt tatcatttGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAALPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYTLDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RAAQEQUESM AKNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKN
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMF LFMLDLAVPR DIEAEVGLDN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVF LIKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAQAQI YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA CCGCTGTCTGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAAG CTGGCGTTTG CCGCCGCCGC CCTGCCATAA GCCGTCGCGA
101 ATCTTGCCCC AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGTGAT TCGGAAGAAA TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACGCGCTGGA TATGCAGGAG ACTGTGCGCC ATGCTTCCG CGTCGCTGC

```

997

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CCGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACCT GGTTCCTATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCCGCTGA TGACGGTTGC CAACCGGAC CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTT TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCGG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAAATGCG ATGAAACAGC TTGCCAAAAG
1101 CGCAACGGCA GAAGAGCTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTTGG TTCACGCCGT CGCGCAGATT TATCATTTGG ACAATAAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAAACLP AVRNLAARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGME TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMF LFMLDLAVPR DIEAEVGDNL DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQCGGRQSV LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHVAQI YHLDK*

m622/a622 98.1% identity in 415 aa overlap

          10      20      30      40      50      60
m622.pep MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLAARSNAATEAVILSTCNRTELYCVGD
          |||
a622      MQLTAVGLNHQTAPLSIREKLAFAAAACLP AVRNLAARSNAATEAVILSTCNRTELYCVGD
          10      20      30      40      50      60

          70      80      90     100     110     120
m622.pep SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
          |||
a622      SEEIIRWLADYHSLPIEEISPYLYTLGMEQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
          70      80      90     100     110     120

          130     140     150     160     170     180
m622.pep RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
          |||
a622      RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
          130     140     150     160     170     180
```

999

```

              70      80      90      100      110      120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g624          HNWEQNGAVPRKAKIFAISMITASCLIMFWHFPQXWWVGAVSSVFCSLVTIFMWHRPESX
              70      80      90      100      110      120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```

a624.seq
1      ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TGCTGTTGGG
51     TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTAAGTC
101    TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTCA CCGCTGGCTG
151    CACCGGCACC GCTATTTCGG TCCGATGGTT CATAACTGGG AACAAAACGG
201    CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251    CCTGCCTGAT AATGTTTGGG CAGTTTCCCC AACGCTGGTG GGTGCGGGCG
301    GTTTCATCGG TTTTGTGTTT CCTTGTCGCC ATATGGATGT GGCACAGGCC
351    CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```

a624.pep
1      MIRYLLIACG CISLLGLIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51     HRRHYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101    VSSVFCSLVA IWMWRRPES*

```

m624/a624: 99.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
m624.pep      MIRYLLIACGCISLLGLIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRRHYFGPMV
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a624          MIRYLLIACGCISLLGLIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRRHYFGPMV
              10      20      30      40      50      60

              70      80      90      100      110      120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a624          HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              70      80      90      100      110      120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```

a625.seq
1      ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51     ACGGtTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101    CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151    GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201    TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251    CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301    AAACtGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351    GTAA

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```

g625.seq
1      atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51     ACGGtTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttGCGCGC
101    CGGtcgttCc CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151    GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201    TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATATATTCTT
251    CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301    AAACtGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351    gTAA

```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```

g625.pep
1      MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA

```

1001

```

501 GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGccg actTTCTTcc
551 ggtaTatgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CatcgTACAT
601 ACCCTcgtCT TTTTcgTTtt cAAACTACTg taa

```

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

```

g627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
  51 FNFEPIAEVG KFLGLGIFITI FVLISILKAG EAGALGGVVS LVHDTAGHPI
 101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
 201 TLVFFVFKLL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

```

m627.seq
  1 ATGTCCGGCC TTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
  51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTATCCTG ATTGCATTGA
 101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
 151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
 201 CATCACCATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
 251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
 301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCCGCAT TCTTGATAA
 351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGCGGCG GATGCCCAAG
 401 CCTTGATGAC GGGTACCCTG TTTTATTCGC TGCTGGCGGT TTCTATGGGT
 451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
 501 GGTCRAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTTCTTCG
 551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
 601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

```

m627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
  51 FNFEPIAEVG KFLGLGIFITI FVLISILKAG EAGALGGVVS LVHDTAGHPI
 101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
 201 TLVFFVFKLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	IALTAVSMAITPKQVRAGNEFNFEPIAEVG				
g627	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	ITLTAVSMAITPKQVRAGNEFNFEPIAEVG				

1003

a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX
190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq
1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC
101 ACACATGGAT TTTACGTTTC GTCAGGCGGC TCAATACCAA CAGGCCGCGT
151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
301 GATTGAATCA GGTGCGGCG CACTTTTTCG CTGCTCAATT TTGCCAGCGC
351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep
1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRRLNTNRPR
51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101 D*IRLRRTF LNFASASGT *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq
1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT
51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
101 AAACATGGAT TTTGCGTTTC GTCAAACGGC TCAATACCAA CAGGCCGCGT
151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG
301 GATTGGATCA GGTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAGCGC
351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep
1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQTWILRS VKRLNTNRPR
51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101 DWIRLRRTSS PLKFASASGA *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m628/g628 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	SDGTSAPALQ	TWILRSVKRLNTNRPR	LKSSAASLIM		
g628	MCVPLKPAGCGPPNSCVSILAAFS	SDGTSAPALHTWILRSVRR	LNTNRPR	LKSSAASLMM		
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRR	TSPLKFASASGA			
g628	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRR	TSPLKFASASGT			
	70	80	90	100	110	120
m628.pep	X					
g628	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

1005

```

151 VEAVATFVAY EFEMLOMLGV WQQGFSSVL LGRYELLWIT GGLAVFAYLI
201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
251 LVVPNIISRL MGDRLRQSLP AVALLGASLV LLCDIIGRMI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAY AV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2023>:

```

m629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACCAACCTGC TGCTGCTGGC
51  GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CTGATGTGTT TTTACTGTCC GACAGCCAGC AGGTCATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCGAT TGTGCTGACG GCGCGCTCGA TGGCGGTGGC
201 CGGCATGATT ATGCAGATTT TGATGCGCAA CCGTTTTGTC GAACCGTCTGA
251 TGGTGGGCGC AAGCCAAAGC GCGGCTTTAG GTTTGCTGCT GATGACCCCTG
301 CTGCTGCCGG CCGCGCCGCT GCCGGCGAAA ATGTCGGTTG CCGCCGTTGC
351 CCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC
401 CGACCGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGTGTG
451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAAACGAAA TGCTGCAAAT
501 GCTCGGCGTG TGGCAGCAGG GCGATTTTTC GAGCGTGCTG CTGGGCGGCT
551 ACGAGCTGCT TTGGATTACG GCGGTTTGG CCGTGTTTGC CTATCTGATT
601 GCCGACCGGC TGACGATTTT GGGCTGGGC GAAACGGTAA GCGTGAATTT
651 GGGTTTGAAC CGGACGGCGG TGTGTGGTC GGGTTTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTTCGGTCG GCAATATTCC GTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCCTG ATGGGCGACA GGTGCGCCA
801 AAGCCTGCCT GCGGTGGCCT TGCTGGGCGC TCTTTGCTG TTGCTGTGCG
851 ACATTATCGG ACGCGTGATT GTGTTTCCG TCGAAATTC GGTCTCTACG
901 GTTTTGGTG TATTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTGAGGAA
951 ACCCGCCTAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

```

m629.pep
1  MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51  LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMVGASQS AALGLLMTL
101 LLPAAPLPAK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGIIFGGV
151 IEAVATFIAY ENEMLOMLGV WQQGFSSVL LGRYELLWIT GGLAVFAYLI
201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
251 LVVPNIISRL MGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAY AV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m629/g629 95.7% identity in 322 aa overlap

	10	20	30	40	50	60
m629.pep	MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
	: : : : : : : : : :					
g629	MTAKPFSLNLNLLPAVLFAVSLSVGIADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m629.pep	GASMAVAGMIMQILMRNRFVEPSMVGASQSAAALGLLMTLLLPAAPLPAKMSVAAVAALI					
	: : : : : : : : :					
g629	GASIAVAGMIMQILMRNRFVEPSMAGQSAAALGLLMSLLLPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIIFGGVIEAVATFIAYENEMLOMLGVWQQGFSSVL					
	: : : : : : : : :					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEFEMLOMLGVWQQGFSSVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLV					
	: : : : : : : : :					

1007

```

a629      GMLVFMMILIRRLPPTAQLMVPLVGIIIFGGVVEAVATFIIAYENEMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180

           190      200      210      220      230      240
m629.pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATTT TGGTGTGGCT ggctttgttt ccccccatgt tttacggcat
51  gtacaacgtc GGCGCACAGG CATTCGGTGC CTTAACGCCC GAtttgctgc
101 aacaaagcat cggccacgac ggcaattacg ccctcgccaa cgctttgggc
151 atcaatatgt cccccgaaGc gggcgtgtTg ggcaaaatgc tgttcgGCGC
201 GATttacttc ctgccgattt acgcgaccgt aTTTATTGTG GGcggcttct
251 ggGaaagtCTT GTTCGCATCc gtACGCAAAc ACgAAATCAa CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAaa AACTTCATGa ACCCTGCGCT GGCAGGCCGT
451 GCCTTCCTGT TCTTCGCCTa CCCCGCCAAc TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAc CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAAcGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCc GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTt GCCCGCATCG
701 CTtcttgGCG CATTATTGCC ggCGTGATGa TCGGTatGat tGcgatgTCT
751 tcgctgatta acttcatCGg ttctgacacc aaagctatgt ttgctatgca
801 cttggtacat ggcacttggt GGAaagatGa ttAtcactca ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF PPMFYGMYNV GAQAFGALTP DLLQOSIAHD GNYALANALG
51  INMSPEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFA VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVGTQITIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLINFIGSDT KAMFAMHLVH GTWWKDDYHS LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GTACAACGTC GGCGCGCAGG CATTCGGTGC GTTAACGCCT GATTGTCTGC
101 AACAAAACAT CGCCAACGAC TGGCATTACG CCTTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTGc GACAAATGc TGTTTGGCGC
201 GATTTACTTC CTGCCGATTt ACGCGACTGT ATTTGTTGTG GGCGGTTTCT
251 GGGAAAGTTT GTTCGCCACC GTGCGCAAAc ACgAAATCAa CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAaa AACTTCATGa ACCCTGCGCT GGCAGGCCGT
451 GCTTTCCTGT TCTTCGCCTa CCCTGCCAAc TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAc CGCACTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAAcGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCc GGCTCCATG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTt GCCCGCATCG
701 CTtcttgGCG CATTATTGCC GGCGTGATGa TCGGTATGAT TGCGATGTCT
751 TCGCTGTTCa ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC

```


1009

```

701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGCTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCCTTTCC GCTTCCTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGCGCAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTCTT CGACTATTTC GTGCGACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALT PDLLQQSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA Q'AAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
351 ARSNG*

m630/a630 98.3% identity in 355 aa overlap

          10      20      30      40      50      60
m630.pep  MMILVWLALFPAMFYGMYNVGAQAFGALT PDLLQQNIANDWHYAFANALGINMSSEAGVS
          |||
a630      MMILVWLALFPAMFYGMYNVGAQAFGALT PDLLQQSIANDWHYALANALGINMSSEAGVL
          10      20      30      40      50      60

          70      80      90      100     110     120
m630.pep  DKMLFGAIYFLPIYATVFVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA
          |||
a630      GKMLFGAIYFLPIYATVFVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA
          70      80      90      100     110     120

          130     140     150     160     170     180
m630.pep  ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
          |||
a630      ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
          130     140     150     160     170     180

          190     200     210     220     230     240
m630.pep  QWAAHGADGLKNAITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA
          |||
a630      QWAAHGADGLKNAITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA
          190     200     210     220     230     240

          250     260     270     280     290     300
m630.pep  GVMIGMIAMSSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW
          |||
a630      GVMIGMIAMSSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW
          250     260     270     280     290     300

          310     320     330     340     350
m630.pep  YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX
          |||
a630      YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX
          310     320     330     340     350

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

```

g635.seq
1  ATGACCCGGC GACGGGTCGG CAAGCAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTGG TCTTGCGGT ATTCAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTCGAAA JACAGGGCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTC CTTACCCAGT TTTTCCAACA CTTCTTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGGA

```

1011

```

m635.pep    MTQRRVVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIAPFRFKTQIRHNAP
a635        MTQRRVVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIAPFRFKTQIRHDAP
              10      20      30      40      50      60

              70      80      90      100     110     120
m635.pep    HILKRRGHLILLIQFFXHVLFRQLLPVKIVQKRHHRSRPAGKIQILLYNIEIAPFFPTLHF
a635        HILKRRGHLILLIQFFXHVLFRQLLPVKIVQKRHHRSRPAGKIQILLYNIEIAPFFPTLHF
              70      80      90      100     110     120

              130
m635.pep    DFSISNRIIVDX
a635        DFSISNRIIVDX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc atGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTGCAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 AAATATTGCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCgcgggg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTACAG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCGGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GCGCGGGGCA AAAATTTCGG CAGGTTTTC TCGCGGGGAA ACGTGGACGA
801 CGGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCACG
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCGSTAT GGCCGAACAA AATAAGCAT CATTCAAATG TGCCTGTTTT
951 TATAGCGAAA CCGCCTGAAA CGGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGKNLARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 IGKNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYAERI IKNIIVFNQG ARGGFFEINT GIHCWQAHTG TNGNQVAERY
201 VRRVYGYGTP ALVPFDGCGT VGRPFNRNRF VDIKFLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFIK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCCTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTGCAATAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCGG
201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAT CGCTGAAGCG GTTGTTTTTG TAGGTGTTGT GCGTGCCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCGGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCGGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCG CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCAATGTGA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GCGCGGGGCA AATGCGGGAT ACGGATCAGC ATAATCGGTT CGTGA

```

1013

251 GAGKCGIPIS IIDSW*

m638/a635 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLDNVVVNIGIVDIVEHNALIAAADGDIVEYFEPLGKHQHI					
a638	MIGGQFIVVGIVGKNALARFVDNVVVNIGIVDIVEHDALVAAADGDIVKHFEPLGKHQHI					
	10	20	30	40	50	60
m638.pep	AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFVGVRAGIGKNAVPPFGNVVADDLRTG					
a638	AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFVIGVRAGIGKNAVPPFGNIVADDLRTG					
	70	80	90	100	110	120
m638.pep	AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFVIGVRAGIGKNAVPPFGNIVADDLRTG					
a638	AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFVIGVRAGIGKNAVPPFGNIVADDLRTG					
	70	80	90	100	110	120
m638.pep	CVPNGNAVALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIIVFNQARGSFEEINT					
a638	RVPNGNAIALVHAQSRVADDFILPHHRIGRTMQIDADRIIQNIIVFNQARGSFEEINT					
	130	140	150	160	170	180
m638.pep	GIHCGQAHTGTGNGQVAERYVRRVYGYGTAPVAFDGCCTVGRPFNRNRFVNVKFGFIYA					
a638	GIHCGQAHTGTGNGQVAERYVRRVYGYGTAPVAFDGCCTVGRPFNRNRFVNVKFGFIYA					
	190	200	210	220	230	240
m638.pep	GIHCGQAHTGTGNGQVAERYVRRVYGYGTAPVAFDGCCTVGRPFNRNRFVNVKFGFIYA					
a638	GIHCGQAHTGTGNGQVAERYVRRVYGYGTAPVAFDGCCTVGRPFNRNRFVNVKFGFIYA					
	190	200	210	220	230	240
m638.pep	GSQFERIARPGAGKCGIPISIIIGSX					
a638	GSQFERIARPGAGKCGIPISIIIDSX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 GCGCGCCGCG GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACA CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCG GATATTCACG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCGCCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGCGGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAAATGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGGCAG GCGGAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNPAG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEVSGN ISVGNMGGYV LMFSERLKVF DNIIVGSRD*
151 GIMLYVNYN DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIMHFTA
201 AIEGTSLDHN SFINNGSQVK YVSTRFLDWS EGGHGNYSWD NSPFDLNGDG
251 FGDSAYRPDG IIDQIIWRAP VSRLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLKEAET ROSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1015

```

1   ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAACTGCCCC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTTC GTCCGGCTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA TATTTCCAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAAAC CCTATAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCGT CCACATATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCAATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAACATTAT
501 CAACAAAGCG GGCAAGTGGC TTTTTCCTTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGTCAAAA TACGTACGCA CGCGCTTTCT CCACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CCGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACCC GTATCGCGCC TCTTGATGAA CAGTCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAA TTTCCCGCCG TTTTGCTGG CCGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGGGC TGCTCAAAAA AGTCGAAACG CGGCAGTTGG
1001 AATGGGGCAG GGCGGAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1   MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVWAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVAVHYM YTNDSEISGN ISVGNNMGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLVNVNYS DIHDNIINKA GKCIFYAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSWD NSAFDLNGDG
251 FGDSAYRPNQ IIDQIIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

a639-1/m639-1 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
a639-1.pep	NGVTVWVWAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVAVHYMYTNDSEISGN					
m639-1	NGVTVWVWAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVAVHYMYTNDSEISGN					
	70	80	90	100	110	120
a639-1.pep	ISVGNNMGYVLMFSERLKVF DNIAGVSRDQGIMLVNVNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNNMGYVLMFSERLKVF DNIAGVSRDQGIMLVNVNYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
a639-1.pep	YDKLSANHFENCQIGIHFTAAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSWD					
m639-1	YDKLFANHFENCQIGIHFTAAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSWD					
	190	200	210	220	230	240
a639-1.pep	NSAFDLNGDGFSGDSAYRPNQIIDQIIWRAPVSRLLMNSPAISIVKWAQAOFPVLPGGVV					
m639-1	NSAFDLNGDGFSGDSAYRPNQIIDQIIWRAPVSRLLMNSPAISIVKWAQAOFPVLPGGVV					
	250	260	270	280	290	300
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLN					
m639-1	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLN					
	310	320	330	340		

1017

```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
               |||
g640          IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAN
               70      80      90      100     110     120

               130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
               |||
g640          DGTIAGAKLVDHHEPIMLIGIPQSRVDKFIDKYIGLNFIFKNPPTPSVAPGDIISGATVTL
               130      140      150      160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATGTG
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGTT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51 AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

               10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
               |||
a640          MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
               10      20      30      40      50      60

               70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
               |||
a640          IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAK
               70      80      90      100     110     120

               130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
               |||
a640          DGTIAGAKLVDHHEPIMLIGIPH
               130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1  ATGCGGTATC CGCCGCAATC GCGGTTTTG CAGAATGCCG CGCGTTGCCT
51 TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTTGCCCG CTATCCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGTCTTCG GTTTCCTCCT GTACGAAGAC AAAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTGC AGGGCGCAGG CGTCGGTCAG GGTGTGTTCC
251 TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgtCgc gGGCAACGGC
301 GGcaaagcgG ACatcggtTT Gcacggcgtc gagCAGGGtt tggTTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CGGTGGCGCG GACGAAC TGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATTT GCGCGCGCgc gTAAGTGTAT
551 TCCGTGGCGa ggTTTTTGac gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCCG
651 AAACCTGATG GCGGCGTTGG ATTTCCGCGC GTTCGTAATC GACGAATCTG

```

1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep			10	20	30	
			ACRRICPLPAISAVQYIFADVVQQEGCGVFVFRLYED			
g642	MRYPFQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADVVQQEGCGVFVFLLYED					
	10	20	30	40	50	60
m642.pep	40	50	60	70	80	90
	KESGDDFADKDFLQAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFLVQLH					
g642	KKSGDDFADEDFLQAGVGQGVFLQEAADVFGQSVVAGNGGKADIGLHGVEQGLVFLVQLN					
	70	80	90	100	110	120
m642.pep	100	110	120	130	140	150
	ACFFFFGGGADKLVVNFGIKHIVRAFKNREGADVDSIAGGVSAFKTLRTQEFQLHLRGG					
g642	ACFFFFGGGADELVVNFGIKHIVRAFKNREGADIDGDIAGWVSAFKTLRAQEFQLHLRGG					
	130	140	150	160	170	180
m642.pep	160	170	180	190	200	210
	VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVS					
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVKDFGNLMAALDFAAFVIDESDIVADIS					
	190	200	210	220	230	240
m642.pep	220	230	240	250	260	270
	FQIFKDVFNHNAVRHADQLQAAADKDVLERAQTSVALGEFHHGGCRHFGIDAVDGVTDGA					
g642	VQVVKDVFNHNAVRHADQLQAAADKDVLERAQTSVAPGEFHHGGCRHFGIDAVDGVTDGA					
	250	260	270	280	290	300
m642.pep	280	290	300	310	320	330
	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRVLPVFRGVDVNGLSVDI					
g642	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRIALPVFRGVDVNGLFVGI					
	310	320	330	340	350	360
m642.pep	340	350	360	370	380	390
	FVVGHLHFACNRRAGGFGFGNTQTAAALAFENHLQTLRDLRFIAELLQWLQHQRAFDAGTQR					
g642	FVAGLHFACNRRAGGFGFGNAQTAAAFENHVQTLCDLRFIAELLQRLQHQRAFDAGTQP					
	370	380	390	400	410	420
m642.pep	400					
	NGHAVMPRNP					
g642	NGHAVMPRNPX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1 GCCTGCCGCC GTATTTGCCC GCTATCCGCA ATATCGGCAG TCCAATATGT
51 CTTTGCGGAT GTCGTTTCAGC AGGAAGGCTG CGGTGTCTTC GTGTTCCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTTC
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTCCGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAATTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TCGCGGCGCG CGTAAGTGTA TTCCGTGGCG AGGCTTTTGA
501 CGATGTTCGC CTCCATCAGT TGATGGGCGA CGGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGCCCG
601 GATTTCCGCG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATTCATAA TGCCGTGCGT CATGCCGATC

```

g643.seq

q643.ppt

m643.seq

m643.pcp

m643/q643

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2067>:

1023

1451 TCGCCCGACT TTTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pep
 1 MPSEPADCC PVHFVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAA^F LKHIESAFRR IFSGDIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKHGGRRKS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLDMIF KGESRRLGVT EPETSGAAIA REMQSCYEY DEQTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNI^FFIRSRL QLIGMTHGIM
 301 EYILDNLNRY VRNDIRFVDY ERREIQRHQ VSEILYRYVC HSVSPVAPVA
 351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGH^PPAG NIAIDIRPFT
 401 IFEGPN^DMLY AEIYDQFVRA TAEKEAGIK LDKNQTL^LLDA VQTDVRF^AAV
 451 ARDYALPEDI RSFLQ^EHTLT DACALQKVFI GKIIARLFVF VQEHEDTTA
 501 FLLNDIRKDI LDCRYCG^{*}

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq
 1 ATGCCGCTCG AAAGTTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG CGCGTTTGAC CGGCCGCCGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAGCACA TCGAATCCGC
 201 ATTCGCCCGC ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCCCTT AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
 301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TCCAAGAAGT
 351 CcTGC^GGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
 451 CAAGTCGCGC AAGGTTTGA GATGATTTC AAAGCGAGG GCGGCGGTTT
 501 GGGTGTTACC GAACCGAAA CCTCCGGCGC GCGGATTGCA CGCGAAATGC
 551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCGCG
 601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCTCTCTCG TTGCCGCCAA
 651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
 701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
 751 TCCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCGCT
 801 GATGAAACTC TCCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
 851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGAAAACT GGAACGATAC GTCCGCAACG ACATCAAATT
 951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCCGAGA
 1001 TTCTTTACCG CTACGTCTGC CATTCGGTTT CGCCTGTGTC CCCCGTCGCC
 1051 CATCAGCTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
 1101 TTACGCCGCC GCGCAAAATG TGCAAAACT CTTGGGTGCG AAGGGTTTGT
 1151 AACCGGGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
 1201 ATTTTGAAG GCCCGAACGA TATGCTTAT GCCGAAATTT ACGACCA^GTT
 1251 TGTCGCGGCC ACCGCCGAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
 1301 ACCAAACCTT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
 1351 GCCCCGCACT ACACTTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCTGACC GATGCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
 1451 TCGCCGACT CTTTGCTCTC GTACAGGCGA AACACGAAGA CACCGCAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 GTAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pep
 1 MPSE^SADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAA^F LKHIESAFRR IFSGDIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKYGGRRKS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLEMIF KEGGGGLGVT EPETSGAAIA REMQSY^YEYI DGQTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI^FFIRSRL QLIGMTHGIM
 301 EYILENLERY VRNDIKFVDY ERREIRRHQ VSEILYRYVC HSVSPVAPVA
 351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGH^TAG NIAIDIRPFT
 401 IFEGPN^DMLY AEIYDQFVRA TAEKEAGMK LDKNQTL^LDR LQTDARF^AAV
 451 ARDYTL^PEDI RSFLQ^EHTLT DACALQKVFI GKIIARLFVF VQAKHEDTAA
 501 FLLNDIRKDI LDCRYCG^{*}

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSE ^S ADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAA ^F					
g644	MPSE ^R PADCCPVHFVVKFRKLTNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAA ^F					

1025

```

851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTGT
1151 AACCGCGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTAT GCCGAAATTT ACGACCATTT
1251 TGTCGCGGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCGCTC
1351 GCCCGCGACT ACACCTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GATGCCTGCG CCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

a644.pep

```

1 MPERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51 QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKYGGGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGEA
151 QIAQGGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYTDGQTIYVNAA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSL QLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HVSVPVAPVA
351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHGTA NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

```

m644/a644 97.3% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
a644	MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
a644	LKHIESAFRRIFSDGIDLMLRYPEDKWLALKQAGLLLPFLDKKYGGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
a644	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQVAQGLEMIFKGGGGGLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
a644	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
a644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIIFIRSLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
a644	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					
	310	320	330	340	350	360
m644.pep	EYILENLERYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					
a644	EYILENLERYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					

1027

851 TTTCCTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

m645.pep

```

1  MMMVLALGIS IPVSMMVEQS NTLNRCKKKS RMTCSSSRSR SCPCATPMRA
51  SGRVSSRSR IFSIVSTSLC RKNTCPPLRS SRNTASRTLK SLKGLTKVLT
101 ARRLGAVVI SEKSRSPSHA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLK
201 RERLATFTGK SAKRSAKFCA CCSTKSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/g645 93.7% identity in 286 aa overlap

m645.pep	10	20	30	40	50	60
	MMVLALGISIPVSMVEQSNLTNRCKKSRMTCSSSRSRSCPCATPMRASGRVSSRSR					
g645	MMVLALGMSMPVSMVEQSNLTNRCKKSRMTCSSSRSRSCPCATPIRASGRVSSRSR					
	10	20	30	40	50	60
m645.pep	70	80	90	100	110	120
	IFSIVSTSLCRKNTCPPLRSSRNTASRTLP SLKGLTKVLTARRRLGAVVISEKSRSPSNA					
g645	IFSIVSTSLCRKNTCPPLRSSRNTASRTLP SLNGLTKVFTARRRLGAVVISEKSRSPSSA					
	70	80	90	100	110	120
m645.pep	130	140	150	160	170	180
	ILKVRGIGVAVMVRISTLARRLSCSFRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI					
g645	MLRVRGIGVAVMVRISTLARRLSCSFRTPKRCSSSIITKPKFLNLMSSCTNLCVPITI					
	130	140	150	160	170	180
m645.pep	190	200	210	220	230	240
	STVPSAMPSSAALVALLLKRERLATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT					
g645	STVPSAMPSSVALVALLLKRERLATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT					
	190	200	210	220	230	240
m645.pep	250	260	270	280		
	ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX					
g645	ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq

```

1  ATGATGATGG TGTGGCGTT GGAATGTCC ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
201 TTCATTGTGC AGGAAAAATA CTGCCCCGCC GCGTTTGAGT TCGCGCAATA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTGACAAA GGTTTGGACG
301 GCGAGGCGGC GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGCTTTTGCT GTTGTTGAAA
601 CGCGAAAGGC TGCGGACTTT CACGGGAAA TCAGCGAAGC GGTGCGGAAA
651 ATTTTGGCGC TGCTGCTCGA CCAGAAGCGT GGTGCGTGC AGTACGGCAA
701 CTGTTTGCC ACCATTACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGCGGCGAT GCGGCTGCC TGGTCTTCGG
851 TTTCTTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep

```

1  MMMVLALGMS IPVSMMVEQS NTLNRCKKKS RMTCSSSRSR SCPCATPMRA

```

1029

51 GFKGTVGQTE RGTAVADTV FRQIISIVNH ADAERTAHS RGRGFYRIS
101 LII*

m647/g647 91.3% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	: : : : : :					
g647	MQRLAADGIQIFFVSDGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGRGFYRISLIIX					
	: : : : : :					
g647	RGTAVADTVFRQIVGVDDTDAERTAVHSRGRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2085>:

a647.seq
1 GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCCTTTTGT TAGGTGTCTGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGACGCA
101 CCGTATTCTT TGGCAAGGT TCGCGATGCT TTGAGCAGGT AATACTSTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGCTGTAGC
201 GGACACCGTT TTTGCGCCAA TAATACGCAT AGTTGATCAC GCCGATACCG
251 AGCGAACGGC GGCCCATAGT GGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2086; ORF 647.a>:

a647.pep
1 VQRLVTHSVQ VFFVGVDDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAHS GGRGFYRIS
101 LII*

m647/a647 87.4% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	: : : : : : : : :					
a647	VQRLVTHSVQVFFVGVDDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGRGFYRISLIIX					
	: : : : : : :					
a647	RGAVAVADTVFRQIIRIVDHADTERTAHSRGRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2087>:

g648.seq
1 ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51 CGACGTTTGT AATGTAGATG CGCCCGGTCC CGGCACGCTC CTGCATCAGC
101 GTGGAAAAACA GGTGCGCAGC CGGAATGATA CGCTTGCGTA TGTTCGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTGG TCGGCAAAAA
201 ACGCTTCGTA CAACCCGAA ACCTCGTTGG GCGAAAAAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCATA
301 ATCAAGCTGG CGGATACGGT TGTCTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCA ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCGCG GCACGCCACC TTGCGAACAA GATTGACCG CCGCTGAAA
451 CATCTTAAAG AAGGGAATGC AGCCGTATG CCGGGCTCA CCGCCCGGA
501 TTTGCTGTC CAGCCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCG
551 CGTTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAAATC
601 CAAACTATCG TCGCATCAA TCAGCACACA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2088; ORF 648.ng>:

g648.pep

1031

```

501 TTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
601 CAGGCTGTCTG TCGCATTCTGA TCAATACGCA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

```

a648.pep
  1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
  51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGFDCLRK
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
 201 QAVVAFDQYA A*

m648/a648 93.8% identity in 211 aa overlap

m648.pep      10      20      30      40      50      60
MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a648          10      20      30      40      50      60
MNRRNARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK

m648.pep      70      80      90     100     110     120
FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a648          70      80      90     100     110     120
FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHAPVVFQHQQA

m648.pep     130     140     150     160     170     180
FGFDMPQGV E QGCRAAAHAALRTGFDRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a648         130     140     150     160     170     180
FGFDMPQGV E QGCRAAAHATLRTGFDCLRKHFKEGNAAGMPCFAAPDFAVQSADTSGIDA

m648.pep     190     200     210
DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a648         190     200     210
DARTLGNVFHNRAGSGVDGIQAVVAFDQYAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

```

g649.seq
  1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACTGC
  51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAAA CATATCCGCA
 101 AGGCAAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGG
 301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

```

g649.pep
  1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER
  51 RAAWYRSQGN VQELRENKKA RKAFTLPYA EQKIQCAAAY EAFDDFDGGR
 101 FRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

```

m649.seq
  1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
  51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
 101 AGGCAAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGT
 301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1033

```

751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCCGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTGAATCC TGCATTCAAC GTCCCGCGt tcatCCCCAA AAACaaacgc
901 aaactGCTGC TTCCTGTCGC GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCGTTTC CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCcggcag gcaCGGTGAA CGTCAGCATt gccCgaatcc aacCCgccgc
1251 cgcaCAGACA gcggacatta ccgtcgcacc ttgtccgcaa gaaaccgtcc
1301 gtacgggaac ccgatccccct tgtccgcaTt accgaacccg ccctTGCGAC
1351 AGCCGCAGCG CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

g650 . pep

```

1 MSKLTIALT ASGLSVCPGF LYAONTSSHQ VGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWDE LRQGFMRGEV NPFLVRRHES KFIASRSYFD RVVNRSRPYM
101 YHIANEVKKR NMPAEAAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKPKR
301 KLLLPPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPTDYSRN
401 MPAGTVNVSI ARIQPAQAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

m650 . seq

```

1 ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACGGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGCG AATATGCCCG CCGAAGCCGC
351 CTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCCTGGAAG AAACACCCGT TTACGACGGC AGGCACGACG TTTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT TGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCGC
701 TGGCGAATAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCGCGT TTATCCCCAA AAGCAAACGC
901 AAATGCTGTC TTCCTGTGCG GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAA GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGGAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCGA AAAACCGTCC
1301 GTACGG . AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

m650 . pep

```

1 MSKLTIALT ASGLSVCPGF LYAONTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWGE LRQGFMRGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTDYSRN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1035

```

901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CAAAACCAG CTGTGTCGAC ATCTCGACG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCTT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

```

a650.pep
  1  MSKLKTIALT ASGLSVCPGF LYAQTSSSHQ IGLAIMRLNS SILDLPPTKQ
 51  YFQSGSLWSE LRQGFRMGEV NPELVRRHES KFIASHSYFN RVINRSRPFY
101  YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151  GLEKTPVYDG RHDYIYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEQNVG
201  RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAA PQSFGMNISD
251  IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301  KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351  DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTNRYRSN
401  MPAGTVNVGI ARIRPAAQOT ADITVAPLPQ KTVRTXTRSP CPYCRCTPCD
451  SRSATSNRKT DRHAV*

m650/a650  99.1% identity in 465 aa overlap

      10      20      30      40      50      60
m650.pep  MSKLKTIALTASGLSVCPGFLYAQTSSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE
          |||
a650      MSKLKTIALTASGLSVCPGFLYAQTSSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWSE
          |||

      70      80      90      100     110     120
m650.pep  LRQGFRMGEVNPPELVRRHESKFIASHSYFNRVINRSRPFYHIANEVKKRNMPAEALLP
          |||
a650      LRQGFRMGEVNPPELVRRHESKFIASHSYFNRVINRSRPFYHIANEVKKRNMPAEALLP
          |||

      130     140     150     160     170     180
m650.pep  FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG
          |||
a650      FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDYIYAATDAALNYLQYLYG
          |||

      190     200     210     220     230     240
m650.pep  LFGDWPLAFAAYNWGEQNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT
          |||
a650      LFGDWPLAFAAYNWGEQNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAA
          |||

      250     260     270     280     290     300
m650.pep  PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
          |||
a650      PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
          |||

      310     320     330     340     350     360
m650.pep  KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
          |||
a650      KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
          |||

      370     380     390     400     410     420
m650.pep  NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTNRYRSNMPAGTVNVGIARIRPAAQOT
          |||
a650      NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTNRYRSNMPAGTVNVGIARIRPAAQOT
          |||

```

1037

```

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPIIS IEDGMDENDW
201 EGWKLLEKLL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAKYNQ LLRIEELAE AADYPSKAAF YQLGK*

```

m652/g652 98.2% identity in 335 aa overlap

```

              10      20      30      40      50      60
m652.pep      MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              |||||
g652          MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              10      20      30      40      50      60

              70      80      90      100     110     120
m652.pep      EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDSKGFPTTVGDEGGFAPNLN
              |||||
g652          EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDSKGFPTTVGDEGGFAPNLN
              70      80      90      100     110     120

              130     140     150     160     170     180
m652.pep      SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              |||||
g652          SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              130     140     150     160     170     180

              190     200     210     220     230     240
m652.pep      GLVNEFPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
              |||||
g652          GLVNEFPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
              190     200     210     220     230     240

              250     260     270     280     290     300
m652.pep      LLVKVNQIGTSLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
              |||||
g652          LLVKVNQIGTSLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
              250     260     270     280     290     300

              310     320     330
m652.pep      RSDRMAKYNQLLRIEELAEAAADYPSKAAFYQLGKX
              |||||
g652          RSDRMAKYNQLLRIEELAEAAADYPSKAAFYQLGKX
              310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

```

a652.seq
1  ATGATCGAAT TGGACGGTAC TGAACACAAA GGCAATTTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCTGCGCGCT TTACCGCTAC TTGGGCGGCG CAGGCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCGCGCGG CTACAAAGCG GCGGAAGACG TATTATTCGC ATTGACTGTC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCA ATATCTGGAA GGCCTGGTCA
551 ACGAGTCCC CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGGGCAAAG TCCAACCTCGT
651 TGGCGACGAC CTCTTCGTTA CCAACCCGAA AATCCTTGCC GAAGGCATTG
701 AAAAAGGCGT GGCAAAACGCA CTATTGGTCA AAGTCAACCA AATCGGTACT
751 TTGAGTGAAA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGCGGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCCGACT ACCCCAGCAA AGCCGCATTG TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

```

a652.pep
1  MIELDGTENK GNLGNATLA VSMVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGA SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

```

g652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNV
151 NGGEHANNLS NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKQVLV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSETLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAYYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCCCGCG GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGTTATTTC GGCAAGGGCG TATTGAAGGC
201 GGTGGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGCGACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTTCCGCGA AGCGTTGCGC TGCGGTGCGG
551 AATTTTCCCA CGCCTTGAAA AAATGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGCGC ACGAAGGCGG TTTGCCCGCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGCGC TACAAGCGG
701 CGGAAGACGT ATTATTGCGA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAT ACCACTTGA AGCCGAAGGC CGCTCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGTAGAGT TCAATTGGTT GCGCAGCACT TGTTCGTAA
951 CAATCCAAAA ATCTTGGCGG AAGGCATCGA AAAAGGCGTA GCAACCGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 CTCGACTTAG CCAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGGGAAACC GAAGACAGCA CCATTGCCGA CTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCGGACTA
1251 CCCAGCAAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNV
151 NGGEHANNLS NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKQVLV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSETLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLESVMGRAAVPSGASTGQKEALELRDGDKSRY					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLESVMGRAAVPSGASTGQKEALELRDGDKSRY					
	10	20	30	40	50	60
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNLSNIQEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNLSNIQEFMIMPVGAKSFREALR					
	130	140	150	160	170	180
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNLSNIQEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNLSNIQEFMIMPVGAKSFREALR					
	130	140	150	160	170	180

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLLESQVGMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLLESQVGMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

              70      80      90      100     110     120
m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

              130     140     150     160     170     180
m652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
              130     140     150     160     170     180

              190     200     210     220     230     240
m652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

              250     260     270     280     290     300
m652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFIISIEDGMDENDWEGWKLTT
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFIISIEDGMDENDWEGWKLTT
              250     260     270     280     290     300

              310     320     330     340     350     360
m652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

              370     380     390     400     410     420
m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK
              370     380     390     400     410     420

              429
m652-1      AAFYQLGKX
a652-1      AAFYQLGKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcgg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGTtgacggT GATGTGCGCt ttgcccAAG
101 CGGCTtcggc ggctttgcCg gtgaTTTCA TCGGTTGCAG GtcgacgaGG
151 AAaacgTGGC TTTCGGTGCG GCCGGAaagc atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTTCACTTGT TTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TtgGCGGCG
301 ATAACGTgca tcaACGGAcc gCCTTGcAGG CTGGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTTGTGG GTGGTAGTgG ttACgaaGTc GCAGaAtggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAEPMRMPE VTYGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMTAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRVLW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTtgacggT GATGTGCGCt TTGCCCCAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG

```

1043

130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2123>:

```
g656.seq
1  ATGCCGCGTT TCTCCGGTTC GATTTCCTCG ATGATTTCCTCA TCGCGCGGAC
51  TTTtggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGc ctTCGACGTT GGAACGATG
151 TGCATCACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TGACTTTGAC
201 TTCGCCTGTT TTGCTGATGC GTCCGACATC GTTGGCGCCC AAATCGATAA
251 GCATAACGTG TTCGGCgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTCTG
301 TTGGCAAGGT CTTGGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACGTcat CGCGTTCGCG GCGGACGAGG ATTCGGGGCG
401 AGGAACCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2124; ORF 656.ng>:

```
g656.pep
1  MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIISITCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRTR ISGEEPTMWK SPKS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2125>:

```
m656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTCA TGGCGCGGAC
51  TTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTTCGACGTT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TAACCTTGAC
201 TTCGCCGTT TTACTIONGATGC GGCCGACGTC GTTGGCGTCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCTG
301 TTGGCAAGGT CTTGGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATAACGTCGT TCGGTTTCGCG TCGGACGAGG ATTCGGGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CSTAG
```

This corresponds to the amino acid sequence <SEQ ID 2126; ORF 656>:

```
m656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT ITSLSRSTR ISGEEPTMWK SPKS*
```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m656/g656 91.0% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGA	PESVPAGKVAARMSMLVMPs	FRPSTLETMCITWEYFSIT			
	: : :	: :	: :	: :	: :	: :
g656	MPRFSGSISSMISIARTFGA	PESVPAGKVAARMSILVTPS	FKQPSTLETMCITWEYFSIT			
	10	20	30	40	50	60
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRP	KSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
	: :	: :	: :	: :	: :	: :
g656	ILSVTLTSPVLLMRPTSLRP	KSIISITCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLSRSTRISGEEPTMWK	SPKSX				
	: :					
g656	MTSSRSRTRISGEEPTMWK	SPKSX				
	130	140				

1045

g657.ppe

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	KTLDDELKAAF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADEL DYGV

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR					
	: : : : : : : : : : :					
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVDGTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
	: : : : : : : : : :					
g657	LADEL DYVGV LAVEMFVVDGTHELVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHRNAHLHLYGKKTAKHGRKMGHFTVL					
	: : : : : : : : : :					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAKHGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSXL					
	: : : : : : : : : :					
g657	TTDSDTAFQEAKKLHQSXL					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGCGCG
51  CGGACAATTA GGCAGAATGT TTA CTGTTGCG TGCCAAAACC ATGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTGCGC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAACTCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGCTC GAACAATGAC
601 AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATTCACGAAA ACGGTATCCT
651 CGCCTACTCC ATCGTCCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAT GGCGCAGCGT TTGGCCGATG AATTGAAC TA CGTCGGCGTA
751 TTGGCGGTAG AAATGTTTGT TGTGCGCGAC ACGCATGAAT TGGTCGTC AA
801 CGAAATCGCG CGCGGTCCGC ACAATTCGGC CCACCATACC GTCGACCGCT
851 GCGCGGCAGA CCAATTCCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGCTGACA CCAAAATGCT GAGTTCTTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCCGGCCGGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGGCGACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTALEELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESI QF LPGILKTATL
151 GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQQARQMAQR LADELNYVGV
251 LAVEMFVVDG THELVVNEIA PRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGEPDWL PLQSRPDAHL HLYGKKTAKH
351 GRKMGHFTIL STDSDTAFQE AKKLHQSXL*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPDPAFAAEFDRHLCAPFDN					

1049

```

101  NAIHAAVFGK  RGFEFVQREF  ADLTFVVAQ  RSRFQDAGQK  LRACFSNVFG
151  LANRLIRRGL  QACFAYPRFF  LNAVLCNGHA  VAAGGNVGM  L  CQRAHRVGD
201  VFKEGRNRR  FCQFVQRPV  VKRRAQMAVG  KFRRRRIRVG  IENGYFVAHG
251  FSGNGKHSAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```

m658.seq
1   ATGGTGTCG  GAATTGTGCG  GCGCGGGGCG  GATTTCTGTTG  ACGACCAATT
51  CATGCGTGT  ACCGACAACA  AACATTTCTA  CCGCCAATAC  GCCGACATAA
101 TCCAATTCGT  CCGCCAAGCG  TTGCGCCATC  TGCCGCGCCT  GTTGCTGCAC
151 GTCGGCACT  AGTCGCGCGG  GGACGATGGA  ATAAGCCAAG  ATGCCGTTT
201 CGTGGATGT  TTCGGCAGGG  TCGAAAGTTT  GCACGTTGTC  ATTGTTCAAA
251 CCGCATACGA  TTACGGAAAT  TTCACTGCGC  AAATCCACCA  TTTTTCCAA
301 AACGCAATCC  ACGCCGCCGT  GTTCGGCAAA  CGCGGCTTTG  AGTTCATCCA
351 ATGTTTTTAC  GCGGATTGGA  CCTTTGCCGT  CGTAGCCCAA  CGTAGCCGTT
401 TTCAGGATGC  CGGGCAAAAA  TTGCGCGCTT  GCTTCAGTGA  TGTCTCAGC
451 CTTACAAACC  ACTTGATACG  GCGCGGTTTG  CAATCCCGCT  TTGCGTATCC
501 ATGCCTTTTC  CTGAATGCGG  TTTTGTGCAA  TCGCCACACA  ATCGCCGCTA
551 GGGGAAACAT  TGGTATGTTT  TGCCAAAAAG  CGCATCGCAT  CGGCATTGAC
601 GTTTTCAAAT  TCAGTGGTCA  CCGCCGCGCA  TTTTGCCAAT  TCGTCCAAAG
651 CAGCTTGGTC  GTTAAACGGC  GCGCACAAAT  GCGGTCGGGC  AAATTCGTCT
701 GCCGCGCGCT  CCGGATCGGG  GTCGAGAACG  GTTACTTTGT  AGCCCATGGT
751 TTTGGCGGCA  ACGGTAAACA  TTCTGCCTA

```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```

m658.pep
1   MVSGIVRARG  DFVDDQFMRV  TDNKHFYRQY  ADIIQFVRQA  LRHLPRLLLLH
51  VGTQSRGDDG  ISQDAVFVDV  FGRVESLHV  IVQTAYDYG  N  FTAQIHFFQ
101 NAIHAAVFGK  RGFEFIQCFY  ADLTFVVAQ  RSRFQDAGQK  LRACFSDVFS
151 LTNHLIRRGL  QSRFAYPCLF  LNAVLCNRHT  IAARGNIGMF  CQKAHRIGID
201 VFKEFSGHRR  FCQFVQSSLV  VKRRAQMAVG  KFCCRRVRIG  VENGYFVAHG
251 FGGNGKHSAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

```

              10      20      30      40      50      60
m658.pep      MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLHVGTSRGGDDG
              ||:|||||  |:|:|  |:|||||  ||:|||||  ||:|||||  ||:|||||
g658           MVAGIVRARGGFIDEQFMCVADNKHFYRQYADIIQFVRQALRRLPRLLHVGTPRGDDG
              10      20      30      40      50      60

              70      80      90      100     110     120
m658.pep      ISQDAVFVDVFGRVESLHVIVQTAYDYGNTAQIHFFQNAIHAAVFGKRGFEFIQCFY
              ||:|||||  ||:|  |:|:|  ||:|||||  ||:|||||  ||:|||||
g658           ISQDAVFVDVFGGVEGLHVFIVQTAYDHGNLAAQVHHFFQNAIHAAVFGKRGFEFVQREFD
              70      80      90      100     110     120

              130     140     150     160     170     180
m658.pep      ADLTFVVAQSRFQDAGQKLACFSDVFSLTNHLIRRGLQSRFAYPCLFLNAVLCNRHT
              ||:|||||  ||:|||||  ||:|||||  ||:|||||  ||:|||||  ||:|
g658           ADLTFVVAQSRFQDAGQKLACFSNVFGLANRLIRRGLQACFAYPRFFLNAVLCNGHA
              130     140     150     160     170     180

              190     200     210     220     230     240
m658.pep      IAARGNIGMFCQKAHRIGIDVFKEFSGHRRFCQFVQSSLVVKRRAQMAVGKFCCRRVRIG
              :||  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
g658           VAAGGNVGMQLCQRAHRVGDVFKEFGRNRRFCQFVQRPVVKRRAQMAVGKFRRRIRVG
              190     200     210     220     230     240

              250     260
m658.pep      VENGYFVAHGFGGNGKHSAX

```

1051

```

g661.seq
1  ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT GCCGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
151 ACCGGA AAAA CCctgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
201 TGCCGTGCAG ATTGCCGGCA GCGACCcga acaGATGGCG Gatgcggcgc
251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
301 ccgcceaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
351 CGAGccgctg gttgcCgcca tTTtgaggc ggtggtcAAG GCGGCGGcg
401 TACCCGTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
451 ctgcCgcgcg tcgccaaaat cgcgaagat tgcggcattg ccgccCttgc
501 cgttccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GCGgcGTTAC
551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCG cctGggtCAA
601 CGGCGACATC actTCgcgcg AAAAAGCCGC CGccgTCCTC AAACAAACCG
651 CCGCCGACGG CATCATGATA GGGCGCGCGC CGCAAGGCAG GCCGTGGTTT
701 TTCCGCGATT TGAAGCATTa TGCCGAACAC GCGGTTTTAC CGCCTGCCTT
751 GAGTTTGGA GAATGCAGAG CCGCATTTTT GAACCATATC CGCGCCATGC
801 ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGGCGAAAT GCCCACGGC GAACAGGCGC GCGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

```

g661.pep
1  MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
51  TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDDHQN
151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
201 RRHHFAAKSR RRPQTNRRRR HHDARRARRQ AVVFRFEAL CRTRFTACL
251 EFGRMQSRHF EPHPRHARVL WXDRCARHT QTHRLVHRRN ARRTTGA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

```

m661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT ACCGACAAAC CGTTCGCCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCCGCG
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGAAGC CGTCGTCCGT GCGGCGAGCG
401 TACCCGTAC CCTCAAAACC CGTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCCTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC
501 CGTCC.AC GG ACGCACGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
551 GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG
651 CCGCCGACGG CATTATGATA GGGCGCGCGC CGCAAGGCAG GCCGTGGTTC
701 TTCCGCGATT TGAAACATTa TGCCGAACAC GGTGTTTTGC CGCCTGCCTT
751 GAGTTTGGA GAATGCGCCG CCGCTATTTT GAACCATATC CGCGCCATAC
801 ACGCGTTTTA CCGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

```

m661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPFRFETL CRTRCFACIL
251 EFGRMRRRYF EPHPRHTRVL RRHRCARHT QTHRLVHRRN ARRTDTS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 98.5% identity in 295 aa overlap

1053

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a661      MHIGGYFIDNPIALAPMAGITDKPFRRILCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60

           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120

           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180

           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPFRFETL
           |||||
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPFRFETL
           190     200     210     220     230     240

           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCARHTQTHRLVHRRNARRRTDTSX
           |||||
a661      RRTRCFTACLEFGRMYRHYFEPHPSHARVLRHRRCARHTQTHRLVHRRNARRRTDTSX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGCA
151 AAATGTTTTC CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGTctGC CAAATGCCTG AAATCGCTGG TGCCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAaggqctg cgCGCCctcg TCAAACAGTT CCGCAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTTGCGAC GCAACAATTC GGTTTTGTG
601 GATTTTTTCG GCATtcagaC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTTGGAAATC CTTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTGA TCGAAGAACG
801 CGTGCGCGAA CACCCGGAAC AATATTCTG GCTGCACAAG CGTTTCAAAA
851 CCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLOFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRRNSVFV
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVTLO FYPAWSFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DEFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTGAAACA

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1055

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151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAACCG TGTTGAAACA
201 GCATTTCAAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCCGC CGGCGGTTTG AATCACTGG TCGCTACCG CAACAAACAT
301 TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACCTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTTTCCTTA TCGGGCGCAC
501 CGAAGGCTG CGCGCCCTCG TCAACAGTT CGCAAAAGC AGCGCGCGCT
551 TTCTGTATCT JCCCGATCAG GATTTCCGAC GCAACGATTC GGTTTTGTGTC
601 GATTTCTTCG GTATTTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCTGTGC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCGT CTGCGGAATC CTTTCCGAGT
751 GAAGATCGCG AGGCCGACGC GCAGCGCATG AACCGTTTA TCGAGGAACG
801 CGTGCGCGAA CATCCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

a663.pep

```

1 MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51 KCFPEWDGKK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNRDSVFV
201 DFFGIRTATI TGLSRIAALA NAKVIPAIPV READNTVTLH FYPAWESFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

m663/a663 96.2% identity in 293 aa overlap

	10	20	30	40	50	60
m663.pep	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP	RRRIGEINLAKCFSEWSEEK				
a663	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP	RRRIGEINLAKCFPEWDGKK				
	10	20	30	40	50	60
m663.pep	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
a663	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
	70	80	90	100	110	120
m663.pep	AFEMAVYALNQDIPISMYSHQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
a663	AFEMAVYALNQDIPISMYSHQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
	130	140	150	160	170	180
m663.pep	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALA	NAKVIPAIPVREADNTVTLH				
a663	SAPFLYLPDQDFGRNDSVFVDFFGIRTATITGLSRIAALA	NAKVIPAIPVREADNTVTLH				
	190	200	210	220	230	240
m663.pep	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHK	RFKTRPEGSPDFYX				
a663	FYPAWSFPSEDAQADAQRMNRFIEERVREHPEQYFWLHK	RFKTRPEGSPDFYX				
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

g664.seq

```

1 ATGATACATC CGCACCCTT CCGCGCCTTT TTCATAAAGC GTCATGGTGT
51 AGAAATTGTT CATCTCCTCA TAGTGAcg gGCGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTTCCGGGAA CTGGTTCTGG CGCAGCAGGC GGATGTTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGGAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAG TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAACCCCT TGTTTCCAT CGCGCCATA
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCcaa
451 cCgaagcgc gtttcgtcCc acttcatcgC gttTTTCAA cgaTTCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT

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1057

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201 GGAACACGGT CAACCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCTT TGTTCCTCAT CGCACCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGATAA ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
1  VIHPHHFRAF FINGHGVEIV HLLISGGAHR MCGRTC VFGE LVLAQQADV F
51  DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

          10      20      30      40      50      60
m664.pep  VIHPHYFRAFFINGHGVEIVHLLIAGG  HRMGGRA CVFGE LVLAQQADV DAAHGAAGAV
          |||||:|||||:|||||:|||||  ||:|||||:|||||:|||||
a664       VIHPHHFRAFFINGHGVEIVHLLISGGAHRMCGRTC VFGE LVLAQQADV DTAHGAAGAV
          10      20      30      40      50      60

          70      80      90      100     110     120
m664.pep  AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGA AVGKDELG
          |||||:|||||:|||||:|||||:|||||:|||||
a664       AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
          70      80      90      100     110     120

          130     140     150     160     170     180
m664.pep  VKDVQTLVFHRAHIEIAHGD DHENIQVVFQTEARFVPFHRVFXTIPRQSRPWACPLRWCK
          |||||:|||||:|||||:|||||:|||||:|||||
a664       VKDVQTLVFHRTHEIAHGD DHENIQVVFQTEARFVPLHCVFXAIPRQSRPWACPLRWCK
          130     140     150     160     170     180

m664.pep  TRFX
          |||
a664       TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
1  atgaagtGgG acgaaacgGg cttcgGgttg GAAtatgact tggatatttT
51  CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACRAGG
101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACC GCC
151 ACCGATACCG ATTTCAAGG CATTGAATCC GTGGTCGGAC ACGAATATT
201 CCACAACCTG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
301 CGCGCCGCC GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
351 GAACCACTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GCGCGGAAG TGGTGGCGAT GTATCATACC CTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTCCaaGg CCACGACGGA CAGGCAGTGA
551 CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
601 GACCACTTCG CCTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGAAAGC
651 CGAAGGCCGT CTGAAAAACA ATGTTTTCGA GTTAACCATT AAACAAACCG
701 TGCCGCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
801 GGGCAACCGC GCAACCGAAG CCGTGTGCT GATGACCGAA GCCGAACagg
851 CCTCCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCAGTGTA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCACG ACAGCGACGC TTTACGTGC TGGGAAGCCG

```

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1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGGC CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTGCGCT CAAGCCGCGC CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCACACAA
1651 GCCCGTTTCG TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACGGCTTCAA CCCGCAGGTC GCCGCCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1 MKWDETRFGL EYDLDFIMVV AVGDFNMGMAM ENKGLNIFNT KFLVADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHQF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFORHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNIFELTV KQTVPPPTDM TDKQPMMPV
251 KVGLLNRNGE AVAFDYQGKR ATEAVLLLTE AEQTFLLLEGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAQTLRYR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQAA KQENQSYEYS PEAAGWRTL
451 NVCRAFLRA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFS DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFAEDG SGYRFIADKV IEIDRENPOV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

	10	20	30	40	50	60
m665.pep	MKWDETRFGL EYDLDFIMVVAVGDFNMGMAMENKGLNIFNTKFLVADSRTATDTDFEGIES					
g665	MKWDETRFGL EYDLDFIMVVAVGDFNMGMAMENKGLNIFNTKFLVADSRTATDTDFEGIES					
	10	20	30	40	50	60
m665.pep	VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQF					
g665	VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNF					
	70	80	90	100	110	120
m665.pep	VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQF					
g665	VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNF					
	70	80	90	100	110	120
m665.pep	PEDAGPTAHPVRPASYEEMN NFYTMTVYEK GAEVVRMYHTLLGEEGFQKG MKLYFORHDG					
g665	PEDAGPTAHPVRPVSYEEMN NFYTMTVYEK GAEVVRMYHTLLGEEGFQKG MKLYFORHDG					
	130	140	150	160	170	180
m665.pep	PEDAGPTAHPVRPASYEEMN NFYTMTVYEK GAEVVRMYHTLLGEEGFQKG MKLYFORHDG					
g665	PEDAGPTAHPVRPVSYEEMN NFYTMTVYEK GAEVVRMYHTLLGEEGFQKG MKLYFORHDG					
	130	140	150	160	170	180
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPPTDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPPPTDM					
	190	200	210	220	230	240
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPPTDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPPPTDM					
	190	200	210	220	230	240
m665.pep	TDKQPMMPV KVGLLNRNGE AVAFDYQGKR ATEAVLLLTEAEQTFLLLEGVTEAVVPSLLR					
g665	ADKQPMMPV KVGLLNRNGE AVAFDYQGKR ATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300
m665.pep	TDKQPMMPV KVGLLNRNGE AVAFDYQGKR ATEAVLLLTEAEQTFLLLEGVTEAVVPSLLR					
g665	ADKQPMMPV KVGLLNRNGE AVAFDYQGKR ATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

1061

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTCCGC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCGCGCTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCCGCCGCCG TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

```

a665.pep
1  MKWDETRFGL EYOLDIFMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
51  TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEGFQKGM MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPPTPDM ADKQPMIPV
251 KIGLLNCNGE AVAFDYQGRK ATEAVLLLTE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEEAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLNDNAFKA LLLGVPSAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNQAA KQENQSYEYS PEAAGWRTLK
451 NVCRAFLVLA DPAHIETVAE KYAEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFSK DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLNPNK
551 ARSLIGSFSR NVPHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

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m665/a665 97.3% identity in 638 aa overlap

```

m665.pep      10      20      30      40      50      60
MKWDETRFGLEYDLDIFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES
a665          10      20      30      40      50      60
MKWDETRFGLEYDLDIFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES

m665.pep      70      80      90      100     110     120
VVGHEYFHNWVTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
a665          70      80      90      100     110     120
VVGHEYFHNWVTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF

m665.pep      130     140     150     160     170     180
PEDAGPTAHPVRPASYEEMNFFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
a665          130     140     150     160     170     180
PEDAGPTAHPVRPARYEEMNFFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG

m665.pep      190     200     210     220     230     240
QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPTPDM
a665          190     200     210     220     230     240
QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQGRKNNVFELTIKQTVPPTPDM

m665.pep      250     260     270     280     290     300
TDKQPMMPVVKVGLLNRRNGEAVAFDYQGRKATEAVLLLTEAEQTFLEGVTEAVVPSLLR
a665          250     260     270     280     290     300
ADKQPMMPVVKIGLLNCNGEAVAFDYQGRKATEAVLLLTEAEQTFQFESVTEAVVPSLLR

m665.pep      310     320     330     340     350     360
GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEEAQTLYRRAVAANLATLSDGVELPKHEK
a665          310     320     330     340     350     360
GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEEAQTLYRRAVAANLAALS DGVELPKHEK

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```

1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTTCAGAC
1801 GACCTCTTGG ACAACGCCTT CAAAGCCCTG CTTTGGGGCG TGCCGTCCGA
1851 AGCCGAAGTG TGGACGGCA CGAAAAACAT CGACCCGCTG CGCTACCATC
1901 AGCGCGCGCA AGCCTTGTG GATACGCTTG CCGTCCGCTT CCTGCCGAAA
1951 TGGCACGAAT TGGACCGTCA GCGGCGGAAG CAGGAAAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCGCGGCACA TCGAAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGTGT GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTT
2251 ATCGGCTCAA GCCGCCGAG CGACACCTG CAACAGGTTT AAACCCGCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAACCC CAACAAAGCC CGTTGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCTGG TGCAGGCGTT CAACCTCTGC AACAGGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG AATTGCAGTG CATTGCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pap

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWEDTRFGL EYLDIFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRVRRRIEN IRLLRQNFQF
351 EDAGPTAHPV RPVSYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFORHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPPPTDMA DRQPMMPVK VGLLNNGEA VAFDYQGRRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNYP YSDDDLLLLL
551 ARLSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNFAFKL LLGVPSAEAL WDGTEINIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTLNR VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSRRSDTL QVQTLALQHP KFSLENPNKA RSLIGSFSRN VPHFAQDGS
801 GYRFIADKVI EIDRFNPOVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTAC ATTTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGTT GAGCCGACAG GGTAGGGGGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAACACAAA
301 TCCTGTATGG GGCTGTATGC TTCCGGCGGC AATTGTGTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCTAAGT CACCACCACC ATCGTCGCGC ACAAACACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGAGTTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTTG
551 CTTTGGTCGC GGGCGATTG GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGAA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGGCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTGG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GGAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTTGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CCGCGACCGC GCCAGCCGCG
1001 CCGTGGCGCG CATCGAAAAA ATCCGCTGCG TCGCGCAGCA CCAGTTCCCG
1051 GAAGACGCGA GCCCGACCGC CCATCCGGTG CGCCCCGCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAACAAAGC GCGGAAGTAG
1151 TCGCGGATGTA TCACACCTG CTCGGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCTT
1301 TGTGTACAG CCAGCGGGC ACGCCGTTT TGAAGCGGGA AGGTCTGCTG
1351 AAAACATAA TTTTCGAGTT GACCGTCAA CAAACCGTGC CGCCACGCGC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTG ACTATCAGG CAAACGCGCG

```

	250	260	270	280	290	300
	310	320	330	340	350	360
m665-1.pep	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRRIENIRLLRQHQPEDAGPTAHPV					
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRRIENIRLLRQHQFPEDAGPTAHPV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665-1.pep	RPASYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
g665-1	RPVSYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665-1.pep	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPMDTKQPMMPVK					
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPPTPMDTKQPMMPVK					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665-1.pep	VGLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLRGFSAPVHLNYP					
g665-1	VGLLNRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLRGFSAPVHLNYP					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665-1.pep	YSDDDLLLLLAHDSDAFTRWEEAQTLYRRAVANLATLSDGVL LPKHEKLLAAVEKVISD					
g665-1	YSDDDLLLLLAHDSDAFTCWEAAQTLYRRAVANLAALS DGIGLPKHEKLLAAVEKVISD					
	550	560	570	580	590	600
	610	620	630	640	650	660
m665-1.pep	DLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNRAAK					
g665-1	DLLDNAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDROAAK					
	610	620	630	640	650	660
	670	680	690	700	710	720
m665-1.pep	QENQSYEYSPAAAGWRTLNRNVCRAFVLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
g665-1	QENQSYEYSPETADWRTLNRNVCRAFVLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
	670	680	690	700	710	720
	730	740	750	760	770	780
m665-1.pep	NESDTRNLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVVRTALQHPKFSLENPNKA					
g665-1	NESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQHPKFSLENPNKA					
	730	740	750	760	770	780
	790	800	810	820	830	840
m665-1.pep	RSLIGSF SRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	RSLIGSF SRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
	850	860				
m665-1.pep	VKQALQIRIQEGLSKDVGEIVGKILD					
g665-1	VKQELQCIQAEGLSKDVGEIVGKILGX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTAC  ATTTTGATAT TAACGAACCG CAAACCATTG
101 TGAAGTCGCG TTTGACGGTC  GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151 TTGACCGGTT CGGCGAAACT  CTTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGGCG  AGACGCTGAC GATTGCGGAC GTGCCGTCGG
251 AACGCTTCAC CGTCGAAGTG  GAAACCGAAA TCCTGCCGGC GAAAAACAAA
301 TCGCTGATGG GGCTGTATGC  GTCCGCCGGT AACCTGTTTA CCCAGTGC GA
351 GCCGGAGGGC TTCCGCAAAA  TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC  ATCGTCGGCG ACAAAAACG CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA  AATCGACGGC GGCGAGTATT CAGACGCGCG

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a665-1.pep	KINGVAADYVLEGETLTITADVPSEKRTTVEVETEILPAENKSLMGLYASAGNLFQCEPEG				
m665-1	KINGAAADYVLEGETLTITAGVPSEKRTTVEVETEILPAENKSLMGLYASGGNLFQCEPEG	70	80	90	100
		110	120		
a665-1.pep	FRKITFYIDRDPVMSKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS	130	140	150	160
m665-1	FRKITFYIDRDPVMSKFTTTIVADKKRYPVLLSNGNKIDGGEFS DGRHWVKWEDPFSKPS	170	180		
		190	200	210	220
a665-1.pep	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGF AVESLKNAMKWDETRFGLF	230	240		
m665-1	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGF AVESLKNAMKWDETRFGLF	250	260	270	280
		290	300		
a665-1.pep	YDLDFIMVVAVGDFNMGMAMENKGLNIFNTK FVLADSRATDTDFEGIESVVGHEYFHNWT	310	320	330	340
m665-1	YDLDFIMVVAVGDFNMGMAMENKGLNIFNTK FVLADSRATDTDFEGIESVVGHEYFHNWT	350	360		
		370	380	390	400
a665-1.pep	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQH QFPEDAGPTAHPV	410	420		
m665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQH QFPEDAGPTAHPV	430	440	450	460
		470	480		
a665-1.pep	RPARYEEMNNFYMTVYEKGAEEVVRMYHTLLGEEGFQKGMKLYFQR HDGQAVTCDDFRAA	490	500	510	520
m665-1	RPASYEEMNNFYMTVYEKGAEEVVRMYHTLLGEEGFQKGMKLYFQR HDGQAVTCDDFRAA	530	540		
		550	560	570	580
a665-1.pep	MVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTVPPTPDMADKQPMMPVK	590	600		
m665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTVKQTVPPTP DMTPDKQPMMPVK	610	620	630	640
		650	660		
a665-1.pep	IGLLNCNGEAVAFDYQGRKRATEAVLLLTAE AQTFQFESVTEAVVPSSLRGFSAPVHLNYP	670	680	690	700
m665-1	VGLLNRNGEAVAFDYQGRKRATEAVLLLTAE AQTFLLGVTEAVVPSSLRGFSAPVHLNYP	710	720		
		730	740	750	760
a665-1.pep	YSDDDLLLLLAHDSDAFTRWEEAAQTL YRRRAVAANLAALSDGVLPKHEKLLAAVEKVISD	770	780		
m665-1	YSDDDLLLLLAHDSDAFTRWEEAAQTL YRRRAVAANLATLSDGVLPKHEKLLAAVEKVISD	790	800	810	820
		830	840		
a665-1.pep	DLLDNAFKALLLGVPSAEALWDGAENIDPL RYHQAREALLDILAVRFLPKWHELNRQA AK	850	860	870	880
m665-1	DLLDNAFKALLLGVPSAEALWDGAENIDPL RYHQAREALLDTLAVHFLPKWHELNRQA AK	890	900		
		910	920		
a665-1.pep	QENQSYEYSP EAGWRTLNRNVCRAFLVRADPAHIETVAEKYAE MAQNMTHEWGILSAVNG	930	940	950	960
m665-1	QENQSYEYSP EAGWRTLNRNVCRAFLVRADPAHIETVAEKYAE MAQNMTHEWGILSAVNG	970	980		
		990	1000		
a665-1.pep	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTAL QHPKFSLENPNKA	1010	1020		
m665-1	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTAL QHPKFSLENPNKA	1030	1040	1050	1060
		1070	1080		
a665-1.pep	RSLIGSFSRNVP HFAEDGSGYRFIADKVI EIDRFPQVAARLVQAFNL CNKLEPHRKNL	1090	1100		
m665-1	RSLIGSFSRNVP HFAEDGSGYRFIADKVI EIDRFPQVAARLVQAFNL CNKLEPHRKNL	1110	1120		

```

g666      HVTGLTEQKQVIASDFIVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL
           70          80          90          100          110          120
           130          140          150          160          170          180
m666.pep  GGGAFVLYWDNTAKTLTTFDGREAPMRATPELFLDKDGGQPLKFMEAVVVVARWVRLSL
           |||||
g666      GGGAFVLYWDNTAKTLTTFDGREAPMRATPELFLDKDGGXPLKFMEAVV--ARXVRLSL
           130          140          150          160          170
m666.pep  NX
           ||
g666      NX
           180

```

```
a666.seq
1  ATGCCTTGTA  TGAATCATCA  ATCAAACCTCA  GGCGAAGGAG  TGCTTGTGGC
51  TAAACATCAT  TTATTGACTG  CATTGATAAT  GTCTATGACA  ATCTCTGGAT
101 GTCAAGTCAT  CCATGCCAAT  CAAGGTAAGG  TTAATACTCA  TTCTGCTGTC
151 ATCACAGGTG  CAGACGCTCA  CACGCCTGAA  CATGCAACGG  GACTGACCGA
201 ACAAAGCAG  GTCATTGCAA  GTGATTTTAT  GGTAGCGTCA  GCCAATCCAT
251 TAGCAACACA  AGCTGGCTAT  GATATCTTAA  AGCAAGCGCG  TAGCGCTGCA
301 GATGCCGATG  TGCGGCTGCA  GACGACACTA  AGCTTGGTAG  AGCCACAGTC
351 GTCAGGCTTG  GGCGGTGGTG  CATTGTGTTT  GTATTGGGAT  AATACCGCCA
401 AAACATTGAC  CATATTGTAT  GGGCGTGACA  CGGCACCCAT  GCGTGCACAG
451 CCGGAATTAT  TTTTGGATAA  AGATGGTGAA  CCATTGAAAT  TTATGGAAGC
501 GGTGGTCTGT  GTCGCTCGGT  GGGTACGCCT  GCTATCCCTA  AACTGA
```

```
a666.pep
  1  MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSAV
51  ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGSAA
101 DAMVAQVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTDED GRETAPMRAT
151 PELFLDKDQG PLKFMEAVVV VARVRLLSL N*
```

		10	20	30	40	50	60
m666.pep		MPCMNHQSNSSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
a666		MPCMNHQSNSSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
a666		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWDNTAKTLTTFDGRETA	PMRATPELFLDKD	GGQPLKFMEAVVVVARWVRLSL			
a666		GGGAFVLYWDNTAKTLTTFDGRETA	PMRATPELFLDKD	GGQPLKFMEAVVVVARWVRLSL			
		130	140	150	160	170	180
m666.pep	NX						
a666	NX						

```
a667.seq
1  ATGCGGTTTG  TCTTCTGTTT  GGGCGGAGAG  ATAGTTTCTG  ATCCGCTTGA
51  TTTCATTTCT  GTATTCGTCT  GCGTCGAATC  TCGCGCTGAC  CAGACAGAA
101 CGCAGATACA  TCAGATAGGT  ATTTACCGCA  TCGGTTTCGC  AATAATTGCG
151 GATTTCTTTC  AGCCTGCCCG  CGTGGAACGC  CTCCACACC  TTGCTGCCGT
201 CCATACCCAG  CTTGCCCGGA  AAACCGCACA  GTTTCGCCAT  ATCGTCCAAC
251 GGCACATTTT  CCGTCGGCTG  GTAAAGCGCG  AGCAATCCA  TCAATCGCA
301 ATGACGTTGG  TGGTAGCGGC  TGATGTAGTT  GTTCCACTTG  AAATCGCGGC
351 TGTGCGCGAA  ATCGCGCTCG  CCCATATCCC  AATAGCGCGC  GGCCTGTGAT
401 CCGTGTAGCA  GCGAAGCGTA  CCGACAGAACC  GGCAGGTGCA  AACCGCGCCG
451 TTGCTCAACTG  ACCAGTTGCG  GCGTATGTTT  TTCAATCAAC  TCGAAAAATT
501 TGGCGATAAC  CACTTCTCTG  CCGTATCCCA  TCTCGCCGAT  TGTACCGACA
551 TGGACTTTAT  CCTGCCCCCA  ACGCATGCGA  CACGAAATCG  CCACAATCTG
601 ATGAAGATGA  TGCTGCATAA  AATCCCCACC  CGTCTGAGCA  CGCGGCTTTT
651 GCTGGGCAAA  CAGCACCCT  TCATCGTCCG  GCAGCGAGGA  CGGCAAGTCA
701 TACAGCGTAC  GGATACACTG  CACATCGGGT  ACGGTTTCAA  TATCGAAAGC
751 CAAAATCGTG  GTCATGACAG  CACCTTGTAT  TTAAAA.CAG  ACTTGCGCCT
801 ATTGTGTCAT  TAA
```

```
a667.pap
1  MRFVFLGLGE  IVSDPLDFHF  VFVCVESAAD  QTETQIHQIG  IYRIGFAIIA
51  DFLQPARVER  LPHLAAVHTQ  LARKTAQFRH  IVQRHIRPRL  VKREQIHQIA
101 MTLVVAAADV  VPLEIAAAVE  IAVAHIPIAR  GVDV*QRTV  MQNRQVETAA
151 VPTDQLRRMF  FNQLEKFGDN  HFLAVIHLAD  CTMDFILPP  THAARNRHNH
201 MKMMLHKIPT  RLSTAFLLGK  QHHFIVGQRG  RQVIQRTDTL  HIGYGFNIES
251 QNRGHDSTLY  LKXDRLRLCH  *
```

	10	20	30	40	50	60
m667.pep	MRLFPGLCGQVIPHFDHFVFVRIQPAADQTETQVHQISVCRVGFATIADFLQPAMEC					
a667	::: :: :: : : : :					
	10	20	30	40	50	60
	MRFVFCLGGEIVSDPLDHFHVFVCVESAADQTETQIHQIGIYRIGFAITADFLOPARVER					
	70	80	90	100	110	120
m667.pep	LPNLAAVHTQLARKTAQFRHHVQRHVCPRLVKREQIHQIAVALVITADVVPLEIAAAVE					
a667	: : : : : : : : : : :					
	LPHLA AVHTQLARKTAQFRHHVQRHIRPRLVKREQIHQIAMTLVV AADVVPLEIAAAVE					

1073

```

m669.pep      FRHVQSSNRQNGRPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
               |||||:|||||
g669          FRHVQSSNRQSGRPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
               70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1  ATGCGCCGCA TCATTAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51 TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1  MRRIKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRLRRQHGI
51 EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

               10      20      30      40      50      60
m669.pep      MRRIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHHDSLRRQHGIEGMGFDFKQI
               |||||:|||||
a669          MRRIKKHQPVNAPHIVLEIRIMKLHRAFVFLGRKRPHHHDSLRRQHGIEGMGFDFKQI
               10      20      30      40      50      60

               70      80      90      100
m669.pep      FRHVQSSNRQNGRPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
               |||||:|||||
a669          FRHVQSSNRQNGRPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
               70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1  ATGACTTGTT GCAGGAAGTG CTTGGCGCGT TCGTGTTTCG GGTGGTGAA
51 AAACGCTTCC GGCGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC GCCTAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNVTVC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1  ATGACCTGTT GCAGGAAGTG CTTGGCGCGT TCGTGTTTCG GGTGGTAAA
51 AAACGCTTCG GGCGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTCGTCA AACAACTTA

```

1075

```

              70      80      90      100      110      120
m670.pep    FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
a670        FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              70      80      90      100      110      120

              130      140      150
m670.pep    SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX
a670        SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX
              130      140      150

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

```

g671.seq
1  ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51  GCCCCAAATG CGGTTGGCAA AGCCAGACC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAATG ACAGagccaa TGCAAACAgg cggggTTGGA ACGagGCAAA
201 GCGGAGGTcg gcgaaggGTG CGGCaaAGAG TTTggcaaAA AAGAaggAAA
251 ccaccCATGC cACCATCgaa ccTGCTTCCG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCGGC GATGACGcg gAGGCGAGGA GGTGCGCAAT
351 GGGGAGGCTA TTCATTGCTT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

```

g671.pep
1  MISRVTIKTP FNAPNTPPKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKGAAKSLAK KKETTHATIE PASAITPRIV
101 EMTMQAAMTA EARRSAMGRL FIRYLAGDAV HAQFVQIAFG IPCVFIVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

```

m671.seq
1  ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51  GCCCCAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTGGA ACGAGGCCAAA
201 GGCGAGGTCG GCGAAGGAGG CGGCAAAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCCATGC CGCCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTGCGCAAT
351 GGGGAGGCTA TTCATTGCTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

```

m671.pep
1  MTSRVTIKTP FNAPNTPPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETTHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

```

              10      20      30      40      50      60
m671.pep    MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDANANR
g671        MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDANANR
              10      20      30      40      50      60

              70      80      90      100      110      120
m671.pep    RGWNEAKARSAKEAAKSLAKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL

```

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```
g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATRFQ NAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDPKVAAFI
201 ATANRLSR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```
m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCTAG CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GCGGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAATC GGTGATGTA TCCGGCGGTG
551 TGGAAGCGTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```
m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQSSRAV DIARAKKITA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATRFQ DAQALLFDAY HPSEYGGTGN RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDAKVAAFI
201 ATANRLSR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICG	ITTPEDAAAA	AAGADAVGL	VFFQSSRAV	DIARAKKITA	ALPPFVSVVA
g672	MRKIRTKICG	ITTPEDALYA	AHAGADALGL	VFYQSPRAI	DIIKAQKIAA	ALPPFVSVVA
	70	80	90	100	110	120
m672.pep	LFNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFHRPY	IKAIRVQTAS	DIRNAATRFQ
g672	LFNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFDRPY	IKAIRVQTAS	DIRNAATRFQ
	130	140	150	160	170	180
m672.pep	DAQALLFDAY	HPSEYGGTGN	RFDWTLLEAY	SGKPWVLAGG	LTPENVGEAV	RITGAESVDV
g672	NAQALLFDAY	HPSEYGGTGH	RFDWTLLEAY	SGKPWVLAGG	LTPENVGEAV	RITGAEAVDV
	190	200	209			
m672.pep	SGGVEASKGK	KDAKVAAFI	ATANRLSRX			
g672	SGGVEASKGK	KDPKVAAFI	ATANRLSRX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

```
a672.seq
```

1079

```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAATAAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRNLQ NVTEALGGVD
101 VVVVFVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELL KPYLPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEDGGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLF D NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA GCGGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGCGGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGTGTGTT
451 GCCCAAGTGC GCGCGAATT TGAATTTGCG GCGCGGAGG CGGTCAACGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRNLQ NVTEALGGVD
101 VVVVFVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYLPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEDGGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLF D TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

m673.pep      10      20      30      40      50      60
MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
|||||
g673          10      20      30      40      50      60
MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI

m673.pep      70      80      90     100     110     120
YDDTAQFVFVDTPGFQTDHRNALNDRNLQNVTEALGGVDVVVFVEAMRFTDADRVVLK
|||||

```

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
a673	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
a673	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR					
a673	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAAACAG CCCGCCGCCG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
101 VIINEAIEVT KTFGGTDGKH FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAAACAG CCCGCCGCCG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGGCAGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCAGCAGAG TATATCCGAC AAATCCGCCC
201 GCTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

```
g675.seq
  1  ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
 51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101  GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcaccgtc
151  gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201  CTCTTCCGAA AAATTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251  GCGAAACCTA CCATTTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301  GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351  CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401  ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451  GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

1085

101 SRVALDYNIP IANAVLT TEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
 151 EEQFEDEE*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLT TEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLT TEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
a675	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTTg
 51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCTCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTTC AATT TCCTCAGCGC CTTCGGGCGT
 151 GTTCAAAACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGG CAACGCGCCA
 201 ACGGCGAAAT CCAAGAAATT TTGTTTGGCG CGGTATCGAT TTCATCGACG
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCGCGCA ACAGACCGAC
 301 GGTCGCGCCG AAAAATACTT GGTCGGTTCG TTCGCGCAAT TCGGGATCGA
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAACGGAT GCGGCGGTGCG
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG
 451 GTCGCGGTTG CCTGCGGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep
 1 MPQILVRIFL IRYSEFIWETV RLCRFRHSR SVDFDVDRK DFNFLTAFRR
 51 VQNHVFAR FNQATRRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT
 101 GRAEKYLVR FAQFGIDDDG SLQTFGOETD AAVDFAHTAF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTTG
 51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCTCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTTC AATT TCCTCAGCGC CTTCGGGCGT
 151 GTTCAAAACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGA CAACGAGCCA
 201 GCGGCGAAAT CCAAGAAATT TTGTTTGGCG CGGTATCGAT TTCATCGATG
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCGAC
 301 CGTCGCGCCG AAAAATACTT GGTCGGTTCG TTCGCGCAAT TCGGGATCGA
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAACGGAT GCGGCGGTGCG
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG
 451 GTCGCGGTTG CCTGCGGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTGTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep
 1 MPQILVRIFL IRYSEFIWETA RLCRFRHSR SVDFDVDRK DFNFLTPFR

1087

```

m677.pep      FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRAEKHLVGRFAQFGIDDDG
                |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a677           FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDGRAEKHLVGRFAQFGINDDG
                70          80          90          100         110         120

                130         140         150         160         170         180
m677.pep      SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
                ::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a677           GFQTLGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFINQLIKLVFQCL
                130         140         150         160         170         180

                190         199
m677.pep      PSGGRNVVFGFGTHIVCGX
                |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a677           PSGGRNVVFGFGTHIVCGX
                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTccgCCG TCATCGCCGC
51 CTGCATCGTC ATTTCCACGA TGCGCGGCGT GATTGCGGAA GCAGgttcGA
101 TGGTgGCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
151 ttcgccgACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTCATTc ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTGCTG GCTGACCGGC GCAGTTTCGG CGGTCGGTCT GGGCTTTGCC
301 AACCGCATTT TGGGCGGTGT ATTCGGTGCA TTGAAAGCGC TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC atacggaCAA CGCaccgaa tCCctcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1  MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGVLIIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTCTT TGCCGCCTCC
151 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCgcCTGT TTGCATTGGC
201 TCTGTCGTTc ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTGCTG GCTGACCAGC GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGCGC TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1  MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTs AVSAVGLGFA
101 NRILGGVFGA LKGVLIIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1089

```

151  CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201  AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251  GGTTCGCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTCG
301  GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGSTTTCGG GCGCGTTCAT
351  GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401  GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTTCG
451  TCGATAAACCC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501  TTCGGCTTTG TTTAAACTGA TGTTTTCTG TTTCACATGG TCGAGCAGCC
551  GTCCGACGGT GCGCAGCACT ATTTTCGCAGC CGGCACGCAG GTCGGCGGTT
601  TGTTTGTTCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651  GTTTTAAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
  1  MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
 51  RRTSSRVTRS TLCLVLQKTI TWFIKRSTIS RSSRLRFWKV STAMMCCSTL
101  ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151  SINPISNMRS ASSRTTISAL FKLMFFCFTW SSSRPTVATT ISQPARRSAV
201  CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
  1  ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
 51  GCGCAGCAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101  GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151  CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTIGCA
201  GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251  GGTTCGCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301  GCGTTGGTGG TGTTTTGGCG GGCGACTTCG ACGSTTTCGG GCGCGTTCAT
351  GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401  GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTTCG
451  TCGATAAAAC CCATATCCAG CATAACGGTC GCTTCGTCCA AAACGACGAT
501  TTCGACTTTG TTCAAATGGA TGTTTTCTG TTTCACGTGG TCGAGCAGCC
551  GTCCGACGGT GCGCAGCAGC ATTTTCGCAGC CGGCACGCAG GTCGGCGGTC
601  TGTTTGTTCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651  GTTTTGTATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
  1  MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
 51  RRTSSRVTRS TLCLVLQNTM TWFIKRSTIS RSSRLRF*MV STAMMCCSTL
101  ALVVFCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151  SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201  CLSIFIPPNK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

                                10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||
g680       MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          |||
                                10      20      30      40      50      60

                                70      80      90     100     110     120
m680.pep  TLCLVLQNTMTWFIKRSTISRSSRLRFKXVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||
g680       TLCLVLQKTTWFIKRSTISRSSRLRFKXVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||
                                70      80      90     100     110     120

                                130     140     150     160     170     180
m680.pep  ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW

```

1091

```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCCgt cgaggttgGG GCGCATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401  TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCTGCGGT
451  GTATTCTGTCG GTTTCGTTCG CGCTGAAGAA ACGCCAGCCG CTGTCTGTTT
501  CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTTTG
551  GCGACGGTGT TGGTGCGGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCACG ATTCGCCGCT TGTCGGCAGA CGGCGGCGGT TTGGTGGTAC
701  AATGTGCGCC GTTTGCAGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

```

m681.pep
  1  MTTTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
 51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101  RLPVNGLEEC AVFGKLPRAA FGLGQCGGF RVFGDVGGEA DDAEVVGVVG
151  VFVGFVAAEE TPAAVVFKNK GFAVEADGP VLFVDGVGVD AAVECRGKCL
201  KCKVHCGNTL GGGKLADEFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251  KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

```

m681.seq
  1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AACTTTTCGG AAGAGGCAAA
 51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101  TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGCATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ATGCGCTGCC TTCGGGTTGG GAGAGCTJTG CGGCGGTTTC AGGGTTGGTT
401  TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GATCGTCCGT
451  GTATTCTGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCTGTTT
501  CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTTTG
551  GCGACGGTGT TGGTGCGGAT ACAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATT
651  TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAA
701  ATGCGCGGTT TGCAGCCTTA AGGTGTTTCT GTATTTTTGG AGTATGGAAA
751  CGCATTCGGG CTGTTTTTTT CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

```

m681.pep
  1  MTTTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
 51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101  RLPVGDGLEC AVFGKLPCAA FGLGQCGGF RVFGDVGGEA DDAEVVRIVG
151  VFVGLVAAEE TPAAVVFKNK GFAVEEADGP VLFVDGVGVD TAVECRGKCL
201  KCKVHYGNTL GXKLTDFTTI RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251  RIRAVFCGR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

m681.pep      10      20      30      40      50      60
               MTTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
               |||
g681          10      20      30      40      50      60
               MTTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV

```

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKNGGF	AVEEADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVR	VVGVFVGLVAAEET	PAAVVFKNGGF	AVEEADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHY	GNTLGXKLTDETT	IRALSADGGGLV	VCAPFAAL	
a681	VLFGDGVGGDAAVE	CRGKCLCKCVH	CGNTXGGKLADFT	TILALSADGGGL	VVCAPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAAT GCCGTCTGAA CCGGATTGGA
251 TTCAGACGGC ATTTGTATG GCAGGATTTA TTCGCTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTC
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCCATTCGGA CAAGGCAGTC AGGCGTTGTT CGGATTTCCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHL STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY... EMAMPSEP DWIQTAFDMA YGFIRFPTDR
101 PIRTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683>:

g683.pep
 1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIC NGNIHTYINK
 51 DSVRKNGLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
 101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..
 1 ATGATTAAGG AAACCCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
 51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
 101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
 151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
 201 TGTACCAAT CTAACAACAG AACGTTTTCG CAACACCCCC GCATACAAGA
 251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
 301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
 351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCTGTCC GGGACATTAA
 401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep..
 1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
 51 DSVRKNGLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
 101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

m683.pep	10	20	30	40	50	60
	MIKETLMRPIFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGLM					
g683						
	MIKETLMRPIFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGLM					
	10	20	30	40	50	60
m683.pep	70	80	90	100	110	120
	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683						
	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
m683.pep	130	140				
	SSLRPMISLSGTLTEKQYETVCGKKLX					
g683						
	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq
 1 ATGATTAAGG AAACCCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
 51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
 101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
 151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
 201 TGTACCAAT CTAACAACAG AACGTTTTCG CNACACCCCC GCATACAAGA
 251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
 301 AGTTCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
 351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCTGTCC GGGACATTAA
 401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep
 1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
 51 DSVRKNGLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL

Homology with a predicted ORF from *N. gonorrhoeae*

m684/g684 97.7% identity in 172 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

Homology with a predicted ORF from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFP	IAAALS	LAACGT	VQSTQY	FVLPDS	RRYIRPAT
a684	MRLFP	IAAALT	LAACGT	VQSTQY	FVLPDS	RRYIRPAT
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRL	NTAQNH	VWADTLD	MDM	LEAALS	NAFNRLD
a684	DPYRL	NTAQNH	VWADTLD	MDM	LEAALS	NAFNRLD
	70	80	90	100	110	120
	130	140	150	160	170	

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPOLVIT
151 GGPAGAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGGK RGLVLSVTGN KVSAGTQSR LASWIHGDIG
251 LPPVDES LRN EGHGQPVSE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQ LKAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

              10      20      30      40      50      60
m685.pep      LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
g685           LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPEPAAEKT
              10      20      30      40      50      60

              70      80      90      100     110
m685.pep      VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
g685           VSAASQAASTPVATLTVPARGDAVVPKNPERVAVYDWAALDTLTPGVNVGATTAPVRV
              70      80      90      100     110     120

              120     130     140     150     160     170
m685.pep      DYLPQAFDKAATVGTLFEPDYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGN
g685           DYLPQAFDKAATVGTLFEPDCESLHRHNPQFVITGGPGAEAYEQLAKNATTIDLTVDNGN
              130     140     150     160     170     180

              180     190     200     210     220     230
m685.pep      IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGGKRGVLVSVTGNKVSAGF
g685           IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKGGKRGVLVSVTGNKVSAGF
              190     200     210     220     230     240

              240     250     260     270     280     290
m685.pep      TQSRLASWIHGDIGLPPVDES LRNEGHGQPVSEYIKEKNPDWIFIIDRTAAIGQEGPAA
g685           TQSRLASWIHGDIGLPPVDES LRNEGHGQPVSEYIKEKNPDWIFIIDRTAAIGQEGPAA
              250     260     270     280     290     300

              300     310     320     330     340     350
m685.pep      VEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQ LKAAFKKAEPV AAGKKX
g685           VEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQ LKAAFEKAEPV AAOX
              310     320     330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TGCGGCGTGG TTTCTGCAGG
51 TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTCGCCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGCCTGTGGA
351 TTATTTGCAG CCTGCATTG ACAAGGCGGC AACGGTGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCTATTAC
451 GCGCGGCCGG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GCGGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAGGA CGCGGGCTGG TGCTGTCTGG TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:

g686.pep (partial)
 1 ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
 51 IIVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
 101 AVGGMVFSV PMDAVKAESV NGTTGFVRIG M*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..
 1 ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTGGC
 51 GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
 101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TCCCGTTGAA
 151 GGCTTCGGCG GCATTGCCCC ATCTGTCCAG CTCGGGGCTG TCTCGGGTGG
 201 CGCGTTTGAA TCCGTCGCCT ACTCCTTGC TCAGCATACT ACCGGCATTG
 251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
 301 GAGCGCGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
 351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
 401 TCGGCGGGAT GGTGTTCTGA TCCGTCCCAA TGGATCGCGT AAAGGCTAAA
 451 TCCGTCAACG GGACTACCG CTTATCAGA ATCGGAATGT GA

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep
 1 MMLKKFVLGG IAALVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
 51 GFGGIARSVQ LGAVSGGA FE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
 101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFSV SVPMDAVKAK
 151 SVNNGTTGFIR IGM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

				10	20	30
g686.pep				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKKFVLGGIAALVLAACGGSEGGSGAXX	XXNFSCSADDVFNDICSAVEGFGGIARSVQLG				
	10	20	30	40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
m686		AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
		70	80	90	100	110
g686.pep		100	110	120	130	
		GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFVRIGMX				
m686		GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFVRIGMX				
		130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)
 1 ..AATTCTCCT GCCGCGCCGA TGATGTTTT GACGATATCT GCAGTGCCGT
 51 TGAAAGCTTC GCGGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
 101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGCTCAGCA TACTACCGGT
 151 ATTGTGAAA CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
 201 GGTTGAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
 251 TCCCTCGGCG CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
 301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC TCAATGGATG CGGTAAAGGC
 351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

```

501 TGCCGCTAC GAGTCCCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGTAATATA AAGTTGAATT TGCTTACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAAAGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>:

```

m687.pep
1  MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYPCHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QIKLQNPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFO IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

```

m687/g687    97.0% identity in 234 aa overlap

          10      20      30      40      50
m687.pep    MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
              |||||
g687         MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
          10      20      30      40      50      60

          60      70      80      90     100     110
m687.pep    QQQAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTHEHVWQKEMLTLARLAAA
              |||||
g687         QQQAGKVEVLEFFGYFCPHCARLEPVLSKHAKSFKDDMYLRTHEHVWQKEMPLPLARLAAA
          70      80      90     100     110     120

          120     130     140     150     160     170
m687.pep    VDMAAADSKDVANSHIFDAMVNVQIKLQNPVLEVLKKWLGEQTAFDGKKVLAAYESPESQAR
              |||||
g687         VDMAAADSKDVANSHIFDAMVNVQIKLQNPVLEVLKKWLGEQTAFDGKKVLAAYESPESQAR
          130     140     150     160     170     180

          180     190     200     210     220     230
m687.pep    ADKMQELTETFOIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
              |
g687         AGKMQELTETFOIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

```

a687.seq
1  ATGAAATCCA AACACCTCGC CCTCGCGGTT GCCGCCCTGT TCGCACTTGC
51  CGCGTGGGAC AGCAAAGTCC AAACCAGCGT CCCCGCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACTGTCCTTG CCAACCCGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTGCAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGTCGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAGA GCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT
501 TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGCAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAAAGCC GCGCACTAA

```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

```

a687.pep
1  MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYPCHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QIKLQNPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFO IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

```


Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m688.pep	VLHYPSRFAQKGISVNKTLILALSALLGLAACSAERVS	LFPSYKLIKIIQGN	LEPR	VAA		
g688	VLHXTSRFAQKGSPVNKTLILALSALFSLTACSV	ERVSLFPSYKLIKIIQGN	LEPR	VAA		
	10	20	30	40	50	60
	70	80	90	100	110	120
m688.pep	LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTF	NTSRNGIIKERSNL	TVYFENGVL	VRTEG		
g688	LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTF	NTSRNGIIKERSNL	TVYFENGVL	VRTEG		
	70	80	90	100	110	120
	130	140				
m688.pep	DVLQNAAEALKDRQNTDKPX					
g688	DALQNAAEALRAKQNA	DKQX				
	130	140				

```

a688.seq
1  GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51  AACCCTCATC CTCGCCCTTT CGGCCCTTCT CGGCCCTTGC GCGTGCAGCG
101 TCGAACCGGT TTA CTGTTCC CCCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGAACAAGT AACTCTCGCGC CGTCCGCTCC CTCGCCCGCC GTATAGACAA
201 AGACCAAGTC CAGTCTCTGC TCGGCAGCCC CATACTCGCG GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAAACGGGG TGCTCGTCCG
351 CACCGGAAGC AACGCCCTGC AAAATGCCCG CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA

```

a688.pep

1	VLHYPSRFAQ	KGISVNKTLI	LALSALLGLA	ACSVRVSLF	PSYCLKIIG
51	NELEPRAVAS	LRPGMTKQDV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KDRSLNTVYF	ENGVLVRTGE	NALONAEEAL	RVKONADKO*	

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

	10	20	30	40	50	60
m688.pep	VLHYP	SRAQKGISVN	KTILILALSALLGLAAC	SAERVS	LFPSYK	LKIIQGN
a688	VLHYP	SRAQKGISVN	KTILILALSALLGLAAC	SVERVS	LFPSYK	LKIIQGN
	10	20	30	40	50	60
m688.pep	LRPGMTK	DQVLL	LLGSPIL	RDAFHTDR	WDYTFNTSR	NGIIKERS
a688	LRPGMTK	DQVLL	LLGSPIL	RDAFHTDR	WDYTFNTSR	NGIKDRS
	70	80	90	100	110	120
m688.pep	LNLT	VYFENG	VLVR	TEG		
a688	LNLT	VYFENG	VLVR	TEG		
	70	80	90	100	110	120
m688.pep	DVLQNA	AEAL	KDRQN	TDK	PKX	
	:::					
a688	NALQNA	AEAL	RVKQN	ADK	QX	
	130	140				

1351 AAAGAAACG GGCAAAGCGA ATACCTTTAA

This corresponds to the amino acid sequence <SEQ ID 2294; ORF 689>:

m689.pep
 1 LLIHIVPVR PVLPGLLLP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
 51 PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
 101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLIVYCLA VAAIVFVSSA
 151 EQLLNLRVVQ AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL
 201 VAPMVGALLQ GLGGWQAI FV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
 251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESS VYQQLYRVTP
 301 HQYAWAFALN IITMFFNRV TAWRLKTGVH POSILLWGIV VQFAANLSQL
 351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
 401 LGVFQSLIGA VGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
 451 KENGQSEYL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

	30	40	50	60	70	80
m689.pep	CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSEKLMAVLMAMLVTLMPFSIDAY					
g689			SPPLPPMSGKLMMAVLMVLAVALMPFSIDAY			
			10	20	30	
	90	100	110	120	130	140
m689.pep	LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLAV					
g689	LPAIPEMAQSLNADIHRIEXSLSLFMFGTAFGQVAGGAVSDIKGRKPVALTGLIVYCLAV					
	40	50	60	70	80	90
	150	160	170	180	190	200
m689.pep	AAIVFVSSAEQLLNLRVVQAFGAGMTVVI VGAMVRDYYSGRKAAQMFALIGIILMVVPLV					
g689	AAIVFASSTEQLLNLRVVQAFGAGMAVVI VGAMVRDYYSGRKAAQMFALIGIILMVVPLA					
	100	110	120	130	140	150
	210	220	230	240	250	260
m689.pep	APMVGALLQGLGGWQAI FV FLAAYSLVLLGLVQYFLPKPAVGGKIGRDVFGVLVAGRFRKRV					
g689	APMVGALLQGLGGWRAIFV FLAAYSPVLPGLVQYFLPNPAVGGKIGRDVFGVLVAGRFRKRV					
	160	170	180	190	200	210
	270	280	290	300	310	320
m689.pep	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMFFNRVT					
g689	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYRQLYHVTPHRYAWVFALNIITMFFSRVT					
	220	230	240	250	260	270
	330	340	350	360	370	380
m689.pep	AWRLKTGVHPOSILLWGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMF SVGTQGLVGAN					
g689	AWRLKTGAHPQSILLRGIVVQFAANPSQLAAVLFFGLPPFWLPVACVMF SVGTQGLVGAD					
	280	290	300	310	320	330
	390	400	410	420	430	440
m689.pep	TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDGSATVMAATMTASTSCGIAL					
g689	TQACFMSYFKEEGGSANAVSGVFRSLIGAGVVMAAT-----VMAATMTASASCGIAL					
	340	350	360	370	380	
	450	460				
m689.pep	LWLCSHRAWKENGQSEYLY					
g689	LWLCSHKAWKENEKRI					
	390	400				

1109

```

|||||
a689      GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFLPKP
          190      200      210      220      230      240

          250      260      270      280      290      300
m689.pep  AVGGKIGRDVFGVLVAGRFRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP
          |||||
a689      AVGGKIGRDVFGVLVAGRFRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYHVTP
          250      260      270      280      290      300

          310      320      330      340      350      360
m689.pep  HQYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFFGLPP
          |||||
a689      HQYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFFGLPP
          310      320      330      340      350      360

          370      380      390      400      410      420
m689.pep  FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMATFLH
          |||||
a689      FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMATFLH
          370      380      390      400      410      420

          430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLLWLCSHRAWKENGQSEYLY
          |||||
a689      DGSATVMAATMTASTSCGIALLLWLCSHRAWKENGQSEYLY
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

```

g690.seq (partial)
1  ATGAAAAACA AACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GCGCCGCGCT TCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTTCCTCAAC CGATTTGCAA
151 CCGGCGGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCTGC ACCCGCCGCG CGGCATTGGC GATCTCATAC
251 AGCAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTCCCAT
301 AACGAACTGG AAACCGTTT CGGCTTACCC GCGCGCGCT ATGACAACAT
351 ACAGCGGctG CTgtttCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACCCGC GGACAAGGCG
551 AGGAACCGAA ACGCGCACGT TATTTTGAAG TTTCCGGAAC ATCtgCctat
601 TTgaaccggC ACAACAacGG ACTTggcgGC AATTTCCAAT ACATCGGCCA
651 ATTGCCCCGC TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCACATC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTtagac
751 ATCCATTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690 >:

```

g690.pep (partial)
1  MNKNTSSLPL WLAAILAAR SPSKEDKKE NGASAASSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQIIAEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSQKTR QGGEPEKRAR YFEVSATSAY
201 LNRHNNGLGG NFQYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPKPFELD
251 IHFDENGKIT RIVVYEKNIIY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

```

m690.seq..
1  ATGAAAAACA AACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCCGGTGCAT
101 CCGCTGCTTC GTCCCTCCGCG TCATCAGCTC CTTCCTCAAC CGATTTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATTGC ACCAGCCTGC ACCCGCCGCG CGGCATTGAC GATCTCATGC
251 AGCAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTCCCAT
301 CACGAACTGG AAACCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAA GCGCACGATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCGC GGACAAGGCG

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1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTATAGACA TCCATTTTGA CGAAAATGGC AAAATCACGC GTATTGTCGT
 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep
 1 MKNKTSLLLL WLAAMMLTAC SPSKEDKKE NGASAASSTA SAASSAPOT
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDPDYHQKII LAIEDLRYGK
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEPEK RTRYFEVSAT
 201 PAYSSRHNNG LGGNFQYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPDKP
 251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

	10	20	30	40	50	
m690.pep	MKNKTSLLLLWLTAIMLTACSPSKDDKTEVGASAASSASSAPS---	QTDLQPTASAPD				
a690	MKNKTSLLLLWLAAMMLTACSPSKDDKTEVGASAASTASAASSAPQTDLQPAASAPD					
	10	20	30	40	50	60
m690.pep	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI					
a690	NVKQAESVPPSNCTDLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPGGGYDNI					
	70	80	90	100	110	120
m690.pep	QRLFPDIRPEDPDYHQKIIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ					
a690	QRLFPDIRPEDPDYHQKIIILAIEDLRYGKRTISRQAQDALMEQERRLREATLLLIQGSQ					
	130	140	150	160	170	180
m690.pep	ETRGQGEPEKRTTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLENQSLFRL					
a690	ETRGQGEPEKRTTRYFEVSATPAYSSRHNNGLGGNFQYIGQLPGYLKIHGEMLENQSLFRL					
	190	200	210	220	230	240
m690.pep	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNTGRIX					
a690	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNLGRX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq
 1 GTGCCGCTGC CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCGGAA CGATTTCCTA CCGAACTGCG ACATACGCCG GCTCGGGCTG
 151 ACACAGGGTC AGCACAATGA GCTGCGTAAA ATCCGCGCCG CCTTCAAAAT
 201 GCGCGGCGAC AGGCGCGGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG
 301 GCGCGCGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTTGGCGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
 401 AGCAGCAAAAT GTGGCTTCTT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep
 1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TQGOHNELRK IRAAFKMGAD RARLKVHSE HSRRRSVVEI ISSDVFNRRNE
 101 ARDYVESRYH SSMDFAVDEL EIQRHFPHIL TPQQQMWLS SCLK*

Homology with a predicted ORF from *N. meningitidis*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. meningitidis*:

m691/a691 97.2% identity in 144 aa overlap

	10	20	30	40	50	60
m691.pep	VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDPQPCDIRRLGLTQSQHNELRK					
a691	VPLXAPCRFAKPAASFLSMALLSCQLSHAATAYIPLNDFQPCDIRRLGLTQSQHNELRK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m691.pep	IRTAFKMAGDRARLKVMHSEHSRRRSVVEIISSDVFNRNEARDYVESRYLSGMDFAVDEL					
a691	IRAAFKMAGDRARLKVMHSEHSRRRSVVEIISSDVFNRNEARDYVESRYLSGMDFAVDEL					
	70	80	90	100	110	120
	130	140				
m691.pep	EIQHRFFHILTPQQQMWLSSCLKX					
a691	EIQHRFFHILTPQQQMWLSSCLKX					
	130	140				

The following partial DNA sequence was identified in *S. gonorrhoeae* <SEQ ID 2309>

g692.seq

```

1  GTATCGCACA CACGCTGTCG CTGTTTCGGAA TCGAtacGCC GGATTTGGCG
51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATGCGGTTCAC GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGT ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTgacGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGCTCT TGGAACAGGG CTTGCGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTGCGCGCG
401 AGTTGTGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCCGC
451 GATGTCGGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTTTCAGC ATCACCAGG CGCGTGCGAA GTTGGAcggG
551 TcgtTGGGCG CGGATACGGT GCTGCCGTCT TGACTTCTT CCAGCGATT
601 CAGTTTGGCC GGATACAGTC CCAAAGGCGC GGTGCGCACT TGAAGGCTT
651 CGGTGATGTC CAGGTTGTGT TCTTTTTTGA AATCGTCAAG ATAGGTTTG
701 TGTTGGAAGA CGTTGATGTC CAACTCGCCC TCCGCCAATG CCAGATTCCG
751 CGGCACATAG TCggtAAATT cgaccaatTT gacgGTGTag cTTTTTTCT
801 CGTAGTCGgc tTGGATTGT TCTTTGACCA TATcgccgaa gtcgcccacg
851 gTCGTGCCGA agacgaTTTC TTTTTTCGCC GcgCGTTAT CGGCAGAAGG
901 GCGGCGGgca gaggtgcGG GCGCGCTGTC TTTTtgaccG ccgCAGGCTG
951 CGAGGATGAG CGCGAGtgcg gcgcggaaa ggGTTTTGAA GAAGGTTTc
1001 atATTTTCTc ctga

```

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692 >:

g692.pep

```

1  VSHTRCRCSE SIRRIWRNGR EWRIKQKCR LNTDAVQTAS FYTTALFGCA
51  FIPCGRVFA LEAFVRVGFE RVGVIGLGYV FKPLAVFVGG FDGRFPVDIGK
101 ARLLEQFGQ LHAAYGVVA VDDGKIHVGA AARQLCGFKL DDFDVQVFR
151 DVGFQCGQRI DAVFEFDPTQ FVQHHQGACE VGRVVGGRYG AAVFDFFQRF
201 QFARIQSQR GRHLEGFGDV QVVFFFEIVK IGFVLEDVDV QLALRQCQIR
251 AHIVGKFDQF DGVAFFLQLG LDLFDDHIAE VAHGRAEDDF FFRAVIGRR
301 GGGRCGGRAV FLTAAGCEDE RECGGKGFE EGFHIFS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

m692.seq

```

1  GTGTTGCACA CGCTTTGTCG CTGTTTCGGAA TCGATACGCC GGATTCGGCG
51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACAGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTGCGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGCG

```

```

51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTCGGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCGGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTGCGGACT TGGAAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTTCGG
751 GCGCACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGGATTGTG TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTT TTTTTCGCC GCGCGGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTATCTTT TTGACCGCCG CAGGCGGCGA
951 GGATGAGCGC GAGTGGGCGG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

```

a692.pep
1  VLHTLCRCSE SIRRIERNR EARIKGQKCR LNTDTVQTAS FYTTALFGCA
51  FIPCGRGFVA LEAFVRVGF E RVGVIGLYV FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFVDFVFG
151 NVRFGCGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVGGRGYG AAVFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVGGG
301 RSGCGGRAIF LTAAGGEDER ECGGGKGFE EGFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

```

m692/a692 98.8% identity in 336 aa overlap

          10      20      30      40      50      60
m692.pep VLHTLCRCSESIRRIERNGREWRIKGQKRLNTDTVQTASFYTTALFGCAFI PCGRGFVA
          |||
a692      VLHTLCRCSESIRRIERNGREWRIKGQKRLNTDTVQTASFYTTALFGCAFI PCGRGFVA
          10      20      30      40      50      60

          70      80      90      100     110     120
m692.pep LEAFVRVGFERFVGVIGLYVFKPLAVFVGFDGRPDIGKARFLEQGFQGLHAAAYGVVA
          |||
a692      LEAFVRVGFERFVGVIGLYVFKPLAVFVGFDGRPDIGKARFLEQGFQGLHAAAYGVVA
          70      80      90      100     110     120

          130     140     150     160     170     180
m692.pep VDDGKIHVGAATRQLRGFKLDDFVQVLDVRFVGGQRI DAVFEFDPTQFVEHHQDAGE
          |||
a692      VDDGKIHVGAATRQLRGFKLDDFVQVFNVRFGCGQRI DAVFEFDPTQFVEHHQDAGE
          130     140     150     160     170     180

          190     200     210     220     230     240
m692.pep VGRVVGGRGYGAAVDFDFQRFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
          |||
a692      VGRVVGGRGYGAAVDFDFQRFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
          190     200     210     220     230     240

          250     260     270     280     290     300
m692.pep QLALSQCQIRAYIVGKLDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDF FFRRAVVGGG
          |||
a692      QLALSQCQIRAHIVGKLDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDF FFRRAVVGGG
          250     260     270     280     290     300

          310     320     330
m692.pep RSGCGGRAVFLTAAGGEDERECCGGKGFE EGFHIFSX
          |||
a692      RSGCGGRAIFLTAAGGEDERECCGGKGFE EGFHIFSX

```

1117

```

151  GRRDIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201  CHISDRFDQK HFARRKLPKR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251  HQRASRIKHA ETALRRRLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301  QVVHDEFVNV DFVAHINRRA ELFOSTFDNT DCPHTSAEA ARIGKDDGFL
351  VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

m694/g694 86.8% identity in 372 aa overlap

	10	20	30	40	50
m694.pep	LVSASGTRQKCR	LPVQTAFVLPKHS	----	TPASTFAQIGFGF	ALAAQLFGQDEHNAFFR
g694		SAFVLPKHPAL	TPASTFAQIGFGF	ALAAQLFGQDEHDAFFR	
		10	20	30	40
	60	70	80	90	100
m694.pep	TLAFAYGFVPP	SAYGCQYFPHQHF	GRGRACRYADFV	FALKPCALQVACI	IHHIRIDSARC
g694	APPPAHGFMPP	SAYGCQYFPHQHF	GRGRACRYADFA	FAFKPRALQVGRV	VHHIRIDSARC
	50	60	70	80	90
	120	130	140	150	160
m694.pep	RHFAQAVAVGR	IGRTDHNHDVAL	FQCQLFDGGLPV	GRRIADIFLVRI	ADIGETRVQRGDDV
g694	RHFAQAVAVGR	IGRTDHNHDVAL	FQCQLFDGGLPV	GRRIADIFLVRI	ADIGETRVQRGDDV
	110	120	130	140	150
	180	190	200	210	220
m694.pep	FGFIDRERGLA	DIGEFVGVSDFE	FCHISDRFDQKH	FARRKLPHRSFD	LDVPLMPDHDDFT
g694	FGFIDRERGLA	DIGEFVGVSDFE	FCHISDRFDQKH	FARRKLPHRAFD	LGVLMPDHDDFT
	170	180	190	200	210
	240	250	260	270	280
m694.pep	VLGIQSGDFLM	FRHQRASRIKHA	ETALRRFLPHRL	RYAVCRINQCR	ARRHFRQVFNKHR
g694	VLGIQSGDFLM	FRHQRASRIKHA	ETALRRFLPHRL	RYAVCRINQCR	ARRHFRQVFNKHR
	230	240	250	260	270
	300	310	320	330	340
m694.pep	TFFTQVVHDEF	VNVDFVAHINRRA	ELFOSTFDNTDC	PIHTSAEAARIG	KDDGFLVHKPGI
g694	AFFAQVVHDEF	VNVDFVAHINRRA	ELFOSTFDNTDC	PIHTGAEAARIG	KDDGFLVHKPGI
	290	300	310	320	330
	360	370	380		
m694.pep	SFSDGINIFLL	GFYGGRCCTPPT	PHRRRX		
g694	PCSDGIHVFL	XXLCDGRYCQAPP	PHRRRX		
	350	360	370		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.seq
1   TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTCTA
51  GACGGCATTT GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTTCGCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGG TTACGCCGAC TTTGTTTTTG CCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGCATGT CGCACTGTTT TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTCTGTCGA TAGCAGATAT CTTCTTGTG CGAATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTCT GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GCGCAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCG GATCATGATG

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695.seq
1  TTGCCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTTGATGTC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATTT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCCTG CTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGCTG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG AGGGCAGCGG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCTATCCCG TTCCACTCT
351 GCAAGACCGT TTGGACTATC TGAAGGCCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAT GTTAAACGGG AAAGTCAAAG CATTGGAGCA TACGAAAATA
451 CACCTTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAACGGC
601 AGGTTTTCTG CCGCAGCCGC CTTGTTGAAG GGGCGGACG GCGGAGACGG
651 CGGAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCGAA GTCATATTC AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGCAAAACG CGCCGCGCGA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695 >:

```
g695.pep
1  LPQTRPARRH HRHROYFVER KGDARSGF*C AAQCONSQR F QSKPAL YAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIWL SVSASCASVL PVPEGSRTM
101 PTOENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRITYVQK LDDRKLKEHY LNTEGGSASA HTVETAONLY NQALKHYONG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQOKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695.seq
1  TTGCCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCCTG CTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGCTCG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGAAGGCCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCTCCG GCAGGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCTG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAAGCGGC
601 AAGTTTTCTG CCGCTGCCTC CCTGTTGAAA GCGCGGACG GAGGCGACGG
651 CGGAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGCAAAACG CGCCGCGCGA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695.pep
1  LPQTRPSRRH HRHROYFAER KGDARSGFRC AAQRHPORF QSKPAERPAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAONLY NQALKHYKSG
201 RFSAAASLLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQOKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

```

      10      20      30      40      50      60
m695.pep  LPQTRPSRRHHRHROFYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR
a695      LPQACPARRHCHROFYFVERKGDARSGFRCAAQRRHPQRFQSKPAERYADCPHHPARRRR
      10      20      30      40      50      60

      70      80      90     100     110
m695.pep  LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQT---EMSTFENASDGIPYPVPTL
a695      FDPASEKIMKTKLPLFIIWLSVSAACSS--PVSRNIQDMRLEPOAEAGSSDAIPYPVPTL
      70      80      90     100     110

      120     130     140     150     160     170
m695.pep  QDRLDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYLNTGGS
a695      QDRLDYLEGLVRLSNEVETLNGKVKALEHAKTHPSRAYVQKLD DRKLKEHYLNTGGS
      120     130     140     150     160     170

      180     190     200     210     220     230
m695.pep  ASAHTVETAQONLYNQALKHYKSGKFSAASLLKGADGGDGGSIQRSMYLLQSRARMGN
a695      ASAHTVETAQONLYNQALKHYKSGRFSAAASLLKGADGGDGGSIQRSMYLLQSRARMGN
      180     190     200     210     220     230

      240     250     260     270     280     290
m695.pep  CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARK
a695      CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARK
      240     250     260     270     280     290

      300
m695.pep  AAAAVRKRKX
a695      AAAAVRKRKX
      300

```

The following partial DNA sequence was identified in *N. gonorrhoeae*
g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>:
g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

```

m696.seq
1  TTGGGTGCC GGCAGGCGGC ATCCCATCAT TTTGCCAAG GCAACAAAT
51  ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTCTCTCG ACGGCAGAAG CGGCAGACTC GCGCGCAGAA
251 GCCGCAGTGT CTTAACATC GGA CTCAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTG GCTTCTTGC AACAACTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

```

m696.pep
1  LGCRQAASHH FCQGNKLFVG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFNL
101 LLFGFLRTSC QGSRHHCGNQ *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:
a696.seq

1123

201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPVIQGAG GLEVVPVAVS FGVVVNIAAP FLMVVFSTLG
 301 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2333>:

m700.seq

1 ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
 51 ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
 101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCG
 151 CGCGTGGAGG ATTTGGGTTT GCGGTTGGAC GATATGGCGT TGACGGTTCT
 201 GTGGCTGTTT GTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
 251 TGGGAAAGTT ATCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
 301 GTCGCGGTGT CGGCAGTGT CGGCAGCTC GGATGCGTGC TGCTCGGATT
 351 TGCATTCGGC AAACGATGC GCGATATTG GATGCCGTCT GAAAGCGCGG
 401 GCATGTATTG TCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAAA
 451 AGCAGCGGCG TATCGTTGCG GCAGGTTTTG GTCAACCGCA GGGGTATTCC
 501 GTTGTCGGTC TGGTTTATGC TTTTATCTCT TCGGGCGGG CTGCTGTTG
 551 CCGCATCGAC AGACGGGTGT TCGTGGACGA AAGGTTTGGC GATGGCTTCC
 601 GGCTTCGGT GGTATCCCT CTGGGTTTG GTCATGACCG AGGCTTACGG
 651 CGCGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGGCA CGAGAGCTGT
 701 TTGCACTGGC ATTTATCCCG CTGCTGATGA AGCGTTTCC AGATGCGGCG
 751 GTGGGGGTTG GCGGTGCGAC CAGTATGGAT TTTACATTGC CCGTGATTCA
 801 GGGTGCGGG GGTGTGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
 851 TGGTCAATAT CGCCGCCCG TTTCTGATGG TGGTGTTTC CGCTTTGGGT
 901 TGA

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

m700.pep

1 MDSLMTLLSV LIPMFAGFFI RVKPYLPAL DKVLSVLVYA VLLIGVSL
 51 RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLPFW RIKGKKGVS
 101 VGVSGSVGQL GCVLLGFAFG KLMRDIWMPES ESAGMYCLML LVFLIGVQLK
 151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASTDGV SWTKGLAMAS
 201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPVIQGAG GLEVVPVAVS FGVVVNIAAP FLMVVFSA
 301 *

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with menB

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVVKPYLPALDKVLSVLVYAVLLIGVSLSRVEDLGSRLD					
g700	MSSLMTLFSVLVPMFAGFFIRVVKPYLPASDKVLSVLVYAVLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKKGKGVSVGVSGSVGQLGCVLLGFAFG					
g700	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKKGKGVSVGVSGSVRQLGCVLLGFAFG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGVSLRQVLNRRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASADGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
	190	200	210	220	230	240

q701.seq

1	ATGTCCTTGGC	ACATATTCCA	AGTTGCAGGG	ATACCGACCG	CTTCGATGGC
51	ACAATCTACG	CCGTCTTCGC	CGACGATGCG	GAAAACTTGT	TTGGAGACGT
101	CGCCGGAAGC	GGGGCTGATG	GATATGGGTGC	CGCCCAACTC	TTTCGCCGGT
151	TTCAAACGGT	TTTCGTCAT	ATCGCACACG	ATAAATGGCG	CAGGGCTATA
201	CAGTTGGGCG	GTCAACAAGG	CGGACATACC	GACAGGGCCG	GCACCTGCGA
251	TGAATACGGT	GTCACCGGGT	TTCATACCGC	CGTATTGCAC	GCCGATTTCG
301	TGGGCGGTGC	GTAAAGCGTC	GTCTCAACAG	AGGGCGATT	CTTCGTTGAC
351	TTGTGCTGTC	GGCGGCACGA	GGCTGTTGTC	GGCATAA	

q701.ppt

1 MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VVWAPNSFAG
51 FKRFSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISLTLSC GGTRLLSA*

m701.seq

1	ATGTCCTTGGC	ACATATTCCA	TGTAGCAGGG	ATACCGACGG	CTTCGATGGC
51	GCAATCCACG	CCGTCTTCGC	CGACGATGGC	AAAGACTTGT	TTGGATACTT
101	CGCCGGGAAG	AGGGCTTAATG	GTATGGGTGTC	CACCCAAATC	TTTCGCCGAT
151	TTCAAACGGT	TTTCGTTCAT	ATCGCAAAAC	ATGATGGCGG	CGGGGATGTA
201	CAGTTGGGGC	GTCAACAGGG	CGGACATAAC	GACAGGGCCT	GCCCCAGCGA
251	TGAATACGGT	GTCGCGGGT	TTGACATCGC	CGTATTGCAC	GCCGATTTCG
301	TGGGCGGTGC	GCAAAAGCGT	GCTCAACAAC	AGGGCGGATT	CTTCGTTGAC
351	ATTATCGGGC	AGCGGAACGA	GGCTGTTGTC	GGCATAA	

m701.pgp

1 MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSP EAGLM VVWAPNSFAS
51 FKRFSISQOT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISSLTLSG SGRLLSA*

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

m701/g701

```

              10      20      30      40      50      60
m701.pep      MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLOTSPEAGLMVWVAPNSFASFKRFSSIQT
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
q701          MSWHIFQVAGIPTASMAQSTPSSPTMAKTCLETSPEAGLMVWVAPNSFAGFKRFSSISHT

```

1127

```

1  MPCSKASWTS PGVATPGIRG MPLLRLPALAR DSCKPGLMAK TAPASSTALS
51  CSGLVTVFPAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

```

m702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAAC TG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

```

m702.pep
1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLM K TAPASSTALS
51  CSGLVTVFPAP TMLGTSLAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

```

m702/g702
m702.pep      10      20      30      40      50      60
MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTVFPAP
g702          10      20      30      40      50      60
MPCSKASWTS PGVATPGIRGMPLLRLPALARDSCKPGLMAKTAPASSTALSCSGLVTVFPAP

m702.pep      70      80      90      100     110     120
TMLGTSLAIRRMASRPTGVRVISRVGMPPSTRAWDKSM AVLKSSIAIT GTTAPAVKIS
g702          70      80      90      100     110     120
MMALGISLAIRRMASPTGVRKVISRVGMPPSTRARDKSTAVLKSSIAIT GTTAPAVRIS

m702.pep      130     140
RGVSLDISVL RVEWGILLRW DRLX
g702          130     140
RGVSLDISVL RVEWGILLRW DRLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

```

a702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAAC TG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

```

a702.pep
1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVFPAP TMLGTSLAI RRMASRPTGV RRVISRVGMP PSTPAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

```

10      20      30      40      50      60

```

1129

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GGCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTGGGC AAGGCAACA
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGVVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
 251 KVPFDEMKG QIAGNLQAEI IDRAVGALLG KANIKPAK*

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVNTVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVNTVVAQEVKRLKLDRAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
g703	EAYALHIKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGVVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGVVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNSREVKVPFDEMKGQIAGNLQAEI IDRAVGALLGKANIKPAKX					
g703	VYYVNSREVKVPFDEMKGQIAGNLQAEI IDRAVGALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

1 ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCCT GTTCCGGCAG
 51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
 101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
 151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACGAG AAGTGGTCAA
 201 CACCGTGGTC GCACAGGAAG TGAACGCTT GAAACTCGAC CGGTCGCGAG
 251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
 301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG
 351 CTTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
 401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
 451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
 501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAGGT TTCGATGCCG
 551 TCTTGAAACA ATATCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
 601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
 651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

1131

```

801 TGC GGGG CAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCCGCCGAGA GGCTGGTGAA GCTGATTCCCT GCGTTTTTGC ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCGTTGAC
1051 GGCACGGTGC TGGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTGCGCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGGCGGC
1201 GGCACGGCAC TGTGCGACAT CGTCCGCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAI
1301 TCGGCGAACT CCTGCTTGCC GTCCCGCTCT TCATCGGCTG GACGCTGTAC
1351 GCCGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCTGCG GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GCGCGCGGAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCTCGC CCCAAACCCAC CGACATCATC TTCGACAAAA CCGGCACGCT
1551 GACCCAAGGC AAACCCGCCG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCCTCGC GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCCTTG CCCGCGCCAT CCTCAACTGC CGCATTTCAG ACGGCAGCGT
1701 CCCCACATC GCTATTAAC AACGCCTCAA CCGCATCGGC GAAGCGTGG
1751 GCGCGCAACT GACCGTCAAC GCGGAAACAC AGGTTTGGGC ATTGGGCAGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAA GAACCGCAA CAGAAGCGCG
1851 CCGCAGCGCG GTTACCTCG GCAGTCAAAG CGGTTTCCAA GCCGTGTTCT
1901 ACCTGCAAGA CCGCTCAA GACAGCGCGG CGGAGGCGGT CCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGCGGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGACGCGC CCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCG CCGTTTGGC
2151 GCAGGCAGAC GTATCCGCCG CCGCAGCGG CGGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATGTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCAC
2251 CTGCTCGATC AGGCGCGCGC CACCCGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGAAAA TGCACTCTGA
2451 AAAAAAGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

a704.pep

```

1 MKKTCFHCGL DVPENLHLTV RYENEDRETCCAGCQAVAS IIDAGLGSYY
51 KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLIE QLLRTDGIV RIDLNYSTHR CRVWDDGKI RLSDILLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMQMFM FALPTYLYG
201 GDIEPDFLQI LHWGGFLMVL PVVFCVAVPF YQALRDLDN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGO GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAEAEQYAS SFIFGELLLA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLLARE GILIGGKQAI
501 ETLAQTDDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSSGFGQ AVFYLDPLK DSAAEAVRQL
651 AGKNLTLHL SGRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQNLIWAG AYNIIAVPLA VLGYPQFWIA ALGMSFSSLA
801 VLGNALRLHK RGKMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLGSYYKQRTADAQKT
          |||
a704      MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLGSYYKQRTADAQKT
          10      20      30      40      50      60

          70      80      90     100     110     120
m704.pep ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLLRTDGIV
          |||
a704      ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLLRTDGIV

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2357>:

g705.seq

1	GTGTTCAATA	ATTTCTcttgc	CTCTCTGCCG	TTTATGACGG	AAACACGGCG
51	TGATATGCTC	ATACAGCGGT	TTTGGCCCAT	GGTTAAAGCC	GGCTTTACAG
101	TGCTCTttgc	TTTGGGCATC	GCTTCTTTCT	TTATCGGCAT	GATTATTGCC
151	GTAGCCGGTT	CTTTGGTAAG	AATCATGCTT	TCCGGCGGTA	TTTTCCAAAA
201	ATGCTTGTGT	AAGCTGGTGG	AATTTTATAT	TTCCGTCGTT	CGCGGTACGC
251	CGCTGTGGT	TCAGCTTGTG	ATTGTGTTTT	ACGGGCTGCC	GTCCGTCGGC
301	ATCTATATCA	ATCCGATTC	CGCCGCCATC	ATCGGCTTTT	CGCTCAATGT
351	CGCGCATAC	GCTTCCGAAA	CCATACGGCG	GGCGATTTTG	TCCGTGCGGA
401	AAGGCGCAGT	GGAAGCAGGT	TTCTCCATCG	GTATGACCTA	TATGACGACG
451	TTCCGCGCGA	TCGTGCGACC	GCAGGCAATC	CGCGTCGCGC	TTCCGCGGTT
501	GAGCAACAGG	TTTATCGGCT	TGTTCAAAAA	CACCTCGCCT	CGCCGCGTGG
551	TAACGGTAA	AGAGCTTTTT	CTTGTCGCAC	AGGAAACGGC	AAACCGCATC
601	TATGACTTTT	TGCCTGTCTA	TATCGAAGCT	GCATTGGTTT	ATTGGTGTTT
651	CTGTAAAGCT	CTGTTTTTGA	TTCAGGCGCG	TTTGGAAAAA	CGTTTTCGACC
701	GTTATGTGCG	CAATAAA			

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

g705.pap

1	VFNFNFLASLP	FMTETRADML	ISAFWPMVKA	GFTVSLPLAI	ASFVIGMIIA
51	VAVALVRIMP	SGGIFQKCLL	KLVEFYISVV	RGTPLLVLQV	IVFYGLPSVG
101	IYINPIPAAI	IGFSLNMGAY	ASETIRAIL	SVPKGQWEAF	FSIGMTYMQT
151	FRRIVAPQAE	RVAVPPLNSE	FIGLFRKLEI	AAVVTVTEAF	RVAQETANRT
201	YDFLPVYIFA	ALUYVCFCKV	LFLLQARLEK	RFDRYVAK*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

```
m705.seq
1      GTGTTCA7TA ATTTCTTGC TTGCTGCCG TTTATGACGG AAACACGCGC
5      CGATATGATT GTACAGCGGT TTTTGCCAT GGTCAAAGCC GGC1TCGCGG
101    TCTCTCTGCC TTTGCGCGCA ATGCTCTTCG TTATCGGTAT GATGATTCGG
151    GTAGCCGTGG CTTTGGTGGC GATTATGCC CC1CGCGCGGA CTGTCGGGAA
201    AATCGTGCTG AAATTTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251    CGCTGTGGGT TCAGCTTGTG ATGTGGTTT AC1GGGGTGCC TTCCGTCGGC
301    ATCTATATCG ACCCGATTCC TTGCGGCATC ATCGGTTTCT GCGCTAATGT
351    CGGCGCATAC GCTTCCGAAA C1CATACGGC GGCAATTTTG TCCGTACCTA
401    AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451    TTCGCCCGCA TTGTGCGCGC CGAGGCATT CCGCGTTGCGG TCGCGCGCTT
501    GAGCAACAGG TTTATCGGTT TGTTTAAAAA CACCTCGCTC CGGGCAGCTG
551    TGACGGTAAC GGAATTATTC GTGTCGCGC AGGAAACGGC AAACCGCATC
601    TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGT1TT
651    TTGTAAGCTG CTGTTCCTGA TTCAGGCGCG TTTGGAAAAA CGTTTCGACC
701    GCTACGTCGC CAAATAAA
```

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

```
m705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRMP AGGVVRKILL KLVEFYISVI RGTPLLVLQV IVFYGLPSVG
101 IYIDPIPAI IGFSNLVGAY ASETIRAIL SVPKGQWEAG FSGTMYMQT
151 FRRIVAPQAF RVAVPPLSNE FIFGLFKNTSL AAVVTVTEL RVAQETANRT
201 YDFLPVYIEA ALVYVQSCFKV LFLIQAARLEK RFDRYVAKF
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

m705/g705 95.0% identity in 238 aa overlap

	10	20	30	40	50	60
m705.pep	VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMI	IAVAVALVRIMP				
g705	VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIAASFVIGMI	IAVAVALVRIMP				
	10	20	30	40	50	60
	70	80	90	100	110	120
m705.pep	AGGIVRKILLKLVEFYISVIRGTPLLVLQVIVFYGLPSVGIYIDPIPA	AIIGFSLNVGAY				
	10	20	30	40	50	60

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

```
g706.seq
1  ATGAAGCTCCT CGCAACGCAA ACGCCTTTCC GgcccGCTGGC TCAACTCCTA
51  CGAAGCGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCggaa
101 ccgtCCTGTT CGCCACCGCA CTCGCCGgc tACTCCACCT CCAacacggc
151 gAATGGATAG GGAtgaCCGT CTTGTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGCgcgatt tActccaacg cggtgGAacg taTGctcggg acggtcatcg
251 ggctgGGCGC GGGTTTGGgc gTTTATGGC TGAACCAGCA TTAttttccac
301 ggcaaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
351 ctGGGCGGCG GTCGGCAAAA acggctacgt ccctatgctg GCGGGGctga
401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGCGCGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AACTCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCGCCCT CATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCCTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCTAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

```
g706.pep
1  MNSSQRKRLS GRWLSYERY RHRLIHAVR LGGTVLFATA LARLLHLQHG
51  EWIGMTVFVV LGMLQFQGA IYNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM AGLTMCMLIG DNGSEWLD SG
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLAD SKMIAEISNG
201 RMTRELERLEQ NMVKMRQINA RMVKSRSILA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTAAALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE ROHLRQSLLE TREHG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

```
m706.seq
1  ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51  CGAAGCGTAC CGTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCTGTT CGCCACCGCC TCGCCCGGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CGGTGGAACG TATGCTCGGC ACGGTCATCG
251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACCAGCA TTATTTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCCGCAAAA ACGGCTACGT CCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC CGCGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CGGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCAAGCT
801 GCAATCTCCC AACTCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCCTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

```
m706.pep
1  MNSSQRNRLV SRWLSYERY RYRRLIHAVR LGGAFLFATA SARLLHLQHG
51  EWIGMTVFVV LGMLQFQGA IYKAVVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM AGLTMCMLIG DNGSEWLD SG
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLAD SKMIAEISNG
201 RMTRELERLEE NMAKMRQINA RMVKSRSILA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTVALING
```


1137

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901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACAGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
1  MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51  EWIGMTVFVV LGMLQFQGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTVG TASALAGWAA VGKNGYVPML AGLTMCMLIG DNGSEWFDSD
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLTDC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSRLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHS*

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a706/m706 99.5% identity in 374 aa overlap

a706.pep	10	20	30	40	50	60
	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG					
m706	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG					
a706.pep	70	80	90	100	110	120
	LGMLQFQGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG					
m706	LGMLQFQGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG					
a706.pep	130	140	150	160	170	180
	VGKNGYVPMLAGLTMCMLIGDNGSEWFDSDGLMRAMNVLIGAAIAIAAAKLL					
m706	VGKNGYVPMLAGLTMCMLIGDNGSEWLDGLMRAMNVLIGAAIAIAAAKLL					
a706.pep	190	200	210	220	230	240
	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSRLA					
m706	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSRLA					
a706.pep	250	260	270	280	290	300
	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD					
m706	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD					
a706.pep	310	320	330	340	350	360
	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQR					
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQR					
a706.pep	370					
	RQHLRQSLLETREHSX					
m706	RQHLRQSLLETREHGX					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

1139

```

751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTG AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTCC CGGATTTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGCGAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTGCGCGGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
1  XKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
51  KLRVSAGEIG DIRYEEKRDX KSAEGSISAF NNXKPLYRNK ILNLRDVEQG
101 LENLRLPSV KTDIPIIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ YQSSLAERM
251 LWXXFXXTS VXMKLWTRQT KYIDDAEIE VQRRRSAGWE AELRHAYLX
301 RWQLDGKLSY KRGTGMRQSM PAPEENGSGT IPXXSRMKII TAGLDAAPX
351 MLGKQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

a707/m707 95.3% identity in 486 aa overlap

a707.pep				10	20	30
				XKETAFKTMCLGSNNLSRLQKAAQQILIVR		
m707	EDET	PCTRVNYISLDDKT	VRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIVR			
	50	60	70	80	90	100
a707.pep		40	50	60	70	80
		GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEEKRDXKSAEGSISAFNNKXPLYRNKI				
m707		GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEEKRDGKSAEGSISAFNNKXPLYRNKI				
		110	120	130	140	150
a707.pep		100	110	120	130	140
		LNLRDVEQGLLENLRLPSVKTDIPIIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT				
m707		LNLRDVEQGLLENLRLPSVKTDIPIIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT				
		170	180	190	200	210
a707.pep		160	170	180	190	200
		GKYQGNVALSXDNPGLGLSDXFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK				
m707		GKYQGNVALSFDNPLGLSDFYVSYGRGLAHKTDLTATGTETESGSRYSVHYSVPVKK				
		230	240	250	260	270
a707.pep		220	230	240	250	260
		WLFNFHNGHRYHEATEGYSVNYDYNKGQYQSSLAERMLWXXFXXTSVXMKLWTRQTY				
m707		WLFNFHNGHRYHEATEGYSVNYDYNKGQYQSSLAERMLWRNRLHKTSGVMKLTWTRQTY				
		290	300	310	320	330
a707.pep		280	290	300	310	320
		KYIDDAEIEVQRRRSAGWEAELRHAYLXRWQLDGKLSYKRGTGMRQSMPEPEENGSGTII				
m707		KYIDDAEIEVQRRRSAGWEAELRHAYLNRWQLDGKLSYKRGTGMRQSMPEPEENGSGDIL				
		350	360	370	380	390
						400

1141

```

      1 MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
     51 DYRQATASIE DALKSDPKNE LAWLVR...Y QYLVNDKAO ESFRQALSIK
    101 PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
    151 SAKQGQFGLA EAYLKRSLAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
    201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
    251 TGQ*

m708/g708 99.2% identity in 253 aa overlap

      10      20      30      40      50      60
m708.pep MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
g708      MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
      10      20      30      40      50      60

      70      80      90     100     110     120
m708.pep DALKSDPKNELAWLVRAEIYQYLVNDKAOESFRQALSIKPDSAEINNNYGWFLCGRLNR
g708      DALKSNPKNELAWLVRAEIYQYLVNDKAOESFRQALSIKPDSAEINNNYGWFLCGRLNR
      70      80      90     100     110     120

      130     140     150     160     170     180
m708.pep PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLAAQPQFPFAFKE
g708      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLAAQPQFPFAFKE
      130     140     150     160     170     180

      190     200     210     220     230     240
m708.pep LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNAQAAYEYEAQLQANF
g708      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNVQAAYEYEAQLQANF
      190     200     210     220     230     240

      250
m708.pep PYSEELQTVLTGQX
g708      PYSEELQTVLTGQX
      250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
      1 ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCCTT
     51 GGGCGCGTGC AGCACTTCCT ACCGCCCCCTC GCGGGCAGAA AAAGCCAATC
    101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
    151 GACTACCGTC AGNGACGGC AGTATTGAA GACGCCTGA AATCAGACCC
    201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
    251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAA
    301 CCCGACAGTG CCGAAATCAA CAACACTAC NGCTGGTTCC TGTGCGGCAG
    351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
    401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
    451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTT
    501 CCTCGCCGCC CAGCCGCACT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
    551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
    601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTGTC TGCTAGGCTG
    651 GAAAAATTGCC AAAGCCCTCG GCAACGCACA GCGGCATAC GAATATGAAG
    701 CACAATTGCA GGCGAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
    751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
      1 MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
     51 DYRQXTASIE DALKSDPKNE LAWLVR...Y QYLVNDKAO ESFRQXLSIK
    101 PDSAEINNNY XWFLCGRLNR PAESMAYFDK ALADPTYXPX YIANLNKGIC
    151 SAKQGQFGLA EAYLKRSLAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
    201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
    251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1143

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
 1 ATGTTTCGCTT TCAAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
 51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTTCATTGG
 101 AGTGGTTGCC GCATATGTCC ATTTATGCCG CCATCGTCGT GCTGATTTTG
 151 TACGGCTTGG CCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
 201 AGGCGCGTTG AATCAGGGA TGGCGCGGAT TTACCTGTTT TTCTTCATCG
 251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
 301 TATTACGGTT TCGGACTGAT TTCCCGGACT TATTTTATT TTTCTCCTT
 351 CCGCTGTGT TCCGTCATCG GCGTGTCCAT CCGCAGCAGC CTGACCACTT
 401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGCGGCG GTTTCAGGCC
 451 GATATGGCGA TGACGGCGGG CCGGATTGTT TCGGCGCAT TTTTGGCGA
 501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCCGCG TCCATCGTCG
 551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
 601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTCCG
 651 CCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
 701 CCGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCCTT GTTGGTCATT
 751 TTGGCATTGA TGCGCATCAA CGCCGTCGTC GCCATGCTCT TACCGTCAT
 801 GGTGTCCGTT GCTGTAACGT ATCTGCACAG CACGCCGAT CTGCGTCAGC
 851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA
 901 GATGTTGTCA AACTGATTTT CCGCGCGGCT TTGGAAGTA TGTTTTTCAC
 951 GCAAAACATC GTGATTCTCG GGATGATTTT GGGCGGACTG TTGTTTGGCG
 1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT
 1051 GCCCGACGCG CGACGTTTCA CGTTGCCATG ACTTCGTCG GGGTTAATTT
 1101 CCGTATCGGC GAGCAATATT TGAGTATTTT GTTGTGCGGT GAAACGTTC
 1151 AACCCGTTTA CGATAAGCTC GGTCTGCATT CCGCAATCT GTCGCGGACG
 1201 CTGGAAGATG CCGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG
 1251 CGCGGTGTTT ATCAGCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
 1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCTT GTTATTGGGT
 1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
 1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
 51 YGLARGLKYN DMQQGMIGAL NQMGAIYLF FFIGLMVSAL MMSGAIPTLM
 101 YYGFGILISPT YFYFSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAFOA
 151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFEH IKNMYYTTIP
 201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
 251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
 301 DVVKLISRGG LESMFFTQTI VILGMSLGL LFALGVIPSL LEAIRFTLTN
 351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVV	ALIAAMGYTI	ISLEWLPHMS	IIAAIVVLIL	YGLARGLKYN	
g709	MFAFKSLDDMPRGEALAVVV	ALIAAMGYTI	ISLEWLPHMS	IIAAIVVLIL	YGLARGLKYN	
	10	20	30	40	50	60
m709.pep	DMQQGMIGALNQMGAIYLF	FFIGLMVSAL	MMSGAIPTLM	YYGFGILISPT	YFYFSSFALC	
g709	DMQAGMIGALNQMGAVYLF	FFIGLMVSAL	MMSGAIPTLM	YYGFGILISPT	YFYFSAFALC	
	70	80	90	100	110	120
m709.pep	SVIGVSIGSSLTTCATVGVA	FMGMAAFOA	DMAMTAGAIV	SGAFFGDKMS	PLSDTTGISA	
g709	SVIGVSIGSSLTACATVGVA	FMGMAAFOA	DMAMTAGAIV	SGVFFGDKMS	PLSDTTGISA	
	130	140	150	160	170	180
m709.pep	SIVGIDLFEHIKNMYYTTIP	AWLISAALML	WLLPNVAAQD	LNSVESFRSQ	LEATGLVHGY	
g709	SIVGIDLFEHIKNMYYTTIP	AWLISAALML	WLLPSVAAQD	LNSVESFRSQ	LEATGLVHGY	
	190	200	210	220	230	240

1145

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
451 WTGLTSLSKK*

a709/m709 91.1% identity in 459 aa overlap

	10	20	30	40	50	60
a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTII	XLEWLPHMSIIAAIVVLILYGLARGLKYN				
m709	MFAFKSLDMPRGEALAVVVALIAAMGYTII	SLEWLPHMSIIAAIVVLILYGLARGLKYN				
	10	20	30	40	50	60
a709.pep	DMQQGMIGALNQGMGAIYLF	FFIGLMVSALMMSGAIP	TLMYYGFLISPTYFYFS	AFALC		
m709	DMQQGMIGALNQGMGAIYLF	FFIGLMVSALMMSGAIP	TLMYYGFLISPTYFYFSS	FALC		
	70	80	90	100	110	120
a709.pep	SVIGVSIGSSLTTCATVGVA	MXXXXAFXAXMXXXXXIVXXAXXGXKMSPLSDTXGXSA				
m709	SVIGVSIGSSLTTCATVGVA	FMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA				
	130	140	150	160	170	180
a709.pep	SIVGIDLFEHIKNMMYTTIPAWLISXXLMLXLLPSVAAQDLNSVESFRSQLEATGLVHCY					
m709	SIVGIDLFEHIKNMMYTTIPAWLISAAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
a709.pep	SLIPFALLVVLALMRVNAVAMLF	TVMVAVVAVTYLHSTPDLRQLGAWFYGGYKLEGEAXX				
m709	SLIPFALLVILALMRINAVAMLF	TVMVAVVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK				
	250	260	270	280	290	300
a709.pep	DIAKLISRGGLESMTFTQ	TIVILGMSLGGLLFALGAIPSLDAVRSFLT	NAGRXTFSVAM			
m709	DVVKLISRGGLESMTFTQ	TIVILGMSLGGLLFALGVIPSLLEAIRFTLN	AGRATFSVAM			
	310	320	330	340	350	360
a709.pep	TSVGVNFLIGEYQYLSI	LLSGSETFKPVYDKLGLHSRNL	SRTLEDAGTVINPLVPWSVCGVF			
m709	TSVGVNFLIGEYQYLSI	LLSGSETFKPVYDKLGLHSRNL	SRTLEDAGTVINPLVPWSVCGVF			
	370	380	390	400	410	420
a709.pep	IXHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLSKKX					
m709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLSKKX					
	430	440	450	460		

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq

1	ATGGAAACCC	ACGAAAAAAT	CCGCCTGATG	CGCGAATTGA	ATAAATGGTC
51	CCAGGAGGAT	ATGGCGGAAA	AGCTGGCGAT	GTCCGCAGGC	GGGTATGCCA
101	AAATCGAACG	GGGCGAAACG	CAGTTAAATA	TCCGCGGTTT	GGAGCAGTTG
151	GCTCAGATTT	TCAAAATCGA	TATGTGGGAC	TTGCTCAAA	CGGGCGGTGG
201	TGGGATGGTG	TTTCAGATTA	ATGAAGGTGA	TAGTGGTGGC	GATATTGCGT
251	TGTATGCGTC	GGGTGATGTT	TCGATGAAAA	TAGAATTTTT	AAAAATGGAG

1147

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
1  ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAGTA AAAAGGTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTGCCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTAGA CAAGTACGAC CGTGCCTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACAGC TTTAAACCTA
851 TTGAAAAACA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAA CTGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKD IID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYDYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRDLIDGK
301 PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
1  ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAGTA AAAAGGTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTGCCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTAGA CAAGTACGAC CGTGCCTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
```

a711.pep	AKFMAKKKVLKX
m711	AKFMAKKKVLKX
	430

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```

m713.seq
1  ATGCAAAATA  ATTCATACGG  CTATGCCGTG  TCGGTGCGCG  TGGGCGGTAA
51  AGAGCACC GC  CACTGGGAGC  GCTACGACAT  CGACAGCGAC  TTTTAAATCC
101 CTGCCGACAG  CTTCGATTTT  GTCATCGGCA  GGTGGGGACC  GGAGGCGGCC
151 ATACCCGATT  TAAGCGGAGA  GAGCTGCGAG  GTAGTGATAG  ACGGGCAAAT
201 CGTGATGACG  GGCATCATCG  GCAGCCAGCG  CCACGGCAAA  AGCAAGGGCA
251 GCCGCGAGTT  GAGCTTGAGC  GGGCGTGATT  TGGCCGGTTT  TTTGGTGGAT
301 TGCTCCGCGC  CGCAGCTCAA  TGTAAAGGGC  ATGACGGTAT  TGGATGCAGC
351 CAAAAAGCTG  GCCGCGCCGT  GGCCGCAGAT  TAAAGCGGTG  GTGCTTAAGG
401 CCGAAAACAA  CCCCCTTTG  GGCAAAATCG  ACATCGAGCC  GGGCGAAACC
451 GTATGGCAGG  CATTAACCCA  TATTGCCAAC  TCGGTCGGGC  TGCATCCGTG
501 GCTGGAGCCG  GACGGCACGT  TGGTGGTGGG  CGGTGCGGAT  TACAGCAGCC
551 CGCCGGTGGC  GACATTGTGT  TGGAGCCGCA  CCGACAGCCG  CTGCAATATC
601 GAGCGCATGG  ACATTGAGTG  GGATACCGAC  AACCCTTTT  CTGAGGTTAC
651 TTTTTTGGCG  CAATCGCACG  GCCGCAGCGG  CGACAGCGCC  AAACACGATT
701 TAAAGTGGGT  GTACAAAGAC  CCGACGATGA  CGCTGCACCG  CCTAAAACG
751 GTGGTGGTGT  CCGATGCCGA  CAATTGGGCC  GCATTGCAAA  AGCAGGCTAA
801 AAAGCAGCTG  GCCACTGGC  GGCTGGAGGG  ATTTTCTC  ACGATAACCG
851 TGGGCGGCCA  TAAACCCGC  GACGGCGTAT  TGTGGCAACC  TGGCCTGCGT
901 GTGCATGTGA  TCGACGACGA  GCACGGTATC  GATGCGGTGT  TTTTCTGAT
951 GGGGCGGCGG  TTTATGCTAT  CCGCATGGA  TGGTACGCAA  ACCGAGCTGC
1001 GGCTCAAAGA  GGACGGTATT  TGGACACCCG  ACGCTTACCC  CAAAAGGCC
1051 GAGGCGGCGC  GCAAGCGCAA  AGGCAAACGC  AAAGCGTGA  GCCATAAGGG
1101 CAAAAAGGC  GGCAAAAAC  AAGCAGAAAC  GCGGTGTTT  GAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```

m713.pep
1  MQNNSYGYAV  SVRVGKKEHR  HWERYDIDSD  FLIPADSFDF  VIGRLGPEAA
51  IPDLSGESCE  VVIDGQIVMT  GIIGSQRHGK  SKGSRELSLS  GRDLAGFLVD
101 CSAPQLNVKG  MTVLDAAKKL  AAPWPQIKAV  VLKAENNPAL  GKIDIEPGET
151 VWQALTHIAN  SVGLHPWLEP  DGTLVVGGAD  YSSPPVATLC  WSRTDSRCNI
201 ERMIDIEWDTD  NRFSEVTFLA  QSHGRSGDSA  KHDLEWVYKD  PTMTLHRPKT
251 VVVSADANLA  ALQKQAKKQL  ADWRLEGFTL  TITVGGHKTR  DGVWLQPGLR
301 VHVIDDEHGI  DAVFFLMGRR  FMLSMDGTQ  TELRLKEDGI  WTPDAYPKKA
351 EAARKRKGR  KGVSHKGGK  GKQQAETAVF  E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```

a713.seq
1  ATGCAAAATA  ATTCATACGG  CTATGCCGTG  TCGGTGCGCG  TGGGCGGTAA
51  AGAGCACC GC  CACTGGGAGC  GCTACGACAT  CGACAGCGAC  TTTTAAATCC
101 CTGCCGACAG  CTTCGATTTT  GTCATCGGCA  GGTGGGGACC  GGAGGCGGCC
151 ATACCCGATT  TAAGCGGAGA  GAGCTGCGAG  GTAGTGATAG  ACGGGCAAAT
201 CGTGATGACG  GGCATCATCG  GCAGCCAGCG  CCACGGCAAA  AGCAAGGGCG
251 GCCGCGAGTT  GAGCTTGAGC  GGGCGTGATT  TGGCCGGTTT  TTTGGTGGAT
301 TGCTCCGCGC  CGCAGCTCAA  TGTAAAGGGC  ATGACGGTAT  TGGATGCAGC
351 CAAAAAGCTG  GCCGCGCCGT  GGCCGCAGAT  TAAAGCGGTG  GTGCTTAAGG
401 TCGAAAACAA  CCCCCTTTG  GACAAAATCG  ACATCGAGCC  GGGCGAAACC
451 GTATGGCAGG  CATTAACCCA  TATTGCCAAC  TCGGTCGGGC  TGCATCCGTG
501 GCTGGAGCCG  GACGGCACGT  TGGTGGTGGG  CGGTGTGGAT  TACAGCAGCC
551 CGCCGGTGGC  GACATTGTGT  TGGAGCCGCA  CCGACAGCCG  CCGCAATATC
601 GAGCGCATGG  ACATTGAGTG  GGATACCGAC  AACCCTTTT  CTGAGGTTAC
651 TTTTTTGGCG  CAATCGCACG  GCCGCAGCGG  CGACAGCGCC  AAACACGATT
701 TAAAGTGGGT  GTACAAAGAC  CCGACGATGA  CGCTGCACCG  CCTAAAACG
751 GTGGTGGTGT  CCGATGCCGA  CAATTGGGCC  GCATTGCAAA  AGCAGGCTAA
801 AAAGCAGCTG  GCCACTGGC  GGCTGGAGGG  ATTTTACTC  ACGATAACCG
851 TGGGCGGCCA  TAAACCCGC  GACGGCGTAT  TGTGGCAACC  TGGCCAGCGT
901 GTGCATGTGA  TCGACGACGA  GCACGGTATC  GATGCGGTGT  TTTTCTGAT
951 GGGGCGGCGG  TTTATGCTAT  CTCGCATGGA  TGGCAGCAA  ACCGAGCTGC
1001 GGCTCAAAGA  GGACGGTATT  TGGACACCCG  ACGCTTACCC  CAAAAGGCC
1051 GAGGCGGCGC  GCAAGCGCAA  AGGCAAACGC  AAAGCGTGA  GCCATAAGGG

```


1153

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```

m714.seq
  1  ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
 51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101  TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151  CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201  CGGTACGGGC AAAAACC GCCGCGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
251  TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301  GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351  TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401  GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451  GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501  CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551  CCTACCGCTA A

```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```

m714.pep
  1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVADAVDP
 51  RSAGQMLADW ERVLGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
101  AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151  GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```

a714.seq
  1  ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
 51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101  TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151  AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201  CGGTACGGGC AAAAACC GCCGCGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
251  TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301  GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351  TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401  GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451  GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501  CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551  CCTACCGATA A

```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```

a714.pep
  1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVADAVDP
 51  SSAGQMLADW ERVLGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
101  AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151  GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVADAVDPRSAGQMLADW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
	:					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a714.pep	AGDRLAPQEI MWVWHVNVRG GNNRITRFRAGISAAGDRLT DYSDAVIESL FNRLKPAHTA					

1155

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

```
m716.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

```
m716.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----				
g716	MNKNIAAALAGALSLSLAAGAVPAHKPASNATGVOKSAQGSAGGSCGASKSAEGSCGASKSAEG				
	10	20	30	40	50
	60	70	80	90	100
m716.pep	----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX				
g716	SCGAASKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

```
a716.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

```
a716.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

```
g717.seq
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

```

m717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDOA YVREYYATAD KDTLFTLFL PPLLSAAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLMEGRAL AFSSAQLVPK
151 LAILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 HAPFSPAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LQSFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
351 RKTRPIALAT LGALAANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAYLAG
451 CILHRKDLH KLFHYLKKQG FPL*

m717/g717 96.4% identity in 473 aa overlap

      10      20      30      40      50      60
m717.pep MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
g717      MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
      10      20      30      40      50      60
      70      80      90     100     110     120
m717.pep YVREYYATADKDTLFTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE
g717      YVREYYAAADKDTLFTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE
      70      80      90     100     110     120
      130     140     150     160     170     180
m717.pep LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLPLTVGLLHFPANTAVLTAVYALA
g717      LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLPLTVGLLHFPANTSVLTVYALA
      130     140     150     160     170     180
      190     200     210     220     230     240
m717.pep NLAAAFLLFQNRCRLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY
g717      NLAAAFLLFQNRCRLKAVRRAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY
      190     200     210     220     230     240
      250     260     270     280     290     300
m717.pep AGLEQLGVYSMGISFGGAALLQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
g717      AGLEQLGVYSMGISFGGAALLQSFSTVWTPYIFRAIEENATPARLSATAESAAALLAS
      250     260     270     280     290     300
      310     320     330     340     350     360
m717.pep ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
g717      ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFYTLTEISGIGLNVVRKTRPIALAT
      310     320     330     340     350     360
      370     380     390     400     410     420
m717.pep LGALAANLLLGLAVPSGGARGAAVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF
g717      LGALAANLLLGLAVPSGGTRGAAVACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF
      370     380     390     400     410     420
      430     440     450     460     470
m717.pep CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCILHRKDLHKLHLYLKKQGFPLX
g717      CLASSAAYTCFGTPANYPLFAGVWAAYLAGCILHRKDLHKLHLYLKKQGFPLX
      430     440     450     460     470

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

```

a717.seq
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGCGCGG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTTCAAAAC CCTGTTCTCG CCGCCGCTGC

```

```

|||||
m717      AGLEQLGVYSMGISFGGAALLFQSI FSTVWTPYIFRAIEENAPPARLSATAESAAALLS
           250      260      270      280      290      300

           310      320      330      340      350      360
a717.pep  ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLVEISGIGLNVVKRTRPIALAT
           |||||||
m717      ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAEISGIGLNVVKRTRPIALAT
           310      320      330      340      350      360

           370      380      390      400      410      420
a717.pep  LGALAANLLLGLAVPSGGARGA AVACAASFVLFVFKTESSCRLWQPLKRLPLYMHTLF
           |||||||
m717      LGALAANLLLGLAVPSGGARGA AVACAASFVLFVFKTESSCRLWQPLKRLPLYLHTLF
           370      380      390      400      410      420

           430      440      450      460      470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKLHFHYLKKQGFP LX
           ||:|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCI LHRKDLHKLHFHYLKKQGFP LX
           430      440      450      460      470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1      TCAGACGGCC TTTACGTACC CCGAACTTT ATCCACCGCC CGCAAAGCTG
51     GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101    CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTC TACCCAAAAA
151    TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA CGCTTTCCTG
201    GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTGTGG
251    AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301    AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351    CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401    CAAACGGTAC GACGGCAACC AGCAATCCGT TTTGCGAGT GGCCGACTGG
451    TGCGAAAAAT CGGCGCGCGC GCTGATTTG GGGCAAACGC TGACCGCGG
501    TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551    TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601    ACAAGCCAAA TCATCGGACC GTTCCTGCAA ATCAACTATC CCCATGCCGA
651    CCCAAACCGC GTGCCGAAAT TTGAATTTGA CACGCGCGAG CCGAAAGACA
701    TCGCGGTCTT TGCCGACGCT ATCCGAAAC TGGTGGATGT CGGCGTACAA
751    ATCCCCGAAA GCTGGGTGCG CGACAACTG GTCAATCCAG ATGTGCAGGA
801    GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAACAGAA
851    CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901    AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGTTGAGCC
951    CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001   TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051   TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101   GTTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1      SDGLYVPRNF IHRPQSWFKW DKDNGLLLR TRENPEGEALW PLGWVVTQK
51     SRSVQQARNG LFRTLWSLYM FKHYAVHDEA EFLELYGMPI RIGKYGAGAT
101    KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLOMADW
151    CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRRDLLV SDAKQVAQTI
201    TSQIIGPFLLQ INYPHADPNR VPKFEFDTRE PKDIAVFADA IPKLVDVGQV
251    IPESWVRDKL VIPDVQEGEA VLVQRVPDNP VNRTALAALS AHTVPSKATG
301    RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAAALNACNSY EEADAALNAL
351    YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLO					
m718	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLO					
	160	170	180	190	200	210
a718.pep	360	370	380	390	400	410
	INYPHADPNRVPKFEFDTREPKDIAVFADAIPKLVVDVGVIPESWVRDKLVIPDVQEGEA					
m718	INYPHADPNRVPKFEFDTREPKDIAVFADAIPKLVVDVGVIPESWVRDKLVIPDVQEGEA					
	220	230	240	250	260	270
a718.pep	420	430	440	450	460	470
	VLVRQVPDPNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	VLVRQVPDPNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
	280	290	300	310	320	330
a718.pep	480	490	500	510	520	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	340	350	360	370	380	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATGCGGGCC
151 CTCCTCGAGG ACGCAGAAAG CGGCGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGCG GCGTGGTGGC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTGAT GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAACTTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
601 CAGCAGCGCG GCAACGGGCT TTTCCGCACG CTTTCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCCTG TTCGAGCGGT GCGCGAAATC GGTCAACAAC CGGCAGGCAT
801 CAGCCAGAAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CCGCAACCAAG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAATCG
901 CGCGCGCGCG TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCAAC AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTG GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCT GCGTACAAAT CCCCGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGTGTGCG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCGA GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAAGCCC ATTTCAATTG
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACCGCA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPOKMRA
51  LFEDAESGDI RAQHELFADI EERDSIAAN MGTRKRALLT LNWVRVAPPRN
101 ATPEEKLSLD QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFSDDL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNRP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLLRAVAEI GHNAAGIMPE GMEIELHNAA NGTTATSNPF LQMAADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

```

1163

a718.pep	190	200	210	220	230	240
	EGEALWPLGWVVHTQKSRSVQQARNGLFRTLWSWLYMFKHYAVHDFAEFLYGMPIRIGK					
m718-1	EGEALWPLGWVVHTQKSRSVQQARNGLFRTLWSWLYMFKHYAVHDFAEFLYGMPIRIGK					
	190	200	210	220	230	240
a718.pep	250	260	270	280	290	300
	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQADWCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQADWCEKS					
	250	260	270	280	290	300
a718.pep	310	320	330	340	350	360
	AARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKOVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKOVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
a718.pep	370	380	390	400	410	420
	HADPNRPVKFEFDTREPKDIAVFADAI PKLVDVGVIQIPESWVRDKLVI PDVQEGEAVLVR					
m718-1	HADPNRPVKFEFDTREPKDIAVFADAI PKLVDVGVIQIPESWVRDKLVI PDVQEGEAVLVR					
	370	380	390	400	410	420
a718.pep	430	440	450	460	470	480
	QVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAAL					
m718-1	QVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAAL					
	430	440	450	460	470	480
a718.pep	490	500	510	520		
	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

```

1  ATGGCAAACG GGAACATGAA ACTGTCGTTG GTGTTAACCG CCGAGATGA
51  CGGAGCGAGA CGGCTACTGG CTGATACTCA ACGACAATTA GATCGTACCG
101 CGAAATCGCG GCGCAACTT GAACGGCAA GCCATACTTA TCGGTTGACC
151 GGCATCCGCT CAGAAAAACA GATTCAACGC GAAATCATGC TGACACAGGC
201 TCGGTTTAAC CGTTTGGCGC GCAGCGGCAA GGCATCACA AATGATTGG
251 CACGGGCGGC GGTCGCTACG CGTAACCGAA TTCGCGAGCT GAACGCGGAA
301 CTGAAACAGG GCACGGGATT TCGGACAAAG ATGGGAAAAA TCGGAAGATT
351 CGGTGCAGCT GCGGTGGCTG GTGGCGCGGC AGCGTATACG GTGCTTAAGC
401 CTGCTATGGA CAACAGAAAG CAGCTTGATG AGAACATCAA CCGCGTGTCC
451 AGACAGGCAT TTATTGAGGA TAACAGTAAA TCGGCAGCGT GGATTGCAAC
501 TGAAGGTGCG CAACAGATCA AGGATTGGC ACTTGAACCT GTCGAGAAAA
551 ATGGCGGGAC CCACGATAAG GCTTGGATT TAATCAGCGG CATGATGACC
601 ACCGGTCTGA ATTTTGCCCA AACCAAGAAT GAAGCGCAGG CCGCATATGC
651 TTTTGCACCT GCCTCAGAAG GCAGTGGCGA GGATACGGCA AACTGATTA
701 AAACCTGAA AGATGGCGGC ATGAGCGGTA AAGACCTGCA ACTCGGGCTT
751 GAGCACGTCT TGCAATCGGG TTTAGACGGC ACTTTCGAGG TCGGGGATAT
801 GGTTCGGGAG CTGCCGAGCC TGCTCTCTGC CGCGCAACAG GCAGGGATGA
851 ATGGTGTGCG CGGTTTGAC TACCTGCTCT CACTCTTACA ATCTGCGGCG
901 AATAAATCGG GCAGTCTCTG CGAAGCGGCG ACTAATGTGC AAAATCTTTT
951 GAGTAAACT CTGTCGCCTG ACACGATAGG TCGTCTGAAG AAGATGGCAA
1001 ATCCGAATGA CCCGAAGAAA GGTGTCGATT GGATAGGCTC GGTGTGCAA
1051 GGCAAGCAA ACGGCGAAAA CGCAGTGAG GTGTTGTCCC GTCTTGCCGA
1101 TGCCATGCTA GTAAAGGATA AGCAATACCA AGATTATAAG AAACGCGCGG
1151 CTCGAGCGA TAAGACGCGC GCGGAGCAGG CAAATATGCT TAAGGGCGCG
1201 CTTTGGCGC AACTGCTGCC TGATTGTCAG GCAAAACAAG GTTTGCTGGC
1251 TGCAACGGAT ATGACGCAA TCCGTGAATA TATGGCTTCG TTGGCTGGCG

```

1165

```

851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CGGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTCGGTGGC AACGGCATT ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTGA TTGAGGTTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TCCAGACGGC TGCTGCCGAG
1051 TCTGGTGGG TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGCGG CAGGCCGTCT GAATGCGTTG GTTGGCGCGG
1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTAC GCGCATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
1  MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHAKPFVQ GIDLEDMGMT
51  GRQVQINAVF WKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AAEAEIIFVF ENAFLELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAAAVADRA AAIPDNLLTG RFSDDLQNR LRLTAKQVQ VQAVRLLST
301 SLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGGLTANAVY TEAYQTAE SLAAAGRLNAL VAAVINQKP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
1  GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
51  AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTTGATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCIT
201 ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGGCA
301 GGCCGTCTGA ATGCGTTGGT TCGGCGGGTC ATCAACCAAA AGCCGCCGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGCG GCTCAATCCC
451 CATATCCACC ACCCCGCGTT TATCAAGCGC GGCACTTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
1  GLQNRLNRLT AKQVQPVQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51  EVNRRMRRLM QAEIAALRAV QTAAESGGL TANAVYTEAY QTAE SLRAAA
101 GRLNALVA AVINQKPLIVR QAPIDGTI HQIAHEFYGDIA RAE LVRLNP
151 HHHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

                250      260      270      280      290      300
m720.pep      SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNRLNRLTAKQVQPVQAVRLLSTSSLL
                ||||||||||||||||||||||||||||||||||
a720           GLQNRLNRLTAKQVQPVQAVRLLSTSSLL
                10      20      30

                310      320      330      340      350      360
m720.pep      SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a720           SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
                40      50      60      70      80      90

                370      380      390      400      410      420
m720.pep      QTAE SLRAAAAGRLNALVA AVINQKPLIVRQAPIDGTI HQIAHEFYGDIA RAE LVRLNP
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a720           QTAE SLRAAAAGRLNALVA AVINQKPLIVRQAPIDGTI HQIAHEFYGDIA RAE LVRLNP
                100     110     120     130     140     150

                430      440
m720.pep      HHHHPAFIKRGTLVNSYAKX

```

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

```

a721.pep
  1  MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
 51  NGHDVALLAN SSRNQLVVVDY EH*TLYKEKN GQPAPAGWM RWLEFTPCKGM
101  FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151  MDEVLAASA QILKPETEON PMKELLQQLF GLPDAGEEEL KAALSALVEA
201  KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251  AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301  ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351  EGK*

```

a721/m721 99.2% identity in 353 aa overlap

a721.pep	10	20	30	40	50	60
	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
m721	10	20	30	40	50	60
	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
a721.pep	70	80	90	100	110	120
	SSRNQLVVVDYEHXTLYKEKNGQPAPAGWMRWLEFTPCKGMFAEVEWTDKAAAAIAAKEYR					
m721	70	80	90	100	110	120
	SSRNQLVVVDYEHQTLYKEKNGQPAPAGWMRWLEFTPCKGMFAEVEWTDKAAAAIAAKEYR					
a721.pep	130	140	150	160	170	180
	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
m721	130	140	150	160	170	180
	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
a721.pep	190	200	210	220	230	240
	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	190	200	210	220	230	240
	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
a721.pep	250	260	270	280	290	300
	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLKQPGGLAFLTGFI					
m721	250	260	270	280	290	300
	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLKQPGGLAFLTGFI					
a721.pep	310	320	330	340	350	
	ENAQPVAAALAGSQTGGKAPDERVAALTAEEAAAAMKLGMSGEEFVKIKESGKX					
m721	310	320	330	340	350	
	ENAQPVAAALAGSQTGGKAPDERVAALTAEEAAAAMKLGMSGEEFVKIKESGKX					

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
  1  GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
 51  TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101  ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151  CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201  TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GAGCCGCCGC AATCCTACCA
251  CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301  GACGACCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351  CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG

```


g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCCGAACACC TTATTTTAC CGTTTACAAA CACAATACCG
101 TCTTCGCCCG CGGCCACTTC TTCGCCGCTA TCATCCAGGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTGCGGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTTC GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTACTCGACC GCCTTGCGTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTTCGCGCA GCCGCGGTCA AACAGCAGGC CGCCGCGCCA AAATTCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTT CCAAGGCTGT GGTTCAGCAT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTCGGCG GTTTCGTGTT
851 TGTTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
1  MRPKPRFRRS VIACISVIT PEHLIFTVYK HNTVFARGHF FAAI IHAQLH
51  FAFGHSTQQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFSGVHQR GLCDLAVNQP LUVAVGELQD FQLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSAESAFSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGA AVSA VSGLLLVFAM MTPCFRRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pet not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
1  -----+-----+-----+-----+-----+-----+-----+ 60
TACTCAAACTCATTTAACCGCTTTTTCGCGTGTGTTGACGATTTTATAGCCGCTTTGG
a  M S L S K L A K K T A Q T A K N I G E T -
CTGCGCGCGGCCTTTCGGGGAAAAATCACGCTGGTGGTGTGTCGTCGAGCCGATACAGCGC
61  -----+-----+-----+-----+-----+-----+-----+ 120
GACGCGCGCGGAAAGCCCCTTTTGTAGTGCAGACCACACAGCAGGCTCGGCTATGTCGCG
a  L R A A F R G K I T L V V S S E P I Q R -
GTGCAGTTGAGCGGCTTGCCCGACGAAACCCTGCAAGACCTTGAACATTTGCAGGAATAC
121 -----+-----+-----+-----+-----+-----+-----+ 180
CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a  V Q L S G L A D E T L Q D L E H L Q E Y -
GGCTTTGCCAGCCATCCGCCCCAGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181 -----+-----+-----+-----+-----+-----+-----+ 240
CCGAAACGGTCGGTAGGCGGGCTGCCGTGCTTCGCCATCACTATGGCGACCCGCCGTTA
a  G F A S H P P D G S E A V V I P L G G N -
```

1171

```

501 CGGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA
551 ACCAAACGGG CGGCAGCTTT AACACCGACG GCGACGTGGT GGCCGGCAAT
601 ATATCGTTGC GCCAGCACCC GCATACCGAC AGCATCGGCG GCAAAACCTT
651 ACCGGCGGAA CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

a724.pep

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKLNK
101 PGETAIFNHE GAKIVIKQKG IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

a724/m724 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQVRVQLSGLADETLQDLEHLQEY					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQVRVQLSGLADETLQDLEHLQEY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a724.pep	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKLNK PGETAIFNHE GAKIVIKQKG					
m724	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKLNK PGETAIFNHE GAKIVIKQKG					
	70	80	90	100	110	120
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
	190	200	210	220		
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

m725.seq

```

1  ATGGTGCGCA CGGTTAAAAG CTACAACGGC GAGGCCGACG ATTTGGCGGG
51  GCAAATCCAT ACGCTGCCTG CGGTTTGGGT AACGTATGGC GGCAGCAAAG
101 TTGAGCCTGC CAGCACCGGC GCGTATGCG GACGTATATCA GGATACCGCC
151 GAATTTGTGG TGATGGTGGC GGCCCGCAAT CTGCGCAACG AGCAGGCGCA
201 GCGGCAAGGC GGCATCGACA GCCGCGAAAT CGGCAGCAAC GATTTAATCC
251 GCGCTGTTTC CCGCCTGCTT GACGGCCAGC GGCTCGGTTT TGCCGATAGC
301 CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT
351 GCAAACGCC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA
401 ACACCTGCGG GTTGGAATAA GACCGCTACC CCGAACGCAC CGACAATCCC
451 GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC
501 GTGGCCTGAT TTCGAGGGGT TGGACGGCAA AATTACGAC CCGCAATCCG
551 CCGATGAAAT ACCTGTAAAC CTAACCCTTA AGGATAAGCA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

m725.pep

```

1  MVRTVKSUNG EADDLAQIHL TPAVWVTYG GSKVEPASTG GVCGRYQDTA
51  EFVVMVAARN LRNEQAQRQG GIDSREIGSN DLIRAVRRLD DGQRLGFADS
101 RGLVPKAVRA IANHVLVQNA AVSIYAVEYA IRFNTCGLEN DRYPERTDNP
151 DDPNHIFTKY QGTLSEPWPD FEGLDGKIYD PQSADEIPVN LTLKDKQ*

```

1173

```

              70      80      90      100      110      120
a726.pep      HEWDGKKWEIGAAAAARFAEQKTATAFRLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
              |||||:::|||||:||||| ||||| ||||| ||||| ||||| |||||
m726          HEWDGKKWKISKAAAAARFAKQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep      LARQADNNAPTMLAQIAAARGVELDVLEIKVVEKSARLAVAAGAIIGKRQQLEDKLNIT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m726          LARQADNNAPTMLAQIAAARGVELDVLEIKVIEKSARLAVAAGAIIGKRQQLEDKLNIT
              130      140      150      160      170      180

              190      200
a726.pep      ETAPGLDALEKEIEEWTLNIGX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m726          ETAPGLDALEKEIEEWTLNIGX
              190      200

```

g727.seq not found yet

g727.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1   ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51  CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTGTC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAC
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1   MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51  AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPPD SRNPNTGFRL FSPQIPPNET QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1   ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51  CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCAGCGTGC GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGCTGAA AACGGAAAAA
301 AAAAAGGAAA TCGAAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1   MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51  AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DFGHHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1175

```

501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTCGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGCGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGAAAAATT TGGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACCTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

m728.pep

```

1 MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSV DA AGRGKIGEDV
201 YEHLGICYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
251 MRELMPRGMK ANSLVVGYYDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

	10	20	30	40	50	60
m728.pep	MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA					
g728	MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEVPENPNNAFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLAALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLAALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
g728	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	190	200	210	220	230	240
m728.pep	DSRNSVFYQNMRELMPRGMKANSLVVGYYDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
g728	DSRDYVFYQNMRELMPRGMKANSLVVGYYDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
	250	260	270	280	290	300
m728.pep	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
g728	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
m728.pep	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
g728	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

1177

	180	190	200	210	220	230
a728.pep	WQPDGSVFDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGSVFDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSLVVGVDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
m728	DSRNSVFYQNMRELMPRGMKANSLVVGVDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEKEVSR					
m728	IAQSSTVALKADGVVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAARRSGGRRDLSHX					
m728	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA CATTGAAAAC TACCTTGACC TCTGTTGCAG CAGCCTTTGC
51  ATTGTCTGCC TGCACCATGA TTCCTCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCGGAAAC CTCCAAAAC GACACATCGG TTTCTTCCAT CCGCGCGGTT
151 GATTGGGGTT GGCATGACTA TTTTSCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACAGCC GTATTGAACA
251 GCGAAATCTA CCGCAAAACA TACATGATCG AGCGCAACAA CCTCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGGCTCGCGC CAAGGCAGCT TGAGCGGCg
351 caaTGTCAGC AGCAGCTACA ATGTCGGACT GGGTGcGGca tCTTACGAAC
401 TCGATCTGTT CgGGCGCGTG CGCagcaacA GcgaagcAGC ACTGcaggGC
451 tATTTTGCCA GCGTTGCCAA CcgGATGCG GCACATTTGa ttCtGATTGC
501 CACCGTTGCC AAAGCCTATT TCAAcgaGcG TTATGCCGAA AAAGcgatgT
551 CTTTGCGCGa gcGTGTCTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATGCGGT ACAAGGCAGG CGTGATTTCG GCCGTCGCCC TCGGCCAGCA
651 GGAAGCCTTG ATTGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCa
701 gcCGGAACA GCGCGCAAT GCCTTGCGAA CCTTGATTAA ccGTCCGATA
751 CCCGAagaCC TGCCCGCCGG TTTGCCGTG GACAagcAGT TTTTGTGTA
801 AAAACTGCCT GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGACA
851 TCCGCGCCGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 gcgCGCGCCg ccTTTTTCCC GTCCATCCGC CTGACCGGAA GCGTCGCTAC
951 GGGTTCTGTC GAATTGGGCG GGCTGTTCAA AAGCGGCACG GCGTTTGGG
1001 CGTTCGCTCC GTCTATTACC CTGCCGATTT TTAATTGGGG AACGAACAAG
1051 GCGAACCTTG ATGTGGCAAA ACTGCGCCAA CAGGCACAAA TTGTTGCCTA
1101 TGAATCCGCC GTCCAATCCG CCTTCAAGA CGTGCGAAAC GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAGCCGC
1201 GCCTCTAAG AAGCGTTGCG CTTGGTCGGA CTGCGTTACA AACACGGCGT
1251 ATCCGCGCGC CTCGATTTGC TCGATGCGGA ACGCATCAGC TATTCGCGCG
1301 AAGGTGCGGC TTTGTCGGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CGCTCgacGG CGGATTGAAA CGGGATACCC AAACCGGCAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFQN DTSVSSIRAV
51  DLGWHDFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANGSR QGSLSGGNVS SSYNVGLGAA SYELDLFGRV RSNSEALQG
151 YFASVANRDA AHLILIATVA KAYFNERYAE KAMSLAQRVL KTREETYKLS

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1179

	70	80	90	100	110	120
m729.pep	PRLQKLIDIALERN	TSRLTAVLNSEI	YRKQYMIERN	NLLPTLAANAND	SRQGSLSGGNVS	
g729	PRLQKLIDIALERN	TSRLTAVLNSEI	YRKQYMIERN	NLLPTLAANANG	SRQGSLSGGNVS	
	70	80	90	100	110	120
	130	140	150	160	170	180
m729.pep	SSYKVGLGAASYEL	DLFGRVRSSEAA	LQGYFASTANRD	AAHLSLIATVAK	AYFNERYAE	
g729	SSYNVGLGAASYEL	DLFGRVRSNSEA	LQGYFASVANRD	AAHLILIIATVAK	AYFNERYAE	
	130	140	150	160	170	180
	190	200	210	220	230	240
m729.pep	EAMSLAQRVLKTR	EETYKLSELR	KAGVISAVALRQ	QEALIESAKAD	YAHAAARSREQ	ARN
g729	KAMSLAQRVLKTR	EETYKLSELR	KAGVISAVALRQ	QEALIESAKAD	YAHAAARSREQ	ARN
	190	200	210	220	230	240
	250	260	270	280	290	300
m729.pep	ALATLINQPIPED	LPAGLPLDKQFF	VEKLPAGLSSEV	LLDRPDIRAAEH	ALKQANANIGA	
g729	ALATLINRPIPED	LPAGLPLDKQFF	VEKLPAGLSSEV	LLDRPDIRAAEH	ALKQANANIGA	
	250	260	270	280	290	300
	310	320	330	340	350	360
m729.pep	ARAAFFPSIRLTG	TGVTGSAELGGL	FKSGTGVWSFAP	SITLPIFTWGTN	KANLDVAKLRQ	
g729	ARAAFFPSIRLTG	SVGTGSVELGGL	FKSGTGVWAFAP	SITLPIFTWGTN	KANLDVAKLRQ	
	310	320	330	340	350	360
	370	380	390	400	410	420
m729.pep	QVQIVAYESAVQS	AFQDVANALAA	REQLDKAYDAL	SKQSRASKEAL	RLVGLRYKHGV	SGA
g729	QAQIVAYESAVQS	AFQDVANALAA	REQLDKAYDAL	SKQSRASKEAL	RLVGLRYKHGV	SGA
	370	380	390	400	410	420
	430	440	450	460		
m729.pep	LDLLDAERSSYAA	EGAALSAQLTRA	ENLADLYKALG	GGGLKRDQT	DKX	
g729	LDLLDAERISYSA	EGAALSAQLTRA	ENLADLYKALD	GGGLKRDQT	GKX	
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

```

1  ATG GATACTA CATTGAAAAC CACCTTGACT TCTGTGTCAG CAGCCTTCGC
51  ATTATCCGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGTGCGGTC
151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAGC AGCAGCTACA AAGTCGGACT GGGTGCGGCA TCTTACGAAC
401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTCCGCC GCACCGCCAA CCGCGATGCG GCACATTGTA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTATGCCGAA GAAGCGATGT
551 CTTTGGCGCA ACGTGTTTTG AAAACGCGCG AGGAACCTA CAAGCTGTCT
601 GAATTACGTT ACAAGGCAGG CGTGATTTCC GCCGTCGCCC TACGTCAGCA
651 GGAAGCCCTA ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GCGCGCAAT GCCTTGCGAA CCCTGATTAA CCAACCGATA
751 CCCGACGACC TGCCCGCCGG TTTGCCGTTG GACAAGCAGT TTTTGTGTA
801 GAAGCTGCCG GCCGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCCG CCTTTTTCCT ATCCATCCGC CTGACCGGAA GCGTCGATAC
951 GCATTCTGCC GAATTGGCGG GGCTGTTCAA AAGCGGCACC GCGGTGTGGT
1001 TGTTTCGACC TTCCATTACC CTGCCGATT TTACTGGGG TACGAACAAG

```

1181

```

          430      440      450      460
a729.pép  LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX
          |||||:|||||
m729      LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

```

g730.seq
1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GCGGTCGCA  CTCATACAGC  CCGCCCTCGC  GGCGGACTTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACACC  CAACGGCAGC  ACTACGAACC  CGGCGGCAAA
151 TACCACCTCT  TCGGcgaCCC  GCGCGGCAGC  GTTTCGACCC  GCACCGGCAA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCA  GATGGGCAAC  CTGCTCATCC
251 AACAGGCGGC  AATCCAAGGC  AATCTTGGTT  ACACCGTCCG  CTTTTCGGGA
301 CACGGACACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 AAGCGAAGAA  AAAGGCAACG  TTGACGACGG  CTTTACCGTG  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCGCGCG  ATGCCTACGA  CGGCCCGAAG
451 GCGCGCAATT  ACCCCAAACC  TACGGGCGCA  CGAGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCCCGCA  GTATCAAAC  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATT  GACAACTACA  ACAACCTCGG  CAGCAATTTT
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TGTCACGGC  GTCGCGCGCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCGA  TGCGCAACAT
801 CGCCCCCTTA  CCCGCGGAGG  GCAAATTCGC  CGCCATCGGC  GGCTTGGGCA
851 GCGCGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTTGA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCGGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  TGGGGATTTT  TCTAAATCCT  ACACCTGCTC  CTTCCACGGC
1051 AGCACCTTGG  TCAAAACGGC  AGACGGCTAC  AAAGCCATTG  CCCATATTCA
1101 AGCCGGAGAC  CGCGTCCTTT  CCAAGGACGA  GGCAAGCGGA  GAAACGGGAT
1151 ACAAAACCGT  TACCGCCCGA  TACGGCAATC  CGTATCAAGA  AACCCTTTAC
1201 ATTGAAGTTT  CAGACGGCAT  CGGCAACAGC  CAAACCTGTA  TTTCCAACCG
1251 CATCCACCGC  TTTTATTCGG  ACGGCAAATG  GATTAAGGCG  GAAGATTTAA
1301 AAGCGGGAAG  CCGGCTGTTA  TCCGAAAGCG  GCAAACCCCA  AACCCTCCGC
1351 AACATCGTTG  TCAAACCAAA  ACCGCTCAAA  GCCTACAATC  TGACCGTTGC
1401 CGATTGGCAT  ACCTACTTCG  TCAAGGGTAA  TCAGGCGGAA  ACGGAAGGGG
1451 TTTGGGTTCA  TAATGATTGT  CCGCCTAAAC  CAAAACCAAC  CAATCATGCC
1501 CAACAAGAA  AAGAAGAAGC  TAAAAACGAT  TCTCATCGAA  GTGTGGGAGA
1551 TTCCAATCGT  GTCGTTTCGG  AAGGAAAGCA  ATATTTAGAT  TCCGACACAG
1601 GAAACCATGT  TTATGTAAAA  GGAGATAAAG  TGGTTATTCT  AACTCCTGAT
1651 GGAAGACAGG  TAACTCAATT  TAAGAAGTCG  AAAGCCAATA  CGTCAAAAAG
1701 GGTAAAAAAT  GGGAAATGGA  CACCAAAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

```

g730.pép
1  VKPLRLTLNL  LAACAVAAVA  LIQPALAADL  AQDPFITDNT  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGKINV  IQDYTHQMG  LLIQAAAIQG  NLGYTVRFSG
101 HGHEEHAPFD  NHAADSASEE  KGNVDDGFTV  YRLNWEHGEH  HPADAYDGP
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIF  DNYNNLGSNF
201 SDRADANRK  MFEHNAKLDR  WGNMSEFVNG  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAAIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVKNLTAAK  PGKAAVSGDF  SKSYTCSFHG
351 STLVKTAGDY  KAIAHIQAGD  RVLSKDEASG  ETGYPVTAR  YGNPYQETVY
401 IEVSDGIGNS  QTLISNRIHP  FYSDGKWIKA  EDLKAGSRLL  SESGKTQTVR
451 NIVVKPKPLK  AYNLTVADWH  TYFVKGNQAE  TEGVWVHND  PPKPKPTNHA
501 QQRKEEAKND  SHRSVGDSNR  VVREGKQYLD  SDTGNHVYVK  GDKVVILTPD
551 GRQVTQFKNS  KANTSKRVKN  GKWTPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

```

m730.seq
1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GCGGCGCGCA  CTCATACAGC  CCGCCCTCGC  GGCGGACTTG  GCGCAAGACC

```

1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAKAAGPGKAAVSGDFSYSYTCFSFHGSTLVKTADGY					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAGPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVTRYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIAKRTISAIKPKNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

a730.seq	1	GTGAAACCGC	TGCGAAGACT	CATCAAGCTC	CTTGCCGCCT	GTGCCGTAGC
	51	GGCGGCCGCA	CTCATACAGC	CCGCCCTCGC	GCCTTCTTG	GCGCAAGACC
	101	CGTTCATTAC	CGATAACGCC	CAACGGCAGC	ACTACGAACC	CGGAGGCAAA
	151	TACCACCTCT	TCGGCGACCC	GCGCGGCAGC	GTCTCCGACC	GCACCGGTCA
	201	AATCAACGTC	ATCCAAGACT	ATACCCACCG	GATGGGCAAC	CTGCTCATCC
	251	AGCAGGCAAA	CATCAACGGC	ACAATCGGCT	ACCACACCCG	CTTTTCCGGA
	301	CACGGATACG	AAGAACACGC	CCCCTTCGAC	AACCACCCCG	CCGACAGCGC
	351	GAGCGAAGAA	AAAGGCAACG	TTGACGAAGG	CTTTACCGTA	TACCGGCTCA
	401	ACTGGGAAGG	ACACGAACAT	CATCCGCCCG	ATGCCCTACG	CGGCCCGAAG
	451	GGCGGCAATT	ACCCCAAAAC	TACGGGTGCA	CGCGACGAAT	ACACCTATCA
	501	CGTCAACGGC	ACAGCACGCA	GCATCAAAC	CAATCCGACC	GACACCCGCA
	551	GCATCCGGCA	ACGCATATCC	GACAATTACA	GCAACCTCGG	CAGCAATTTT
	601	TCCGACCGCG	CCGATGAAGC	CAACAGAAAA	ATGTTTCGAGC	ACAATGCCAA
	651	GCTCGACCGC	TGGGGCAACA	GCATGGAGTT	TATCAACGGC	GTCCGCCCGC
	701	GCGCGCTCAA	CCCCTTTATC	AGCGCGGGCG	AAGCCTTGGG	CATAGGCGAC
	751	ATACTGTACG	GAACGCGCTA	TGCCATAGAC	AAAGCCGCAA	TGCGCAACAT
	801	CGCCCCCTTG	CCCGCCGAGG	GCAAATTCGC	CGTCATCGGC	GGCTTGGGCA
	851	GCGTGGCGGG	CTTTGAAAAA	AATACGCGCG	AAGCCGTGTA	CCGGTGGATA
	901	CAGGAAAACC	CCAATGCCGC	CGAAACCGTC	GAAGCCCTGG	TCAACGTCCT
	951	GCCGTTTGCC	AAAGTCAAAA	ACCTGACAAA	GGCGGCAAAA	CCGGGGGAAG
	1001	CTGCGGTAG	CGGGGATTTT	TCTGCTGCAT	ACAATACAAG	AACAACTAGA
	1051	AAAGTTACTA	CAGAAACAGA	GGGTTAAAT	AGAATCAGAC	AGAACCAGAA
	1101	AAATAGTAAT	ATACATGAGA	AAAATTATGG	AAGAGATAAT	CCTAATCATA
	1151	TTAATGTTTT	ATCTGGAAAT	TCTATACAAC	ATATACTGTA	TGGAGATGAA
	1201	GCAGGAGGTG	GGCATCTTTT	TCCTGGCAAA	CCTGGTAAGA	CAACATTCCC
	1251	CCAACATTGG	TCAGCCAGTA	AAATAACTCA	TGAAATTAGT	GATATCGTTA
	1301	CATCCCCAAA	AACGCAATGG	TATGCACAGA	CTGGAACAGG	CGGCAATAT
	1351	ATTGCTAAAG	GAAGACCAGC	TAGGTGGGTA	TCATATGAAA	CGAGAGATGG
	1401	AATTCGTATC	AGAACAGTTT	ATGAACCTGC	AACAGGAAAA	GTGGTAACTG
	1451	CATTCCCCGA	TAGAACCTCT	AATCCCAAT	ATAACCTGT	AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

a730.pep	1	VKPLRLRIKL	LAACAVAAAA	LIQPALAADL	AQDPFITDNA	QRQHYEPGGK
	51	YHLFGDPRGS	VSDRTGQINV	IQDYTHRMGN	LLIQANING	TIGYHTRFSG
	101	HGYEEHAPFD	NHAADSASEE	KGNVDEGFTV	YRLNWEHGH	HPADAYDGP
	151	GGNYPKPTGA	RDEYTYHVNG	TARSIKLNPT	DTSRIRQIS	DNYSNLGSNF
	201	SDRADEANRK	MFEHNAKLDR	WGNSMEFING	VAAGALNFI	SAGEALGIGD
	251	ILYGTRYAID	KAAMRNIAPL	PAEGKFAVIG	GLGSAAGFEK	NTREAVDRWI
	301	QENPNAAETV	EALVNVLPFA	KVNLTAKAAG	PGKAAVSGDF	SAAYNTRTTR
	351	KVTTETEGLN	RIRQNQKNSN	IHEKNYGRDN	PNHINVLSGN	SIQHILYGDE
	401	AGGGHLFPKG	PGKTTFPQHW	SASKITHEIS	DIVTSPKTQW	YAQTGTGGKY
	451	IAKGRPARWV	SYETRDGIRI	RTVYEPATGK	VVTAFFPDRTS	NPKYNPVK*

1185

```

251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
301 CACCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA
351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

```

m731.pep
  1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE
  51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

```

g731/m731 95.2% identity in 84 aa overlap

```

                                10      20      30
g731.pep                      DFRFSCENGLSVRVRNLDGGKIALRLDGR
                                |||||
m731      LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCEGLSVRVRHLDGKVALRLDGR
              20      30      40      50      60      70

              40      50      60      70      80
g731.pep      RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX
              |||||
m731      RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX
              80      90      100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

```

a731.seq
  1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTGT CTTGGCGGC
  51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGAGGG CATATGCCGC
 101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCCAG
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CATCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

```

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

```

a731.pep
  1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE
  51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

```

a731/m731 94.4% identity in 126 aa overlap

```

              10      20      30      40      50      60
a731.pep      MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTADFRAFSCEGLSVHVRRL
              |||||
m731      MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCEGLSVRVRHL
              10      20      30      40      50      60

              70      80      90      100     110     120
a731.pep      DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE
              |:::|
m731      DSGKVALRLDGRRAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE
              70      80      90      100     110     120

a731.pep      TSCRARX
              |||||
m731      TSCRARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

```

g732.seq
  1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
  51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTTGCC GCCGagaagg
 101 ACGGgcgGGA TAACGAagtC CTGCCGTGC AATCCATCCG TACGATGGCG

```

1187

```

1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GCGCGATTG
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAG ACGACCAGT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51 EVYGOIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMEK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAII KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLAG
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLNSGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNNKDKKD KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

	10	20	30	40	50	60
m732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRDNEVLPVQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	VSPIEDTPAERAEVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m732.pep	IVVNLTRAIKVKSVRHHLIEPDYGIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEDYVYGMGGDSLAG					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKGMVLKAVPEDYVYGMGGDPLAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m732.pep	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLNSGSAV					
g732	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLNSGSAV					
	310	320	330	340	350	360

1189

a732/m732 99.6% identity in 494 aa overlap

a732.pep	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGGQIKANY					
m732	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGGQIKANY					
a732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
m732	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
a732.pep	130	140	150	160	170	180
	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732	130	140	150	160	170	180
	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
a732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLEPDYGYIRVSQFQERTVESVNTAAKELVKENKGPLKGLV					
m732	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLEPDYGYIRVSQFQERTVESVNTAAKELVKENKGPLKGLV					
a732.pep	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAV					
m732	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAV					
a732.pep	310	320	330	340	350	360
	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFQSGSVQTLIPLSNGSAV					
m732	310	320	330	340	350	360
	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFQSGSVQTLIPLSNGSAV					
a732.pep	370	380	390	400	410	420
	KLTTALYYTPNDRSIAQAGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
m732	370	380	390	400	410	420
	KLTTALYYTPNDRSIAQAGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
a732.pep	430	440	450	460	470	480
	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAACK					
m732	430	440	450	460	470	480
	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAACK					
a732.pep	490					
	PVSNDKDKDKDKKX					
m732	490					
	PVSNDKDKDKDKKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGIGTG CGGCGGTCTT
51 GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGGTT TGAAAAACGg cgACACTTCC
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCCG CGGGTGC GCA CGCCATTG GGA CTGCTGC

```

1191

```

      1  MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDSTS
     51  LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
    101  KRLFPESGVF MDFLMKTGKG GKR*

```

a733/m733 100.0% identity in 123 aa overlap

```

      10      20      30      40      50      60
a733.pep  MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDSTSLGKQTEKMEK
          |||
m733      MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDSTSLGKQTEKMEK
          |||
      70      80      90     100     110     120
a733.pep  YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERLFPESGVFMDFLMKTGKG
          |||
m733      YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERLFPESGVFMDFLMKTGKG
          |||
      70      80      90     100     110     120

a733.pep  GKRX
          |||
m733      GKRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

```

g734.seq
      1  ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
     51  GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
    101  AGGATGCAAA CGATGTTTTG CAGGTAAAAA CCACAAAAGA AGATTCGGCG
    151  AAAAGCGAAG CGTTTGCCGA GTTGGAAGCC TTTTGCAAAG GTCAGGACAC
    201  GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
    251  CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
    301  ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
    351  TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
    401  AATGCGGCTT GGAAACAGTG TATTGCACGT CATCTTCTTA TTACGGCGGG
    451  GCTGTTGCTT CCTTAATCCA ACACCTGAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

```

g734.pep
      1  MMKKILAVSA LCLMTAAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
     51  KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
    101  MRVENAVVIT SPRFTSVHGV ALNQCIKKYQ AQGQCGLETV YCTSSSYYG
    151  AVRSLIQHLK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

```

m734.seq (partial)
      1  TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCCG TCGTGTGCGT
     51  GAACAATACC TGTGTGCGCG TGGCATACCC GAAAGCCTTG GGCGCGCTGC
    101  GTGTGACAAA CGCGTCGTG ATTACTTCTC CGCGTTTAC GAGCGTTCAT
    151  CAGGTCGCAC TCAACCAAGT CATCAAAAAA TACGGCGTAC AGGACAAATG
    201  CGGCTTGGA ACAGTGATT GCACATCTTC TTCTTATTAC GGCGGAAGT
    251  TCGCTCTTT GATTCAAAAT CTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

```

m734.pep (partial)
      1  SGIAEDEPTG CRSVSLNNT CVALAYPKAL GALRVDNAV VITSPRFTSVH
     51  QVALNQCIKK YGVQGCGLT TVYCTSSSY GGTVRSLIQN LK*

```

m734/g734 92.4% identity in 92 aa overlap

```

      10      20      30
m734.pep  SGIAEDEPTGCRSVVSLNNTCVALAYPKAL
          :|||
g734      VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKAL

```

1193

351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEYKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNASGGCI DGFGSHGLQL YNRALGYGN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GCGCGCTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEYKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DGFGHHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALV	GTGLAVSHHQGYKSAFAKQQ	AVIEKMKRDKAQALLLSAQN			
m735	MNLVKLLANNWQPIAIIALV	GTGLAVSHHQGYKSAFAKQQ	AVIDKMERDKAQALLLSAQN			
	70	80	90	100	110	120
a735.pep	YARELEQARA	EAKKYEYKAHAVGMALAKKQ	AEVSRLKTENKKEIENVLTQ	DRKNAGGGCI		
m735	YARELELARA	EAKKYEYKAHAVGMALAKKQ	AEVSRLKTENKKEIENVLTQ	DRKNASGGCI		
	130	140				
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCGGCAGT ATCAGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
101 CGGCTTTTGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCT TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCGCGAACT GGGTCCCGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCG CGCGTTTTCG GCGGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGAACAAAC ATTACGATAC ATTACGATGT AATCAACGGT

1195

	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVTVSS					
g736	GIFWPQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCIP*SEGILRASTRVTVSS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

a736.seq

1	ATGAATTTTA	TCCGTTCCGT	CGGGGCGAAA	ACCCTCGGCC	TTATTCAATC
51	TCTCGGCAGT	ATCACGCTGT	TTCTGCTGAA	TATTCTGGCG	AAATCCGGTA
101	CGGCTTTTCG	CCGTCCGCGC	CTGAGCGTGC	GCCAAGTGTA	TTTGCCCGGC
151	GTGCTGTCGG	TGTTGATTGT	TGCCGTTTCA	GGGCTGTTTG	TCCGCATGGT
201	CTTGGGTTTG	CAGGGCTATA	CGCAGTTGTC	GAAATTCAAA	TCCGCCGATA
251	TTTTGGGCTA	TATGGTCGCG	GCTTCGCTGT	TGCGCGAACT	GGGTCCGGTG
301	TTGGCGGCGA	TTCTGTTTGC	CAGCAGCGCG	GGCGGTGCGA	TGACCAGCGA
351	AATCGGTIP3	ATGAAAACGA	CCGAACAGCT	CGAAGCGATG	AACGTGATGG
401	CGGTAAACCC	CGTCCGCCGA	GTGGTTGCGC	CGCGCTTTTG	GGCGGGCGTG
451	TTTTCCATGC	CGCTTTTGGC	TTCGATTTTC	AACGTGGCGG	GTATTTTCGG
501	CGCGTATTTG	GTCGGTGTA	CCTGGCTGGG	CTTGGACAGC	GGTATTTTCT
551	GGTCGCAAT	GCAGAACAA	ATCACGATAC	ATTACGATGT	AATCAACGGT
601	CTGATCAAAT	CCGCCCGGTT	CGGCGTGGCG	GTAACGCTGA	TTGCCGTGCA
651	TCAGGGCTTC	CACTGCGTCC	CGACCTCGGA	AGGCATTTTG	CGCGCCAGCA
701	CGCGCACGGT	GGTTTCGTCC	GCCCTGACGA	TTTTGGCGGT	CGATTTTATA
751	TTGACCGCGT	GGATGTTTAC	AGATTGA		

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

a736.pep

1	MNFIRSVGAK	TLGLIQSLGS	ITLFLNILA	KSGTAFVRPR	LSVRQVYFAG
51	VLSVLIVAVS	GLFVGMVLGL	QGYTQLSKFK	SADILGYMVA	ASLLRELGPV
101	LAAILFASSA	GGAMTSEIGL	MKTTEQLEAM	NVMVNPVAR	VVAPRFWAGV
151	FSPMLLASIF	NVAGIFGAYL	VGVTWGLGDS	GIFWSQMNN	ITIHVDVING
201	LIKSAAFGVA	VTLIAVHQGF	HCVPTSEGIL	RASTRVTVSS	ALTILAVDFI
251	LTAWMFTD*				

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTWGLGDS					
m736	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTWGLGDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVTVSS					

1197

```

a737.seq
1  ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51  CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

```

a737.pep
1  MNFKRLLLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51  AQAEEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLLTA	AATALMGISA	PALAHHDGHG	DDDHGHAHQ	HSKQDKIISR	AQAEEKAALAR
m737	MNIKHL	LLTSAATALLS	ISAPALAHHDGHG	DDDHGHAHQ	HNKQDKIISR	AQAEEKAALAR
	10	20	30	40	50	60
	70	80	90	100	109	
a737.pep	VGGKITDIDLE	HDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
m737	VGGKITDIDLE	HDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

```

g738.seq
1  ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCG CCAAACCTGCC
51  GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGCGC
151 GCGGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC
301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG
351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCAtcgtT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
451 CAGTTTGCCG GCTGGGAAAA CACCCCCCTG CTTCAAAACA TCATCGTTCA
501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCTCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTTCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAAGC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCC AACAAACCTT CCTGATCAAT GCCGAACAGC
1001 ACACCATAA CGACAACTTC CTCAGCACCT TGTTCAACCA TTCCCACAAC
1051 ATCATCCTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
1151 CCCCAGCATC ACTTTTCTTG CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTTCA TCCCTTCTCG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
1401 CCCCAGCGCT GACGACAGT CCAAAACCTT CAACCGGAAA ATCAACGAAC
1451 TGCGCTATAT TTCCGCAAAC AGCCCGATGC TGTCTTTTTA TGCCGACTTC
1501 TCCTTCGTAA ACTTCGCCCT GCCGGAATAC CCGGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCCTAC TCCGCCACCT

```

```

51  AAGLIVLLFL TAGKKLFDVK IPAISFLLFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TLFWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR
201 KIPPAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNIYDNL LSNLFTSHN
351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGI IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALEPY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAEAK
551 QWMRATQSYV PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/g738

```

              10      20      30      40      50      60
m738.pep      MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738           MSAETTVSGARPAAKLPYIILPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL
              10      20      30      40      50      60

              70      80      90      100     110     120
m738.pep      TAGKKLFDVKIPAISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738           TAGKKLFDVKIPAISFLLFAMAAFWWLQARLMNLIYPGMNDIASVWFILLAVSAWACKSL
              70      80      90      100     110     120

              130     140     150     160     170     180
m738.pep      VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738           VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN
              130     140     150     160     170     180

              190     200     210     220     230     240
m738.pep      NLGHYLMWGILAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738           NLGHYLMWGILASAYLNGQRKIPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW
              190     200     210     220     230     240

              250     260     270     280     290     300
m738.pep      YFRSDKSNRRTMLGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738           YFRSDKSNRRTMLGIAAAVFLTALFQFSMNAILETFTGIRYETAVERVANGGFTDLPRQS
              250     260     270     280     290     300

              310     320     330     340     350     360
m738.pep      EWNKALAAFQSAPIFGHGWNSFAQQTFLINAEQHNIYDNL LSNLFTSHNIVLQLLAEMG
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738           EWNKALAAFQSAPIFGHGWNSFAQQTFLINAEQHTIHDNFLSTLFTSHNIIQLLAEMG
              310     320     330     340     350     360

              370     380     390     400     410     420
m738.pep      ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738           ISGTLLVAATLLTGIAGLLKRSLTPASLFLCALAVSMCHSMLEYPLWYVYFLIPFGLML
              370     380     390     400     410     420

              430     440     450     460     470     480
m738.pep      FLSPAESDGI AFKKAANLGILTASAAIFAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g738           FLSPAESDGI AFKKAANLGILTASAAIFAGLLHLDWYTYRLVNSFSPAADDSAKTLNRK

```


1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
 251 TILGIAAAVF LTALFQFSMN TiletFTGIR YETAVERVAN GGFTDLPRQI
 301 EWRKALAAFO SAPIFGHGWN SFAQQTFLIN AEQHNIDNL LSNLFTHSHN
 351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
 401 SMLEYPLWYV YFLIPFGLML FLSPAEASDG IAFKKAANLG ILTASAAIFA
 451 GLLHLDWYTY RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
 501 SLVNFALEPY PETOTWAEAA TLKSLKYRPH SATYRIALYL MRQKVAEAK
 551 QWMRATQSY YPYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
 601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAHAAKLPIYILPCFLWIGIVPFTFALRLQSPDFYHDAAGLIVLLFL					
	:					
m738	MPAETTVSGAHAAKLPIYILPCFLWIGIVPFTFALKLKSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
	70	80	90	100	110	120
a738.pep	TAGKKLFDVKIPISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
	:					
m738	TAGKKLFDVKIPISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a738.pep	VAHYQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
	:					
m738	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a738.pep	NLGHYLMWGILAAAYLNGQRKIPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	:					
m738	NLGHYLMWGILAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
	250	260	270	280	290	300
a738.pep	YFRSDKSNRRRTILGIAAAVFLTALFQFSMN TiletFTGIRYETAVERVANGGFTDLPRQI					
	:					
m738	YFRSDKSNRRRTMLGIAAAVFLTALFQFSMN TiletFTGIRYETAVERVANGGFTDLPRQI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a738.pep	EWRKALAAFO SAPIFGHGWN SFAQQTFLINAEQHNIDNLLSNLFTHSHNIVLQLLAEMG					
	:					
m738	EWNKALAAFO SAPIFGHGWN SFAQQTFLINAEQHNIDNLLSNLFTHSHNIVLQLLAEMG					
	310	320	330	340	350	360
	370	380	390	400	410	420
a738.pep	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	:					
m738	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
	430	440	450	460	470	480
a738.pep	FLSPAEASDGIAFKKAANLGILTASAAIFAGLLHLDWYTYRMVNAFSPATDDSAKTLNRK					
	:					
m738	FLSPAEASDGIAFKKAANLGILTASAAIFAGLLHLDWYTRYLVNAFSPATDDSAKTLNRK					
	430	440	450	460	470	480
	490	500	510	520	530	540
a738.pep	INELRYISANSPMLSFYADFSLVNFALEPYPETOTWAEATLKSLKYRPHSATYRIALYL					
	:					
m738	INELRYISANSPMLSFYADFSLVNFALEPYPETOTWAEATLKSLKYRPHSATYRIALYL					
	490	500	510	520	530	540

1203

	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPQHTDSPRET					
	: : : : : :					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTEPQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
	: : : : : :					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
	:	:	:	:	:	:
g739	ADSLTGTGTQAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPKHEILDKLF					
	: :					
g739	PKNTPAKPKHEILDNLF					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACAA
551 CGCCGCTAA ACCCCATAAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1  MAKKPNKPFRLTPKLLIRAVLLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQADTAQT DRQPDAGAQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD PKNTPPKPKH EILDNLF*

a739/m739 93.9% identity in 197 aa overlap

10 20 30 40 50 60
a739.pep MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTEPQHTDSPRET
|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739 MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPQHTDSPRET
10 20 30 40 50 60

70 80 90 100 110 120
a739.pep EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT
|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739 EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT
70 80 90 100 110 120

130 140 150 160 170 180
a739.pep DRQPDAGAQ AENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPD
|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739 DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD
130 140 150 160 170

```

1205

```

a740.pep  MSRNLLVRWLVLVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
          |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m740      MSRNLLVRWLAVCLIPLATLAVFAANPPEDKLOHLINGIILACEATFLFKFVLFDTIKHH
          10      20      30      40      50      60

          70      80      90
a740.pep  LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m740      LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
          70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1  GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTC
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTG GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAA GCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCTGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCTG CGATTGGGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAG CCGAGTATCA CGGCAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAACTG ACCTATACCA TAGATTTCGC CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1  VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNGTLTL SAQGAEKTFK AGGKDNSLNT GKLNKDISR
101 FDFVQKIEVD GQTITLASGE FQIYQDHSA VVALRIEKIN NPDKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 GHGKIEHLKT PEQNVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGKEV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1  GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCCTAACCG GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GGCGGCACAA GGTGCGGAAA AAACCTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTTCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGAAA CGGCAAAATC
601 GAACATTGTA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAGACGCC ATGCCGTCAT CAGCGGTTCC GTCTTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1  VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHKDKGL
51  QSLTLDSVR KNEKLLAAQ GAEKTYNGND SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQYKQ SHSALTAFQT EQIQDSEHSK KMAKROFRI

```

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
	: : : : : : : : : :					
m741	VNRTAFCCSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLLAAQGAEKTYGNGDSLNTGKLNKDKVSRFDFIRQIEVDGQLITLESGEFQVYKQ					
	: : : : : : : : :					
m741	KNEKLLAAQGAEKTYGNGDSLNTGKLNKDKVSRFDFIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDDD					
	: : : : : : : : :					
m741	SHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDDD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYYTIDFAAKQGHGKIEHLKSPELN DLAASDIKPKDKRHAVISGSVLYNQAEEKGS					
	: : : : : : : : : :					
m741	AGGKLTYYTIDFAAKQGNKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAQKX					
	: : : : :					
m741	YSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAQKX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

m742.seq

1	ATGGTTTACG	GCATTGCCGA	AGCCGATGCG	GGCGACAGCA	GTGTGCTTAC
51	TTTGGGCGGC	ATGTATCAGA	AGAGTAGGGA	GGTTCCTGAT	TTTTCGGGCA
101	TTATTTTGCC	CTGTGAAAAT	CAGAAACTG	CCCCGTTTAC	TTCAACGCCT
151	GCCTGCAACC	GGCCTTTGCA	ACTGCCGCGC	AACACTTATT	TGGGGGAGGA
201	TTGGTCGCGG	TTAAGTGCCG	ACAAATACAA	CCTTTTCTCA	GGATTCAAAAC
251	ATGTGTTTGA	CAACGGTTGG	CAGCTCAATG	CCGAAGTGTC	TTATACCAAG
301	AATGAATCCG	ATGCGAAGGT	GGGGCAGTTT	TTTCTGAAAA	ACGAATATGC
351	GGCGGGTTTG	TCGGGTGAGG	ATGCGGTAGG	CTTTTGTACT	GAAAAAAACG
401	AAGTCATCCC	GTTTCGAGCCG	AAAGATAAGG	CATTGGAGAA	ACTGAAAGCA
451	TATCGTGATG	AAACCGCCAA	GGAATACCGG	GAGCGCAAAG	ACGATTTTGT
501	TAAAAACCGT	TTTCGATAATA	CTGCTTTCTGA	ACAGTATCGC	AGCCGCCGTG
551	CCGCAGAACG	CAAAGCCCGT	TTTGACAAGT	GTATGAGTGA	CCCTTTTCGCG
601	CTGGACTTTA	TCTGTCAAGG	TTCTTGGGGG	GATCCGGGCG	TTGATGCCGA
651	CAAGGCGGAA	TTTGTGCGATA	AAGCCCTTGC	GAAGGAGGGC	ATCTTTAATA
701	ATGCGGCACA	ACGTTTTCCTA	AACAGCCTGT	ATGACTCTTC	CTTTAATCGG
751	AAGGCTACCG	CCAACCGACG	ATACAGTTAT	ATGCCGTTGC	GGCATACCAA
801	AGACGACCGC	CAATGGGGAA	TTAACTTGA	CCTGACCGGC	ACATATGGGC
851	TGTTCCGGCG	GGAGCATGAT	TTCTTTGTGC	GCTATGCCTA	CGGTGATGAA
901	AAGATACGTT	CGGAATATCT	AGAAATCTAC	GAACGCCGCT	ACAGAGTACG
951	TCCGAATACG	GGGGCAACGC	ACGGCGTGTA	TGCGGGAAGT	TGTCAGGAGG
1001	AGCCGGACGG	CGATTTGTCTG	TCTCCTTTGG	TCAGGGGGCA	TAAAGAACCC
1051	GATTGGCAGG	CGTACGATGA	AAAAGGCAAC	CGTACCGTTT	ATGCCGAAGA
1101	ATGCAGGAAC	GCCAAGAAAA	TAAAAACCGA	GCCCAAGCTC	GATGCCGAAG
1151	GCAAGCAGGT	GTATTACTAT	GACGAATACA	GCGGCAGCCG	GACACCGGTA
1201	TATGTGATG	TATATGAGCT	GGACGAAAAA	GGCAACAAGA	TTCAGGAGAC
1251	CAATCCCGAC	GGCAGCCCTG	CCTTTACCGG	TTTTTCCGGT	ACGGTGCCGG
1301	TTTGGAAGAC	CGTCAAAGTG	GCAGACGACC	ATGTTCTCTG	GCTGTATAAC
1351	TACGCCAAAT	ACCTCAACAC	CAACAAAACC	CATTCGCTGA	CTGCCAGCAC
1401	GCGTTTCAAC	GTAACCGGCC	GACTGCACCT	TTTGGGCGGG	CTCCACTACA

1209

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1201 TATGTCGATG TATATGAACT GGATGAAAAA GGCAATAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCCTG CCTTTACCGG TTTTTCGGT ACGGTGCCGG
1301 TTTGGAAAAC CGTCAAAGTG GCCGACGACC ATGTTCTCTG GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTGCTGA CTGCCGGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCATCT TTTGGGCGGG CTGCACTACA
1451 CGCGCTATGA AACCTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAAGGCGG ATCAGGACCA
1551 TTATACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCGTATGATT GACACCGCAA CAGAGTATT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACATAT AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTGCTCG ATTTTGGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGTGTCAGC AGGGGTGCGG
1901 AATTGAGATT GTCGGTGAG TTGAACGAAG ATTGGAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTCGCG AAAAACACAG GCGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCCGTGCA CATATTCGCT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGCGGCGCG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCT AAATTGAGCC TCATCGGTAC GAACCTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAACAAA
2301 CTTCTATGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

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This corresponds to the amino acid sequence <SEQ ID 2542; ORF 742.a>:

```

a742.pep
1  M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L S C E N Q K T A P F S S T P
51  A C N R P L Q L P R N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K
101 N E S D A K V G Q F F L K N E H A A G L S D E D A V G F L T E K N E V I P F E P K D K A L E K L K A
151 Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R S R R A A E R K A G F D E C M S A P F A
201 L D F I C Q G S W G D P G V D A D K S E F V D K A L A K E G I F N N A A Q R F P N S L Y D S S F N R
251 K A T A N R R Y S Y M P L R H T K D D P Q W G T Y L D L T G T Y G L F G R E H D F F V G Y A Y S D E
301 K I R S E Y L E I Y E R R H R V R P N T G A T H G V Y A G S C Q G E P D G D L S S P L V R G H K E P
351 D W Q A Y D E K G N R T V Y A E E C R N A K K I K T E P K L D A E G K Q V Y Y Y D E Y S G S R T P V
401 Y V D V Y E L D E K G N K I Q E T N P D G T P A F T G F S G T V P V W K T V K V A D D H V P A L Y N
451 Y A K Y L N T N K T H S L T A G T R F N V T G R L H L L G G L H Y T R Y E T S Q T K D M P V R Y G Q
501 P A S D F Q T A S S I K A D Q D H Y T A K M Q G H K L T P Y A G I T Y D L T P Q Q S I Y G S Y T K I
551 F K Q Q D N V D V S A K T V L P P L V G T N Y E V G W K G A F L Q G R L N A S F A L F Y L E Q K N R
601 T V V D F G Y V P G A G G K Q G S F Q T V A K P I G K V V S R G A E F E L S G E L N E D W K V F A G
651 Y T Y N K S R Y K N A A E V N A E R L A K N T G A D P Y N F S N E T P V H I F R F G T S F H I P N T
701 G L T V G G G V S A Q S G T S S L Y N I R Q G G Y G L I D G F V R Y E L G K H A K L S L I G T N L N
751 G R T Y F E N N Y N R T R G A N N F Y G E P R T V S M K L D W Q F *

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a742/m742 98.5% identity in 783 aa overlap

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              10      20      30      40      50      60
a742.pep      M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L S C E N Q K T A P F S S T P A C N R P L Q L P R
              |||
m742           M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L P C E N Q K T A P F S S T P A C N R P L Q L P R
              10      20      30      40      50      60

              70      80      90      100     110     120
a742.pep      N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K N E S D A K V G Q F F L K N E H A A G L
              |||
m742           N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K N E S D A K V G Q F F L K N E Y A A G L
              70      80      90      100     110     120

              130     140     150     160     170     180
a742.pep      S D E D A V G F L T E K N E V I P F E P K D K A L E K L K A Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R
              |||
m742           S G E D A V G F L T E K N E V I P F E P K D K A L E K L K A Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R
              130     140     150     160     170     180

              190     200     210     220     230     240
a742.pep      S R R A A E R K A G F D E C M S A P F A L D F I C Q G S W G D P G V D A D K S E F V D K A L A K E G I F N N A A Q R F P

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1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi145723 (X56605)
 pseudobactin uptake protein (*Pseudomonas putida*) Length = 819
 Score = 152 bits (381), Expect = 6e-36
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADDDHV-PALYNYAKYLNTNKTSLTAGTRFNVGTGRLHLLGGLHYTRYETSQTKDM 494
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y
 Sbjct: 511 QTPKPGDDEIIPGI----QYNISNRQSGYFVASRFNLTDDLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPTYAGITYDLTPQQSIYGSYTKIFKQQ 554
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q
 Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPKQ 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRLNASFALFYLEQKNRTVVDFGYVPGAGGK 614
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG
 Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGEFLEGRNLNANIALYMKRDNLAESTNEVVPSDGG 668

Query: 615 QGSFQTVAKPIGKVVSRAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674
 S + + +G + ELSGE+ W VF GY++ ++
 Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +
 Sbjct: 708 ADGKRLTPQLPMDTFRWNTYRLPGWEKLTGGGVNWNNSKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
 RY + + +L N+ + Y Y G+ YG PR ++ L + F
 Sbjct: 768 TSLMARYRINESLAATLNVNNIFDKKY---YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTIATC
 51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
 151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCGCG
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAG
 351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
 401 TGACCGTCAA TGTGTCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
 451 TCTCCGAGTA CCGATTGCGG GGTATTATGAC CATATTGAAG TTGTACGGGG
 501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
 551 TGATCCGTAA GTGA

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep
 1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
 51 GKTEKTRSYT IDRMSTATGM RIAGKDT PQS VSVITRSRLD DKAVHTLEEA
 101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
 151 SPSTD LAVYD HIEVVRGATG LTQSNSEPPG TVNLIRK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTIATC
 51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTGC
 151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCGCG
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAG

1213

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1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGA AAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCCTTA AAGATAGAAA TTATGCAAAAT
1501 ATTTCTCCTA AAATAAAAC TGAACTGAA TATTTAATA TTTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGAACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

```

m744.pep
1 MKPLKLTLEFG FVDAANYRRR ENKDLFNRF VKGEYLDLCL EPNISFLIGE
51 KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLLVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIFNKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEEESQQ ITFTESKFQA NLGFIERKFK
201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQNON TKLQDNSVFL DWRFDYKSYR
301 SSKIFGVFDH LLRTQQEKQD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKKSKEYD VVAEDFDNTS FQREYSIYLL
401 GEIKDHLLFY YSQSDYQNFL KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKFMS TANEFLOFLF DLNVIAYLDN PEDETKPIYH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTFFKNK Q*

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g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

```

m745.seq
1 ATGTTTTGGC AACTGACCGT TGTTCAGTA ACCGCCGTCA TTGCACTGGG
51 GACAATATTC ATCAATAAGA AAACCTCAAA GCAAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTTGCGCCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATTCT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TCGGTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTGG TTTAAACGGC TGCATTGCAC
351 CAACTTCATA AAATGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGGTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTGTG GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

```

m745.pep
1 MFWQLTVVSV TAVIALGTIF INKKTSKQKA TLDVILNDYQ DAQFVEADNH
51 ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPV MKIREEERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

```

g746.seq
1 ATGTCCGAAA ACAAAACAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
51 ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTGC CGACAGCAAT
151 CCCGCACCGC AGGCCGGCGA AACC GGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCACAA ACCCTGCTCT TGAATCCCG CGCCGAAAAC GGGGAAACCG
251 CGCCCGACAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAAAACGTA GCGCGGCCGC TGGTCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGTTTGGAA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCGAAGCA GGCAAAACAA
451 CGCGCTGCCG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACC GAAAAA TGCTGCCGAA AAAACCAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

```

	110	120	130	140	150	160	169
m746.pep	LEDSNIKGLEASEK LQQAETAKTAPKQAKQRAAEKV PATADSTDTVAVEKPKRTAETKPPQ						
g746	LEDSNIKGLEASEK LQQAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPKPPQ						
	130	140	150	160	170	180	
	170	180	190	200	210	220	229
m746.pep	KAERTAKAKPKAKETKTAEKVADKPKTAAEKT KPD TAKSDSAVKEAKKADKAESKKTAEK						
g746	KAERTAEAKPKAKETKTAEKVADKPKTAAEKT KPD TAKSDSAVKEAKKADKAEGKKTAEK						
	190	200	210	220	230	240	
	230	240	250	260	270	280	
m746.pep	DRSDGKKHETAQKTDKADKTKTAEKEKSGK--KAAIQAGYAEKEPALSLQRKMKMAAGID						
g746	DRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKAAIQAGYAEKERALS LQRKMKMAAGID						
	250	260	270	280	290	300	
	290	300	310	320	330		
m746.pep	STITEIMTDNGKVYRVKSSNYKNARDAERDNLKLRVHGIAGQVTNEX						
g746	STITEIMTDNGKVYRVKSSNYKNARDAERDNLKLRVHGIAGQVTNEX						
	310	320	330	340			

a746.seq

1	ATGTCCGAAA	ACAAACAAAA	CGAAGTCCTG	AGCGGTTACG	AACAACCTCAA
51	ACGGGCGCAAC	CGCCGCGCCGC	TGCTTAACGGT	AAGTGTGCCTG	GTTTGGCGCCT
101	CTCTGATCCT	GCTTGGCAGCG	CGCCTCAGTT	CGGGCCCTTCG	GGAACAGACT
151	GCCGCGCGAAA	CAAGCGCGCT	AGAAAAACAA	GCGGCAGGTG	CGGCACAAAC
201	CCCTGCGCTTG	TAACTCCGCGC	CCGCAACAACC	CAGGAGCTTG	CAGCGCGAAG
251	ACAAAGCCTTC	GGCCGCGCAC	AGCGAAATCA	GCGAGCTGCA	AAACGTAGGC
301	GCGCGCGCTGG	TGCTGATTAA	CGACGCGCTC	GAAACACGCA	ACATCAAAGG
351	TTTTGAAGAC	TCCGAAAGAC	TGCAACACGG	AGAAACCGCG	AAATCCCGCAC
401	GGAAGCAGGC	AAAAACAAGC	GCTGCGGAAA	AAGTGGCGGC	AACTGCCGAC
451	AGTACGGATA	CGGTAGCGGT	TGAAAAACCG	AAACGCAGTG	CGGAAACAAA
501	ACCGCAAAAA	GCGAAACGCA	TGCGCAAAAC	CAAGCCCCAA	GCCAAAGAAA
551	CCAAACACCG	CGGAAAACTG	GCGCGAAGAC	CGAAACATGC	CGCGCAAGAAA
601	ACCAACACGG	ATACGGCAAA	ATCCGACAGC	CGGCTAAAAG	AAGCTGAAAA
651	AGCCGACAG	GCTGAAAGCA	AAAAAACACG	CGAAAAGAAC	CGTTCCGCGC
701	GCAGAAAAAC	CGAAGACGCA	CAAAAAACCG	ACAAAGCGGA	CAAGACCAAA
751	ACCGCGGAGA	AGGAAAACTC	CGGTAAAAAA	GCGCGCAATT	AGGACAGGTT
801	TGCGCAAAAA	GAGACGGCCT	TACGGCTTCA	GCGCAAAATC	AAGCGCGGTA
851	GTATCGATT	GACCATCACC	GAAATTATGA	CCGACAAACG	CAAAGTTTAC
901	CGCGTCAATT	CAAGCAACTA	TAAAAACGCA	AGGGATGCGC	ACACGCGATT
951	GAAACAAATG	CGCGTACGAT	GCTTGCGCCG	TCAGGTTAAC	AATGAATA

a746.pep

1	MSENKQNEVL	SGYEQLKRRN	RRRLVTSACL	VVASCILLAA	ALLSSGPAEQT
51	AGETSGVDRN	AAGAATQPTL	KSAADKPQDL	AGEDKPSAAD	SEISEFENVG
101	APLVLLINDL	EDNSIKGLEA	SEKIQQAETA	KTAPKQAQKR	AAEKVPFATAD
151	SDTDTVAEKP	KRTAEATKPK	AERTAKTAEPK	AKETKTAEKV	ADBKPTAAEK
201	TKFDPTAKSD	VAEAKKAADK	AESKKTAEKD	RSDGKKHETA	QKTDKADTKK
251	TAEKESKSGK	AAIQAGYAEK	ERALSLORKM	KAAIGDSTIT	EIMTDNGKVV
301	RVKSSYKNKA	RDAERDLNKL	RVHGIAGQVT	NE*	

Homology with a predicted ORF from *N. meningitidis*

a746/m746; 99.7% identity in 332 aa overlap

```

              10      20      30      40      50      60
a746.pep      MSENKQNEVLSGYEQLKRRNRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
              |||||
m746          MSENKQNEVLSGYEQLKRRNRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
              10      20      30      40      50      60

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a747/m747 97.1% identity in 102 aa overlap

a747/m80195

gi1150271 (M80195) outer membrane protein [Neisseria meningitidis] Length = 272
Score = 59.3 bits (141), Expect = 6e-09
Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLVNGKQLTDSVGLEFPDYR 60
+ PW++ DL + K+ T +D+++ GW G+G N+G+L +S +E P+Y+
Sbjct: 174 INPWSEVKFDLNSRYKLNTGVTNLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95
+T + E + GD + ++ EYG RV F
Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2561>:

```

g748.seq
1      ATGAGTCAAA  ACCAACCCGC  ACAACCGACC  AAACGCAATC  TGTTCAAAAC
51     CGCCCTTGCC  TCGCGCGCAA  TCGGCGCAAT  CGGAGTTTAT  TTCGGCGGCA
101    AAAAACAGGG  CGAAACCGCC  GAACGCACCG  CCGAAGGCCA  ACACTCGGCC
151    CAAGCGCTAT  CTTGCTACGG  CGAACATCAG  CGAGGTTAGC  TTACGCGCCG
201    GCAGGCGTTT  TCCATTATGT  GCGCCTTCGA  CGTAACCCGC  CAAAGTGCCA
251    AGCAGCTGGA  AAACCTGTTC  CGCACACTGA  CCGCCCGCAT  CGAGTTTCTC
301    ACCCAAGGCG  GAGATATACA  AGACCGCGCA  GACAAACTCC  CGTCAGCCGG
351    CAGCGGCATT  TTGGGTAAAG  CTTTCAACSC  CGACGGATTG  ACCGTTACCG
401    TGGGGGTGGG  CAGCAGCCTG  TTTGACGGCC  GGTTCCGAGT  CAAAGACAAA
451    AAAACGGTTT  ATTTGACGGA  AATGCGCGAC  TTCCCAACAG  ATAAGCTGCA
501    AAAAAGATGG  TGCACGCGCG  ATTTGAGCCT  GCAAAATCTG  GCCTTCACCC
551    CCGAAACCTG  CCAAACCGCC  CTGCGCGACA  TCATCAAAAC  CACCCGCAAC
601    ACCGCGTCFA  TCCGCTGGAG  TATFCAGCGG  TGGCAGCCTA  AATCCGAACC
651    CGGCGCGATG  GCGGCGCGAC  ACCTGTTGGG  CTTCGAGAC  GGCACGGGCA
701    ACCCCAAGGT  TTCCGATCCC  AAAACCGCCG  ACGAGGTTTT  ATGGACGGCG
751    GTGGCGGCCA  ACAGCCTCGA  CGAACCGGAG  TGGGCGAAAA  ACGCGAGCTA
801    TCAGGCAGTC  CGCCTATCTC  GCGCCTTTTG  CGAGTTTGGG  GACAGGACGC
851    CGCTTCAAGA  GCAAACCGAC  ATTTTCGGGC  GGCGAAAAAT  CACGGGGGCG
901    CCGATGGACG  GCAAAAAAGA  AGCCGACCAA  CCGGATTTCC  CCAAAGACCC
951    CGAGGGTGAT  ATACGACCCA  AAGACAGCCA  TATGCGCTCG  GCGAATCCGC
1001   GCGATCCCGA  ATTCTCTCAA  AAACACTGCC  TCTTCGCGCG  GCGCTACAGC
1051   TATTTCTCGC  GAGCGCCCTC  AAGCGGACAG  CTTGATGTGC  GGCTGGTGTT
1101   CGCTCTGCTAT  CAGGCAAAAT  TTGCGGACGG  TTTCTATCTT  GTGCAAAACC
1151   TCCTCAACGG  CGAACCGCTG  GAAGAATACA  TCAGCCCCCT  CGCGCGCGCG
1201   TATTTCTCTC  TCTTGGCCGG  CGTGGGAAAA  GCGCGGATTCT  TGGGACAAGG
1251   GCTGCCGGCG  GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

1	MSQNQPAQPT	KRNLFKTALA	VGAIGAIGGY	FGGKKQGETA	ERTAESQHSP
51	QAYPCYGEHQ	AGIVTPROAF	SIMCAFDVTA	QSAQOLENLF	RTLTAIRIEFL
101	TQGGEYQDGD	DKLPSASGSI	LGKAFNPDLG	TVTGVGSSSL	FDGREGLRDKD
151	KTVHLQEMRD	FPNDKLQKSW	CGDGLSLQIC	AFTPETCQTA	LRDIIKHTAQ
201	TATVIRWSDG	WPKKSEPGAM	AARNLLGFRD	GTGNPKVSDP	KTADAEVLWTG
251	VAANSLDEAP	WAKNGSYQAV	RLIRRFVEFV	DRTPLOEQTD	IFGRRKYSGA
301	PMDGKKEADQ	PDFAKDPEDG	ITPKDGHMRL	ANPRDEPFLK	KHCLFRRAYS
351	YSRGPASSGQ	LDVLGVLFVC	QANLADGFIN	VONLNNGPEL	EYELISPFGGG

g748	AFTPETCQTALRDI IKHTAQTA VIRWSIDGWQPKSEPGAMAA RNLLGFRDGTGNPKVSDP 190 200 210 220 230 240
m748.pep	KTAEVLWLTGVAANS LDEPEWAKNGSYQAVRLIRHFVEFWDRTP LQEQTDFIGRRKYSGA 250 260 270 280 290 300
g748	KTAEVLWLTGVAANS LDEPEWAKNGSYQAVRLIRRFVEFWDRTP LQEQTDFIGRRKYSGA 250 260 270 280 290 300
m748.pep	PMDGKK EADQP D FAKDP EGDI TP KD SHIRLANPRDPEFL KKHRLFRRAYSYSRGGLASSGQ 310 320 330 340 350 360
g748	PMDGKK EADQP D FAKDP EGDI TP KD SHMLANPRDPEFL KKHRLFRRAYSYSRGGPASSGQ 310 320 330 340 350 360
m748.pep	LDVGLVFVCYQANLADGF I FVQNLLNGEPL E E YISPFGGGYFFVLPGVKG G FLGQGLLG 370 380 390 400 410 420
g748	LDVGLVFVCYQANLADGF I FVQNLLNGEPL E E YISPFGGGYFFVLPGVKG G FLGQGLPG 370 380 390 400 410 420
m748.pep	VX
g748	VX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2565>:

```

a748.seq
1  ATGAGCAAAA  ACCAACCCGC  ACAACCGACC  AGGCGCACTC  TTTTAAAAAC
51  CGCGATCGCA  GCTGGAGCAG  TCGCGCAAT  CGGAGGTTAT  CTCGCGGCAC
101  AAAAACGGGG  CGAAACCGCC  GAACGACGCG  CCGAAAGCCA  ACATCTCGCC
151  CAAGCGCTATC  CTCTGCTACG  CGAACATCAG  GCAGGCATCG  TTACGCGCCG
201  GCAGGCGTGT  TCGATTATGT  GCGCCTTCGA  CGTAACCGCG  CAAAGTGCCA
251  AGCAGCTGGA  AAACCTGTTC  CGCAGCGTGA  CGCCGCGCAT  CGAGTTTCTC
301  ACCCAAGGCG  CGGAATACCA  AGACCGCGAC  GACAAACTTC  CGCCAGCGCG
351  CAGCGGCATT  TTGGGCAACA  CCTTCAACCC  CAGCGGTTG  ACCGTTACCG
401  TGGGGGTGGG  CAGCAGCGCT  TTTGAGGGCC  GGTTCGGACT  CAAAGACAAA
451  AAACCGATTG  ATTTCGAGGA  AATGCGCGAC  TTCTCCAACG  ATAAGCTGCA
501  AAAAAGCTGG  TGGCAGCGCG  ATTTAGCCTG  GCAAATCTGT  GCCTTCACCC
551  CCGAAACCTG  CCAAGCGCCG  CTCGCGCACA  TCATCAAAAC  CACCGTCCAA
601  ACCCGCGTTA  TCCGCTGGAG  TATCGCGGAG  TGGCAGCCTA  AATCCGAACC
651  CGCGCGGATG  GCGCGCGCGC  ACCTGTTGGG  CTTCCGCGAC  GGCACGGGCA
701  ACCCAAAGT  TTCGACCCCG  AAAAGCTCCG  ACGAGGTTTT  GTGACGCGGG
751  GTGGCGCCGA  ACAGCCTCGA  CGAACCGGAG  TGGCGGAAAA  ACGCGACGTA
801  TCAGGCATGC  CGCCTTATCT  GCCACTTTGT  TGAGTTTGGG  GACAGGACGC
851  CGCTTCAAGA  GCAAAACGAC  ATTTTCGGGC  GGCGCAAAAT  CAGCGGCGCG
901  CGGATGGGAC  GCAAAAAAGA  AGCCGACCAA  CCGGATTTTG  CCAAAGACCC
951  CGAGGGGAAT  ACCACGCCCA  AAGACGCCCA  TATACGCTCG  CGCAATCCGC
1001  GCGATCCCGA  GTTCCTTAAA  AAACACCGCC  CTCTCCGCGC  CGCCTTACAG
1051  TATTCGCGCG  GACTCGCCTC  AAGCGGACAG  CTGTATGTCG  GGCTTGTGTT
1101  CGTCTGCTAT  GACGCCAAAC  TTCCGCGACG  ATTCACTCTC  GTGCAAAAGT
1151  TCCTCAACGG  CGAACCGCTG  GAAGAAATACA  TCAGCCCTTT  CGGCGGCGCG
1201  TATTTCTTCG  TCTTGCCCGG  CGTGAAAAAA  GCGCGCTTTT  TGGGGCAAGG
1251  GCTGCTGGCG  GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2566; ORF 748.a>:

a748.pap

1	MSKNQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGGKKRGETA	ERTAESQHSF
51	QAYPCYGEHQ	AGIVTPQQAQ	SIMCAFDVTA	QSAKQLENLF	RTLTARIEFL
101	TQGGEGYQDQ	DKLPAPGSGI	LGKAFNPDLG	TVTVGVGSSL	FDGRFGLKDK
151	KPIHLQEMRD	FSNDKLOKSG	CDGDLLSQIC	AFTPETCQAA	LRDIIKHTVQ
201	TAVIRWSIDG	WQKSEPGAM	AARNLLGFRD	GTGNPKVSDR	KTADEVLWGT
251	VAANSLEDEP	WAKNGSYQAV	RLIRHFVEVF	DRTPLEQETD	IFGRKRYSGT
301	PMDGKKEADQ	PDFAKDPEN	TTPKDISHRL	ANPRDPEFLK	KHRLFFRAYS
351	YSRGLASSGQ	<u>LDVGLVFVCY</u>	<u>QANLADGFIF</u>	<u>VQNLLNGEPL</u>	EYISPFGGG
401	YFFVLPGVEK	GGFLGQGLLG	V*		

Computer analysis of this amino acid sequence gave the following results:

1221

```

801 GttccctCCG GGCAAAGTGG TCGGCGGCGC GTCCGAAGTG ATTGAAGAAG
851 CGGCGGGCAG TAAATCAGC CTTGAAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TCGGACGGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCGG TTGATTGAGG CCAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGCACCAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCGGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

g749.pep

```

1 MRKFNLTAIS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIQVN
51 DNACEPMNLT VPSGQVVFNI KNSGRKLEW EILKGVVVVD ERENIAFGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
151 DYKAYVQGEV KELAATKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPIV DATEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRGLGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

m749.seq

```

1 ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAAGTACGC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAC
501 CAAACTTTT ACCGAAGCCG TCAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCGGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTTTAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGACGG
751 AAAGTATGTA CCGATGTGTA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCGG CTGATCGAGG CCAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCCT ATTAACGCGC TTGCGGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

m749.pep

```

1 MRKFNLTAIS VMLALGLTAC QPPEAEKAAP AASGEAQTN EGGSVSIQVN
51 DNACEPMELT VPSGQVVFNI KNSGRKLEW EILKGVVVVD ERENIAFGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPIV DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGLGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

              10      20      30      40      50      60
m749.pep  MRKFNLTAISVMLALGLTACQPPEAEKAAPASGEAQTNEGGSVSIQVNDNACEPMELT
          |||
g749      MRKFNLTAISVMLALGLTACQPPEAEKAAPASGETQSANEGGSVGIQVNDNACEPMNLT
              10      20      30      40      50      60

```

1223

301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKOV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
a749.pep	MRKFNLTALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	IAVNDNACEPMELT				
m749	MRKFNLTALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	IAVNDNACEPMELT				
	70	80	90	100	110	120
a749.pep	VPSGQVVFNIKNNSGRKLEWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
m749	VPSGQVVFNIKNNSGRKLEWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	130	140	150	160	170	180
a749.pep	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTTEAVKAGDIE					
m749	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTTEAVKAGDIE					
	190	200	210	220	230	240
a749.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
m749	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	250	260	270	280	290	300
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
	310	320	330	340	350	360
a749.pep	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
m749	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
	370	380	389			
a749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
m749	EADRKALQASINALAEDLAQLRGILGLKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq
 1 GTGAAACCGC GTTTTATTG GGCAGcctGC GCCGTCCTGC CGGCCGCCTG
 51 TTCGCCCGAA CCTGCCGCGG AAAAACTGT ATccgCCGCA TCCCAAGCCG
 101 CATCCACACC TGTCGCCACG CTGACCGTGC CGACCGCGCG GCGCGATGCC
 151 GTTGTGCCGA AGAATCCCGA ACgctcgcc gtgtAcgaCt ggCGGCGTt
 201 ggaTACGCTG ACCGAGCCGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG
 251 TCGCGTGGA CTATTTGCAG CCTGCATTG ACAAGCGCGC AACGGTGGGG
 301 ACGCTGTTTG AGCCCGATTG CGAATCCCTG CACCGCCACA ATCCGCAGTT
 351 TGTCAATTACC GCGGGGCCGG GTGCGGAAGC GTATGAACAG TTGGCGAAAA
 401 ACGCGACCAC CATAGATTG ACGGTGGACA ACGGCAATAT CCGCACCAGC
 451 GGCGAGAAGC AGATGGAGAC CCTGTCGCGG ATTTTCGGTA AGGAAGCGCG
 501 CGTGCGCGAA TTGAATGCGC AGATTGACGC GCTGTTCCGC CAAAAGCGCG
 551 AAGCCGCCAA AGGCAAAGGA CGCGGGCTGG TGCTGTCGGT TACAGGCAAC
 601 AAGGTGTCCG CCTTCGGCAC GCAATCGCGG TTGGCAAGTT GGATACACGG
 651 CGACATCGGC CTGCCGCGCG TGGACGAATC TTACGCAAC GAAGGGCACG
 701 GGCAGCCCGT TTCCTTCGAA TACATCAAG AGAAAAACCC CGGCTGGATT
 751 TTCATCATCG ACCGCACCGC CGCCATCGGG CAGGAAGGGC CGGCTGCCGT

```

g750      GGPGAEEAYEQLAKNATTIDLTVDNGNI RTSSEKQMETLSRIFGKEARVAELNAQIDALFA
           130      140      150      160      170      180
m750.pep  180      190      200      210      220      230
           QTREAAKGKGRGLVLSVTGNKVSAFGTOSRLASWIHGDI GLPPVDES LRNEGHGQPVSFE
           |||||
g750      QKREAAKGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDI GLPPVDES LRNEGHGQPVSFE
           190      200      210      220      230      240
m750.pep  240      250      260      270      280      290
           YIKEKNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWKRRQI IVM PAANYIVAGGA
           |||||
g750      YIKEKNPDWIFIIDRTAAIGQEGPAAVEVL DNALVCGTNAWKRRQI IVM PAANYIVAGGA
           250      260      270      280      290      300
m750.pep  300      310      320
           RQLIQAAEQLKAAFEKAE PVAAAGKKX
           |||||
g750      RQLIQAAEQLKAAFEKAE PVAAQX
           310      320

```

a750.seq

1	GTGA AACCGC	GTTT TATTG	GGCAGCCTGC	GCCGTCCTGC	TGACCGCCTG
51	TTCCGCCGAA	CCTGCCGCCG	AAAAA CTGT	ATCCGCCGCA	TCCGCATCTG
101	CCGCCCACT	GACCGTGCCG	ACCGCGCTGG	GCGATGCCGT	TGTGCCGAAG
151	AATCCCGAAC	CGCTGCGCGT	GTACGACTGG	GCGGCGTTGG	ATACGCTGAC
201	CGAATTGGGT	GTGAATGTGG	GCGCCAACCA	CGCGCGCGTG	CGCGTGGATT
251	ATTTGCA GCG	TGCATTTGAC	AAGGCGGC AA	CGGTGGGGAC	GCTGTTCCGAG
301	CCCGATTACG	AAGCCCTGCA	CCGCTACAAT	CCTCAGCTTG	TCATTACCGG
351	CGGGGATTCG	CGCGAAGCGT	ATGAACGATT	GCGCAAAATTG	GCACCAACCA
401	TAGATCTGAC	GGTGGACAA	GGCAATATCC	GCACCAGCGG	CGAAAAGCAG
451	ATGGAGACCT	TGGCGCCGAT	TTTCGGCAAG	GAAGCGCGCG	CGGCGGAATT
501	GAAGCGCGAC	ATTGACGCGC	TGTTTCCCAA	AACCGCGCAA	CGCCGCAAAG
551	GCAAAGGACG	CGGGCTGGTG	CTGTCCGGTTA	CGGGCAACAA	GGTGTCCGCC
601	TTCCGCGACG	AGTCGCGGTT	GGCAAGTTGG	ATACACGGCG	ACATCGGCCTT
651	ACCGGCTGTA	GAGCAATCTT	TACGCACA	GTCACACGGG	GACGCTGCTT
701	CCTTCGAATA	CATCAAAGAG	AAAAACCCCG	ATTGGATTTT	CATCATCGAC
751	CGTACCGCGC	CCATCGGGCA	GGAAAGGGCCG	CGGGCTGTGC	AAGTATTGGA
801	TAACGCGCTG	GTACGCGGCA	CGAAGCGCTTG	GAAGCGCAAG	CAAAATCATC
851	TCATGCTCTG	CGCGACAATC	ATTGTGCGGG	CGGGCTCGCG	GCAGTTGATT
901	CAGGCGGGCG	AGCAGTTGAA	GGAGGCGGTT	GAAAAGGCAG	AACCCGTTGC
951	GGCGGGGAAA	GAGTAG			

a750.pep	1	5	101	151	201	251	300
	VKPRFYWAAC	AVLLTACSP	PAAEKTVSA	SASAATLTVP	TARGDAVVPK		
	NPERVAVYDW	AALDTLT	VNVGATTAPV	RVDYQLQAFD	KAATVGTLFF		
	PDYEALHRYN	PQVITVGGP	AEAYEQLAKN	ATTIDLTVDN	GNIRTSGEKQ		
	METLALFPGK	EAKAAELKAE	IDALFAQTR	AAGKGKRGVL	LSVTGNKVSQ		
	FGTQSRSLASW	IHGDIGLPPV	DESLRNEGHG	QPVSFYEIKE	KNPDWIFIID		
	RTAAIGQEGP	AAAEVLDNAL	VRGTNAWKRK	QIIVMPAANY	IVAGGSRQLL		
	QAAEQLKEAF	EKAEPVAAGK	E*				

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

	10	20	30	40	50	60
a750.pep	VKPRFYAACAVLLTACSEPEAAEKTVSAASASAATLTVP	TARGDAVVPKNPERVA	VYDW			
m750	VKPRFYAACAVLLTACSEPEAAEKTVSAASASAATLTVP	TARGDAVVPKNPERVA	VYDW			
	10	20	30	40	50	60
	70	80	90	100	110	120
a750.pep	AALDTLT	ELG	VNVGATTAPVRVDYLQPAFDKAATVGT	LFEPDYEALHRYNPQLVITGGPG		
m750	AALDTLT	ELG	VNVGATTAPVRVDYLQPAFDKAATVGT	LFEPDYEALHRYNPQLVITGGPG		

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

```
m752.seq..
1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAAT TGCCAAGCTG CTGAATCTTT
101 CCGCAAAACAA TCCTGATATA GACATTCCTG ATTTTCTTAC TGAAATCAAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCCAGC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
651 TACCAAGTAA GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGCGC TGGAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTCGATTC CTATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTT TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTCATCTA TTACCAATGC GATATTATCA AGCGGCGCGT
1101 TGCCGATTG GAGCACTACA TTTCCGACAA ACAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAAATG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATT TTAGTAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAGGTT
1401 AGAAAAAAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

```
m752.pep
1  MKISRPPEFT LLQOEYMOHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51  DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKLSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTYFIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALFYVAP QDLLERLEKK *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

```
m752-1.seq
1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAAT TGCCAAGCTG CTGAATCTTT
101 CCGCAAAACAA TCCTGATATA GACATTCCTG ATTTTCTTAC TGAAATCAAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCCAGC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
```

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```
m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTGACACAGT ATTTTCCGGA AGGCTTTTGT GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCCG CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTTGC TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAG GTTTTGATGC ATCCGAATAT
601 CCTTGCTTGG CTGCCAATGA ATTTTATGCA ATGCAGACCA TCAAACAAGC
651 CGGCATTGCC GTTGACACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTC AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCGGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGACACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGCGCATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTCGT CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATT
1051 AACCTGACTA ACCACGGTAA GAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAT GAAGAAGGTC TACCGTTTAC ATTCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```
m754.pep
1  MMKSILTVSG NRMKRPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVRND PLFNEWIDGL EMKNPRILTE RDLGINARQ
151 VFQQYMAEIF HHGREVSVSG IQQMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLSSEDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDI SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKKTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*
```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```
m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTACTCCGAT ATTAACCA
101 TCTTGCTAG ACATGGATTT GAGAACATTC AGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTACC
251 GCCTTGAAAG TGATTGAAC GCACAATTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA
```

1231

	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVFPYGAELVSDGNFTAV					
a756	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVFPYGAELVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

m757.seq

```

1  ATGAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAAAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTGAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGGGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGGCG ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

m757.pep (lipoprotein)

```

1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSGLTI LTVDTPKADK
101 ITAVRVVWNT DAMPKAEKL SKAAALIAA TAPEDRTMLR DTGDDIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPSV VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

m758.seq

```

1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAC TGTGGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCGCG
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTCTAGAAA GGATTGAGCC
501 ATGA

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451 ACCGCACTCA GCAGCGTACC CTTGCTTGGA AACGGCCAGC CAAAGGCCAA
501 TGCTTACCTC GATACCGACC GCTTCCCCTA CTTGTACGA CTCGGCTCAG
551 GCACGCAACA AGTCCGCAAA GCASACGGCA CGCGTACACG AACCGCCCCG
601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAATAT TGGGGTTCCA
651 AAACCACGGC TTACTCGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCC CCCTGTTTGC CTCGACAAG
751 CATGAAAACC GCTGGGTGCT TGCGGGCGTA CTCAGCACCT ACGCCGGCTT
801 CGATAATTTT TCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCGGGCT GACCACCAAC
901 GAACTCATAT GGCGCGACAA CGGTAATGGC AACAGCACCC TGCAAGGGCT
951 CAACGAACGC ATCACCCTGC CCATTGCAAA CCCTTCGCTT GCCCCACAAA
1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA
1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
1101 AGGCGCAGCG GCATTGCAGT TCGACAGCAA CTCACCGTC GTCGGTAAAA
1151 ACCACACATG GCAAGGTGCA GCGGTATATG TAGCCGACGG CAAACGCGTC
1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC
1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCAGGGC GACATCAGCA
1301 TCGGGGAAGG CACTGTCGTA CTCGCCAAA AAGCTGCTTC AGACGGCAGC
1351 AAACAAGCAT TCAACCAAGT CCGCATCACC AGCGGCAGGG GCACGGCCGT
1401 CCTCGCCGAC AGCCAGCAAA TCAACCCGA AAACCTCTAT TTCGGCTTCA
1451 GGGGCGGACG GTCGACCTC AACGGCAACA ACCTTGCTT TACCATATC
1501 CGCCATGCGG ACGCGGCGCG GCAATCGTC AATCACAAAC CTGACCAAGC
1551 CGCGACACTG ACGTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTCG
1601 AGTGGGTGCA ATGGGGCAAC CGTCGCGAAG GCAACGCGGC GGTTTACGAA
1651 TACATCAACC CGCACCGBAA CCGTCGGACC GACTACTTCA TACTCAAACC
1701 CGGCGGCAAC CGCGCGGAAT TTTTCCCGTT AAATATGAAA AACTCAACAA
1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCGCA ACAAGTCGCC
1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG
1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG
1901 AAGCAGCCAT AGAAAAAACC CGCATATCG CAAATGCCGC CGTATACGGC
1951 CGGCCCCAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
2001 ACGCACCAGC AGCACGCTGT TGCTCAACGG CGGCATGAAC CTTAAGCGGG
2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTACGGCAG GCCCGTACCC
2101 CATGCCCTAC ACCACCAGGC CAAACGCGAA CCGTTCTTG AAAACGAATG
2151 GACCGACGGC AGCTTCAAGG CTGCACGGTT CACCCTGCGA AACCATGCCC
2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA
2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
2301 ATGCTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCCAACCGCG
2351 TTTTAAAGC CGAAACTAT CGTGCACTAC CTGCAACGCA AGTACGCGGC
2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT
2451 GTACGGCAGC ATCCGTGCGG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG
2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGGCGC ACTGACGCTT
2551 GACGGCGCAC AAATTACCCT GAACCCCGAT TTCGCCAATA ATACACACAA
2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTGCGCA
2651 CATTCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
2701 AAACCTGGAAG GGGACAGCCG CGGCGCATTC CAAATCCAGC TCAAAAACAC
2751 CGGACAAGAA CCTCAAACAA CCGAATCGCT TGCACTTGTG AGCCTCAATC
2801 CGAAACACAG CCACCAAGCC CGATTACCC TCCAAAACGG CTATGCCGAT
2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAA AACACAACG GATACAGCCT
2901 GTACAACCCG CTCAAAGAGG CCGAACTTCA AATTGAAGCC ACGCTGCGG
2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC
3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC
3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG
3151 CGTGCCCAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG
3201 TCAGGTTGCC AAAGCCGCGG ACACGAACGA CCTGACACTC TTCGAAACCG
3251 AACTGGATAC GTATATAGAA CGTGTAGAAA TGGCCGAATC CGAACTTGAC
3301 AAAGCACGGC AAGGCGGCGA TGCGCAAGCC GTCGAAACAG CCCGGCACGC
3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA
3401 CCGCGTTGC CGGCATCCGT ATGCCGAACC TGCCCGAAT GATCAGCCGG
3451 TCGGCCAACA CCGCGTTTC CGAACAGGCC GCCTACAATA CCGGCGGCA
3501 ACAGGCGGGA CGCCGATCG ACCGCCACCT TACCGATCCG CAGCAGCAA
3551 ACATCTGGCT GGAACCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
3601 CACCGTCCCT ACCAACAAC TACCAACTAT GCACATATCG GCATCCAAAC
3651 CGGCATCACC GACCGTCTCA GTGTCGGTAC GATTTTAACC GATGAGCGCA
3701 AAACAACCG TTTTGATGAA GCGTATCCG CCCGAAACCG CAGCAACGGC

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1235

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1  ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCTGCT GCGTGTTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGCGCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCACG CTGCCCCAAC TGTTCGCCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTG TACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGCG AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGGTCTC CGCGTCCCGC CGAGAAAAAC AACCGGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GCGCGGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGCCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTTAAATGTC ACAGCCACGA CGTGTTCCGC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCGGAT CGGAAAGCCG ATTCCAATTA TACGTTGCGG GCGAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGC GCG
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAAGCGT CGCTTTAGAT
1201 GGTTCGCGC CTTTGCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCCTC TGGAAGGTTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCCTC CCAACTCTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCCG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTCGTTC TACCGCATGA AGGATAAAAA CGCCGCGCGA
1651 CCGCTGGACT CAAACAACAA AAAAACCCGT TACGCGCAT TGGGCAACG
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAAAATCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAACACCGC
1801 TCCAATTCGC GCGACGAAGG CATCTTCCTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAGGC
1951 GGTATGCCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAACT
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCC
2051 GCGTCGGCAG CGAGAGCACC TTTAACATTC CCGGTTCCGA GCGCAGCCTG
2101 ACGGCAAACC TCGGTTACAG TTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1  MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKG QRSYNAIATE
51  KNGDYSSFAA TVGTRIPASL REIPQSVSII TNQQVKDRNV DTFDQLARKT
101 PGLRVLNSDD GRSSVYARGY EYSEYNIDGL PAQMOSINGT LPNLFADFVR
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THKQYKAED
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQRRR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHSHDVFA
301 DLKHYFGNGG YGKVGMRYSR RKADSNYTF GSKLNNTGQA DVAGLGTDIK
351 QKAFVVDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSVLAD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHHKI ESGDGKTLHK ASKTKFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME CTEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAY YRFTPKLKLQ INADNIFNRH YYARVGSEST FNIPGSEERSL
701 TANLRYSF*
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1237

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1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATCCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCAGGCT TTGCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

```

m761.pep
1 MKISFHLALL PTLIIASFPV AAADTDNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQITDNLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQOTD NKTLLSSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSASFASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFENSENKL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVENADPE YTRQYETGVK SSWLDDRST TLSAYQIERF NRYRPPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRSLGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFERY TPENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAANLLNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

```

a761.seq
1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCCG CCTACGATAT GCGCGCGGAA AGCATTTTCC TCGCGCGGTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT
451 CCGTCTCTCG TGCTTTATGG GCGTACCAAC GCGCGCGGTG TCATCAACAT
501 GGTCAAGCAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTCGTG GGCAAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AACAAAAACG TCGCCATCCG TCTCACCAGC GAAGTCGGGC GCGCCAATTC
651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT
701 CCGTCAAACT CGACAACGGC TTGAAGTGGA CCGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
801 CTTCCGACTG CCTTACCGCA TGGGGTTTCG CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTTCGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAT
1001 ACGCTTGGA GACAGACGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGTAA AACCACCTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCGATTG AAATTCGTCC
1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCGAAAA CAACTACACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGCGGCT ATTTGAGCAT CGATACGTTG
1501 TCTTCGCGCG GTTCAACGCG CGACCCGAG TACACCCGCC AATACGAAAC
1551 CGGCGTAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCGCA TCCAAAAAAC
1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTTCG GCGGCGTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

```

1239

```

m761.pep  NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
          |||
a761      NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
          370      380      390      400      410      420

          430      440      450      460      470      480
m761.pep  QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSSRQYSGHSFSPNIGAVWNINPVHTLYAS
          |||
a761      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSSRQYSGHSFSPNIGAVWNINPVHTLYAS
          430      440      450      460      470      480

          490      500      510      520      530      540
m761.pep  YNKGFPYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDRLSTTSLAYQIERF
          |||
a761      YNKGFPYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDRLSTTSLAYQIERF
          490      500      510      520      530      540

          550      560      570      580      590      600
m761.pep  NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
          |||
a761      NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
          550      560      570      580      590      600

          610      620      630      640      650      660
m761.pep  RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYSNRNKEVTTLPGFARVDAM
          |||
a761      RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
          610      620      630      640      650      660

          670      680      690      700
m761.pep  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
          |||
a761      LGWNHKNVNVTFAAANLFNQKYWRSDSMPGNPRGYTARVNYRFX
          670      680      690      700

```

g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTATAC GATAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTATGAG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT
401 CACTTTTAGT TTCTAATTTT ATTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1  MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLVLQCTIL FHSQKIYFIT
51  LFLLFIFNEV TKSIYMAIIY PILYFFTICK YYPYSRKVII LLSLALSIYF
101 SEMDFYFFSI YSDNLSYTE PLHLYIPIII NFFSLLVSNF ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTATAC GATAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

```

1241

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

m763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFOASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RKGMSVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

a763.seq

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTCAC CTTGCCACTA
151 TCCCTTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTCCGGTG ATTTTCAAGC GTCCCATTA CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACTTAA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCAAG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCGGCC CATGCGGCGG
551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACCACTT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCAGCTAT CTGCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAAGCA GCGGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAAAT
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCC
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGTTAGGG TTGGAAACGG TATTTCGGGA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

a763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFOASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RKGMSVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

m763 / a763 99.8% identity in 467 aa overlap

```

          10      20      30      40      50      60
m763.pep  MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          10      20      30      40      50      60
a763      MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          10      20      30      40      50      60

```

1242

m763.pep	70	80	90	100	110	120
	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAAFLPHVSNASYQRQPPSISSTRETQ					
a763	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAAFLPHVSNASYQRQPPSISSTRETQ					
	70	80	90	100	110	120
m763.pep	130	140	150	160	170	180
	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
a763	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
	130	140	150	160	170	180
m763.pep	190	200	210	220	230	240
	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEIIVLAEKQTYENQLNDY					
a763	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEIIVLAEKQTYENQLNDY					
	190	200	210	220	230	240
m763.pep	250	260	270	280	290	300
	TDLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
a763	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
	250	260	270	280	290	300
m763.pep	310	320	330	340	350	360
	QNSRYPTVSAHVGYNLYTSSAQNNNDYHYRGKGMVGVQNLPLYTGGELSGKIHEAEA					
a763	QNSRYPTVSAHVGYNLYTSSAQNNNDYHYRGKGMVGVQNLPLYTGGELSGKIHEAEA					
	310	320	330	340	350	360
m763.pep	370	380	390	400	410	420
	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKSTETGQQYGIR					
a763	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKSTETGQQYGIR					
	370	380	390	400	410	420
m763.pep	430	440	450	460		
	NRLEVIRARQEVAQAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
a763	NRLEVIRARQEVAQAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
	430	440	450	460		

1243

g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```

m764.seq
1  ATGTTTCTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCGCGCATT TGGAACGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGT TTTATTATGG CGTTTGCCTG
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGGGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCGGTGGG GCGCATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCGGTTTG CCGGCCGACA ATTTTATTTC GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACCGGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CCGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG CCGGTGTGGT GCAGGCTGCC
1051 CAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGTG GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTCAGG GCGGCTATGA ATGTACGGGC GGAGATTAA
1351 ACGGGTAAAC GCGGGGTGCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

```

m764.pep
1  MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEEQAFI PAHLELTDPF
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDQOHVKQGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGVEQGG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEK
451 TGKRRVLDYL LSLPLQTKLDE SFRER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```

a764.seq (partial)
1  ATGTTTCTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCGCGCATT TGGAACGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGT TTTATTATGG CGTTTGCCTG
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGGGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCGGTGGG GCGCATCGAG CAGCAGAAAA

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1244

```

701 CAGCAGACTA CCGCCGTTTG CGGCGCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAGG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCTT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGTG GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ATATACCTTG AATATTGACG
1301 GCAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

```

a764.pep (partial)
1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEEQAF LPAHLELTDTP
51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVKGQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSAALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVVPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHTDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

m764.pep	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVAVRDQLEPPKRTAEEQAF LPAHLELTDTPVSAAPKWAAR					
a764	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVAVRDQLEPPKRTAEEQAF LPAHLELTDTPVSAAPKWAAR					
m764.pep	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVKGQE					
a764	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVKGQE					
m764.pep	130	140	150	160	170	180
	TLAELEAVGTDSDDVVQSEQALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSGLSDAD					
a764	130	140	150	160	170	180
	TLAELEAVGTDSDDVVQSEQALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSGLSDAD					
m764.pep	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQSAALRGHQAE LQSAKAQE QKLVSVAIEQQKTADYRRL					
a764	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQSAALRGHQAE LQSAKAQE QKLVSVAIEQQKTADYRRL					
m764.pep	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA					
a764	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA					
m764.pep	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVVPDD					
a764	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVVPDD					
m764.pep	370	380	390	400	410	420
	DKMDVEVLVLNKNKDIGFVEQQQDAVVKIESFPYTRYGYLTGKVKSVSHTDAVSHEQLGLVYT					

1245

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|||||
a764      DKMDVEVLVLNKKDIGFEVQQDAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
              370      380      390      400      410      420

              430      440      450      460      470
m764.pep    AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFRERY
              |||||
a764      AVVSLDKHTLNIDGK
              430
```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```
m765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTGAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCCTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTGCGG TCGTTGCTGA TGTTTACGGT CATGATTCCG CCACAATGAA
201 CGCTGCGGCT GCCAAAGATT ATATGAAAAC GGTGAGTTA AACAACTCTG
251 CCGGCAATGT CGATACCACA TCCAGAACAG CCCGCAGGGT GCAGGCAGTA
301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACCGCTGGG
401 CAATGCCCGG TGGAAAAATG GCGTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
751 TNPELVGLGM DILGTYGLTL PYRSLEEEA DEGGMMLMAQ AGYHPAAAVR
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGCGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```
m765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKEYI SFLPSFKRIL CLSAVISVLG
51  ACVVVADVYG HDSATMNAHA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FFRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDDIEIAAI MGHEMTHALH ERGKNKVGQQ ILTNTAAQIG TQIILDKKPD
201 TNPELVGLGM DILGTYGLTL PYRSLEEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT STHPTNNARIE NLKRLPLPTVM PVYEQSVRNK
301 GRVKKRRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```
a765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTGAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCCTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTACGG TCGTTGCTGA TGTTTACGGT CAGGATTCCG CCACAATGAA
201 TGCTGCGGCT GCCGAAGATT ATATGAAAAC GGTGAGTTG AACAACTCTG
251 CCGGCAATGT CGATACTACA TCCAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACCGCTGGG
401 CAATGCCCGG CGGGAAAATG GCGTTTATA CGGGGATAGT CGATAAACTT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAACCGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGCGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```
a765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKEYI SFLPSFKRIL CLSAVISVLG
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1246

```

51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGHHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTGDGEIAAI MGHMETHALH EHGNKVKGQK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSL EEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT STHPTNNARIE NLKRLPTVM PVYEHVSRNK
301 GRVNKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

	10	20	30	40	50	60
m765.pep	MLRCRPKSVLDS	GI FLKFNFLRSKPKYEIS	FLPSFKRILCLSAVIS	VLGACAVVADVYG		
a765	MLRCRPKSVLDS	GI FLKFNFLRSKPKYEIS	FLPSFKRILCLSAVIS	VLGACTVVADVYG		
	10	20	30	40	50	60
m765.pep	HDSATMNAAAKDY	MKTVELNKSAGNVD	TTSRTARRVQAVFRR	MLPYADAANNTSHK	FDW	
a765	QDSATMNAAAKDY	MKTVELNKSAGNVD	TTSRTARRVQAVFR	MLPYADAANNTGHK	FDW	
	70	80	90	100	110	120
m765.pep	KMTVFKNDELNAW	AMPGGKMAFYTGIV	DKLKLTDDEIAAIM	GHMETHALHEHGK	NKVGQ	
a765	KMTVFKNDELNAW	AMPGGKMAFYTGIV	DKLKLTDGEIAAIM	GHMETHALHEHGK	NKVGQ	
	130	140	150	160	170	180
m765.pep	ILTNMAAQIGTQI	ILDKKPDTNPELV	GLGMDILGTYGLT	LPYSRSL EEEA	DEGGMMLMAQ	
a765	ILTNMAAQIGTQI	ILDKKPDTNPELV	GLGMDILGMYGIT	LPYSRSL EEEA	DEGGMMLMAQ	
	190	200	210	220	230	240
m765.pep	AGYHPAAAVRVWE	KMNQENDQNGFIYA	ITSTHPTNNARIEN	LKRLPTVMPVYE	QSVRNK	
a765	AGYHPAAAVRVWE	KMNQENDQNGFIYA	ITSTHPTNNARIEN	LKRLPTVMPVYE	HSVRNK	
	250	260	270	280	290	300
m765.pep	GRVNKNRRRX					
a765	GRVNKNRRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

g767.seq

```

1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTGCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTTCG TACATTGCCA TCATTTGAT CCTTTGTA1 TGAAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTTAAAGCAG TTTACGAACA
351 AAAAATCCGT TTGGAACA GGGCTGTTGC CGGAAATGG GCTTTATCTC
401 AAAAAGGTTT TGACGGCAAA AAAGTATGCG GCGCCTATGA TTCCCCGAA
451 GCTGCCGCCG TCGCATTAAA AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

g767.pep

```

1  MKFKHLLPLL LSAVLQAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEF*G
51  YFCVHCHHFD PLLKLKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

```

1247

```

101 GLKYQANSV FKAVYEOKIR LENRAVAGKW ALSQKGFQDGK KLMRAYDSPE
151 AAAVALKMQK LTEQYQIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

```

m767.seq
1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCCTCA AGAACAGTCG GGTAATAATTG AGGTTTTTGA ATTTTTCGGC
151 TATTTCTGCG TACATTGCCA TCATTTTCGAT CCTTTGTTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATG CCTATTTGAG GACGGAGCAC GTGGTCTGGC
251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CGGCTGCCGT CAATTTGTCTG
301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGGAATAACA GGTGCGTTGC CGGAAATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AAATGATGC GCGCCTATGA TTCCCGCGAA
451 GCTGCCGCGC CCGCATTAAA AATGCAGAAA CTGACGGAAC AATACCGCAT
501 CGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAGAATTT GGTTCGCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

```

m767.pep
1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG
51 YFCVCHHHFD PLLLKLKAL PSDAYLRTEH VVWQPEMLGL ARMAAANLS
101 GLKYQANPAV FKAVYEOKIR LENRSVAGKW ALSQKGFQDGK KLMRAYDSPE
151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

```

m767/g767      95.8% identity in 214 aa overlap

              10      20      30      40      50      60
g767.pep      MKFKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPQEQSGKIEVLEFFGYFCVCHHHFD
              |||
m767           MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPQEQSGKIEVLEFFGYFCVCHHHFD
              10      20      30      40      50      60

              70      80      90      100     110     120
g767.pep      PLLLKLKALPSDYLRTTEHVVRPEMLGLARMAAAVKLSGLKYQANSVFKAVYEOKIR
              |||
m767           PLLLKLKALPSDAYLRTEHVVRPEMLGLARMAAANLSGLKYQANPAVFKAVYEOKIR
              70      80      90      100     110     120

              130     140     150     160     170     180
g767.pep      LENRAVAGKWSQKGFQDGKKLMRAYDSPEAAVALKMQKLTQYQIDSTPTVIVGGKYR
              |||
m767           LENRSVAGKWSQKGFQDGKKLMRAYDSPEAAAAALKMQKLTQYRIDSTPTVIVGGKYR
              130     140     150     160     170     180

              190     200     210
g767.pep      VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
              |||
m767           VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
              190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

```

a767.seq
1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCCTCA AAAACAGTCG GGCATAATTG AGGTTTTTGA ATTTTTCGGC
151 TATTTCTGCG TACATTGCCA TCATTTTCGAT CCTTTGTTAT TGAAATGGG
201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGTCTGGC
251 AGCCTGAAAT GCTCGGTTTG GCAAGAATGG CTGCTGCCGT CAAGCTGTCA
301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGGAATAACA GGTGCGTTGC CGAATAATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AAATGATGC GCGCCTACGA CTCTCTGCG

```

1248

```

451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTGCCCCAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
1  MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPOKQS GKIEVLEFFG
51  YFCVHCHHFD PLLKLGLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
101 GLKYQANPAV FKAUYEQKIR LENRSVAEKW ALSQKGFDDG KLMRAYDSPA
151 AAAAASKMQQ LTEQYRIDST PTVVVGKRYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

```

m767/a767 96.7% identity in 214 aa overlap

      10      20      30      40      50      60
a767.pep MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPOKQSGKIEVLEFFGYFCVHCHHFD
m767      MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPOKQSGKIEVLEFFGYFCVHCHHFD
      10      20      30      40      50      60

      70      80      90     100     110     120
a767.pep PLLKLGLKALPSDAYLRTEHVWQPEMLGLARMAAAVKLSGLKYQANPAVFAVVEQKIR
m767      PLLKLGLKALPSDAYLRTEHVWQPEMLGLARMAAAVNLGLKYQANPAVFAVVEQKIR
      70      80      90     100     110     120

      130     140     150     160     170     180
a767.pep LENRSVAEKWALSQKGFDDGKLMRAYDSPAAAAAASKMQQLTEQYRIDSTPTVVVGKRYR
m767      LENRSVAGKWALSQKGFDDGKLMRAYDSPAAAAALKMQQLTEQYRIDSTPTVVVGKRYR
      130     140     150     160     170     180

      190     200     210
a767.pep VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
m767      VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
      190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
1  ATGAATATCA AACAAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCACGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCAATCA CGCGGTTAT GAAGACCTGC TCAAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
1  MNIKQLITAA LIASAAFATQ AAPQKPVSA QTAQSAVWI DVRSEQEFSE
51  GHLHNAVNI PVDQIVRRIE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
101 YTNVANHGGY EDLLKKGMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
1  ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCACGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGGCATTTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC

```

m768.pgp

```

1  MNIKHLITAA LIA2AAFAAQ AAPQKPVSA AQAQHPAVWI DVRSECEFSF
51  GHLHNAVNIP VDQIVRR2IHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
101 YTNVANHG2GY EDLLKKGMK*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m768/q768 96.6% identity in 119 aa overlap

		10	20	30	40	50	60
g768.pep		MNIKQLITAALIASAAFAATQAA	PQKPVSAQAQ	TAQHS	AVWIDVR	SEQEFS	EGHLHNAVNIP
m768		MNIKHLITAALIASAAFAAAQAA	PQKPVSAQAQ	TAQHPAVWIDVR	SEQEFS	EGHLHNAVNIP	
		10	20	30	40	50	60
		70	80	90	100	110	120
g768.pep		VDQIVRR	IYAAPDKDTPV	NLYCRSGR	RAEAAALQEL	KKAGYTNVAN	HGGYEDLLKKGMKX
m768		VDQIVRR	IIEAAPDKDTPV	NLYCRSGR	RAEAAALQEL	KKAGYTNVAN	HGGYEDLLKKGMKX
		70	80	90	100	110	120

a768.seq

1	ATGAATATCA	AACACCTGAT	TACCGCCGCA	CTCATTGCCT	CAGCCGCCTT
51	TGCCCGCAGC	CGAGCCCGCG	AATACCCCGT	ATCCGCGCGC	CAAAACGGCCG
101	AACATCTACG	CTTTTGGATG	GATGTCCGCA	GCGAACAGGA	ATTATAGCAAA
151	GGTCATTTCG	ACAACGCGGT	CAACATCCCC	GTGCACCAA	TCGTCCGCCG
201	CATACACGAA	CGCCGCGCCG	ACCAAGACAC	CGCGGTCAAC	CTCTACTGCG
251	GCAGCGGACG	CGGTGCGGAA	CGCCGCTTCC	AGGAAGTCAA	AAAGGACAGCG
301	TATACGAATG	TTGCCAATCA	CGGGCGTTAT	GAAGACTCTGC	TCAAAAAGG
351	GATGAAATGA				

a768.ppt

1 MNIKHLITAA LIASAAFAAO AAPQKPVSA AQAQSAVMI DVRSEQEFSE
51 GHLHNAVNI PVDQIVRR IIHE AAPDKDTPVN LYCRSGRAE AALQELKKAG
101 YTNVANHGGY EDLLKKGMK*

Homology with a predicted ORF from *N meningitidis*

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MN	IKHLITAA	LIASAAFAAQAAPQKPVSAQAQHS	AVWIDVRSEQEFSE	GH	LHN
m768	MN	IKHLITAA	LIASAAFAAQAAPQKPVSAQAQHPAVWIDVRSEQEFSE	GH	LHN	AV
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	VDQIVRR	IHEAAPDKDTPV	NLYCRSGRR	EAAQLQELK	KAGYTNVAN	HGGYEDLLKKG
m768	VDQIVRR	IHEAAPDKDTPV	NLYCRSGRR	EAAQLQELK	KAGYTNVAN	HGGYEDLLKKG
	70	80	90	100	110	120

1250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq
 1 TTGATAATGG TTATTTTTTA TTTTATTTT TGTGGGAAGA CATTATATGCC
 51 TGCACGAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
 101 CCGAAGaAAC ACCgtgCGAA CCGGATTTGA GAAGCCGTCC CGAGTTCAGG
 151 CTTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGGAGAAGG TACCGGGGCA
 201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
 251 AAAATCCCCGA ATTGTGTGCG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
 301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
 351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
 401 AGGGCAGGCT GAAGGAGGCG GTTCCCAT ATTCCGGAAT GATTGCCGCC
 451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
 501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
 551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
 601 TTGCGCGAAC GCGATGCGTG GAAGGTAAAC GGCAGTTTCA GCGTTACCCG
 651 CGAACACAAT ATCAACCAAG CCCCAGAAAC GCAGCAGTAC GGCATTTGGA
 701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
 751 GAGAAAAAAT GGTGCTGAA AACCGGTGG TACACGACGG CGGGCGGCGA
 801 CGTGCCCGG AGGGTTTATC CGGGGAATAA GAAATTCAAC GATATGACGG
 851 CAGGTGTTTC CGGCGGCATC GGTTTTGCCG ACCGCGGTAA AGATGTCGGG
 901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
 951 CGCCAACGCG GCACGCCTTT ATTTCAACCG TTGGCAAAAC AGAGATGGC
 1001 AAACGCTGTC TTCGGCGGAG TGGGGGCGTT TGAAGAATAC GCGCCGGGCG
 1051 CGTTCCGACA ATACCCATTT GCAAATTTCC AATTGCTGTT TGTTTTACCG
 1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTAC CCGCAGCGCA
 1151 ACCCCGCGCA CCGTGGCGAC AATTTCACCG GTTACGGCCT GCGCTTTGCC
 1201 TTGGGGCAGG AATGGGGCGG CAGCGGCTTG TCTTCGCTGT TCCGCTCGG
 1251 CGTGGCGAAA CGGCATTATG AAAAACCCTG CTTCTTCAGC AGTTTAAAG
 1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCCTTGAG CCTTTGGCAC
 1351 CGGGCATTGC ATTTCAAAGG CATCACGCGG CGCCTGACGC TGTCGCAACG
 1401 CGAAACGTGG AGCAACGATG TGTTAAACGA ATACGAGAAA AACAGGGCGT
 1451 TTGTCGAGTT TAACAAAACG TTCTGA

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep
 1 LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAEETPCE PDLRSRPEFR
 51 LHEAEVKPID REKVPQVRE KGVVLQVDGE TLLKNPELLS RAMYSVVSN
 101 NIAGIRVILP IYLQARQDK MLALYAOGIL AQAEGRVKEA VSHYRELIAA
 151 QPDAPAVRMR LAAALFEDRQ NEAAADQFDR LKTEDLPPQL MEQVELYRKA
 201 LRERDAWKVN GGFSVTREHN INQAPKQQQY GNWTFPKQVD GTAVNYRFGA
 251 EKKWSLKNGW YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
 301 LAVFHERRTY GNDAYSANG ARLYFNWRQT PRWQTLSSAE WGRLLKNTRRA
 351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDYF RERNPADRGD NFNRYGLRFA
 401 WGQEWGSGSL SSLFRLGVAK RHYEKPFFFS SFKGERRRDK ESDTSLSLWH
 451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq
 1 TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCTGCACG
 51 AAACAGATGG ATGCTGCTGC TGCTTTTATT GGCAAGCGCG GCATATGCCG
 101 AAGAAACACC GCGCAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
 151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGAGGT
 201 CGGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
 251 ATCCCGAATT GTTGTCCGCG GCGATGTATT CCGCAGTGGT CTCAAACAAT
 301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
 351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
 401 GTAGGGTGAA GGAGGCGATT TCCCATTTACC GGAATTGAT TGCCGCCCAA
 451 CCCGACGCGC CGCCGCTCCG TATGCGTTTG GCGGCAGCAT TGTGTAAAAA
 501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
 551 ACCTGCCGCG GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
 601 CGCGAACGCG ATGCGTGAA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
 651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AATGGAATT
 701 TCCCGAAACA GGTGGACGCG ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
 751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
 801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
 851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GCGCGAAAAG TGCCGGGCTG
 901 GCAGTGTTC ACGAACGCGG CACCTACGGC AACGACGCTT ATTCTTACAC
 951 CAACGCGGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
 1001 CGTTGTCTTC GCGGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
 1051 TCCGACAATA CCCATTTGCA AATTTCACAT TCCTGGTGT TTTACCGGAA
 1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGG GAGCGCAACC
 1151 CCGCGGACCG GGGCGACAAT TTCAACCGTT ACGGCTGCG CTTTGCCTGG
 1201 GGGCAGGAAT GGGGCGGCGA CGGCTGTCT TCCTGTGTC GCCTCGGCGC

1251

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1251 GGCAGAACGG CATTATGAAA AACCCGGCTT TTTCAGCGGT TTAAAGGGG
1301 AAAGCGCGAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCGA
1401 AACCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

```

m769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPGQVREK GKVLQIDGET LLKNPELLSR AMYSVVSN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151 PDAPAVRMRL AAALFENRON EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NQAPKQQYQ KWTFFPKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAL
301 AVFHERRYTG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGDFYR ERNPADRGDN FNRYGLRFAW
401 GGEWGGGSL SLLRLGAAKR HYEPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

m769/g769 95.1% identity in 492 aa overlap

```

               10      20      30      40      50      59
g769.pep      LIMVIFYFCGKTFMPARNRWMLL-PLLASAAYAETPCEPDLSRPEFRLHEAEVKPI
               |||||  |||||  |||||  |||||  |||||  |||||
m769          LIMVIFY--FCGKTFMPARNRWMLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPI
               10      20      30      40      50

               60      70      80      90      100     110     119
g769.pep      DREKVPQVREKGVQVLDGETI IYNPEL SRAMYSVVSNNIAGIRVILPIYLQQAQD
               |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769          DREKVPQVREKGVQVLDGETL LKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQD
               60      70      80      90      100     110

               120     130     140     150     160     170     179
g769.pep      KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAADQFD
               |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769          KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAADQFD
               120     130     140     150     160     170

               180     190     200     210     220     230     239
g769.pep      RLKTEDLPPQLMQVELYRKALRERDAWKVNGGFSVTREHNI NQAPKQQYGNWTFPKQV
               |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769          RLKAENLPPQLMQVELYRKALRERDAWKVNGGFSVTREHNI NQAPKQQYGNWTFPKQV
               180     190     200     210     220     230

               240     250     260     270     280     290     299
g769.pep      DGTAVNYRFGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV
               |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769          DGTAVNYRLGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA
               240     250     260     270     280     290

               300     310     320     330     340     350     359
g769.pep      GLAVFHERRYTGNDAYSANGARLYFNRWOTPRWQTLSSAEWGRLKNTRRARS DNTHLQI
               |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769          GLAVFHERRYTGNDAYSYTNGARLYFNRWOTPKWQTLSSAEWGRLKNTRRARS DNTHLQI
               300     310     320     330     340     350

               360     370     380     390     400     410     419
g769.pep      SNSLVFYRNARQYWTGGDFYRERNPADRGDNFNRYGLRFAWGGEWGGGSLSLRLGVA
               |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769          SNSLVFYRNARQYWMGGDFYRERNPADRGDNFNRYGLRFAWGGEWGGGSLSLRLGAA
               360     370     380     390     400     410

               420     430     440     450     460     470     479
g769.pep      KRHYEPGFFSSFFKGERRRDKESDTSLSLWHRALHFKGITPR LTLSHRETRS NDVFNEYE
               |||||  |||||  |||||  |||||  |||||  |||||  |||||

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1252

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m769      KRHYEKPFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSDNVFNEYE
           420      430      440      450      460      470

           480      490
g769.pep  KNRAVFVNKTFX
           |||||
m769      KNRAVFVNKTFX
           490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTT TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCTATGCCC
101 AAGA AACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGAAAAAA GGAAAGTTT TGCAGATTGA CCGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCCGTA TCCGCGTTAT TTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCAACAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATACCG GGAATTGAT TGTGCGCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCGGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGCGCAG GTTATCCGG GGAATAAGAA ATCAACGAT ATGACGCGAG
851 GCGTTTCCGG CCGCATCGGT TTGCGGACC GCGGCAAGA TCGCGGCGT
901 GCAGTGTTC ACGAACGCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAAACCCG AAATGGCAAA
1001 CGTTGTCTTC GCGCGAGTGG GCGCGTTTGA AGAATACGCG CCGGCGCGCT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TCGCGCCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCGACCGG GGGCGCAAT TTCAACCGTT ACGGCGTGGC CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCG CCGCTGTCT TCGCTGTTGC GCCTCGGCGC
1251 CCGAAACGG CTTATGAAA AACCCGCTT TTTACGCGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CTTGAGCCT TTGGCACCGG
1351 RERDQLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRVGLRFAW
1401 AQEWGSGSL SLRLGAAR HYEKPFFSG FGERRRDKE LNTSLSLWHR
1451 ALHFKGITPR LTLSHRETR SDNVFNEYKN RAVFVNKTF *

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAEETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVRMRL AAALFENRQN EAAADOFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTRHNNI NQAPKRQOYG KWTFPKQVDG TAVNYRLGAE
251 KKWSLKNWGY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRVGLRFAW
401 GQEWGSGSL SLRLGAAR HYEKPFFSG FGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETR SDNVFNEYKN RAVFVNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

```

m769/a769  99.8% identity in 490 aa overlap

           10      20      30      40      50      60
a769.pep  LIMVIFYFCGKT FMPARNRWMLLLPLLASAAYAEETPREPD LRSRPEFRLHEAEVKPIDR
           |||||
m769      LIMVIFYFCGKT FMPARNRWMLLLPLLASAAYAEETPREPD LRSRPEFRLHEAEVKPIDR
           10      20      30      40      50      60

           70      80      90      100     110     120
a769.pep  EKVPQVREK GKVLQIDGET LLKNPELLSRAMYS AVVSNNIAGIRVILPIYLQQAQQDKM

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1253

```

m769      |||||
           EKVPQGVREKGV LQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM
           70      80      90      100     110     120

a769.pep   130      140      150      160      170      180
           LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
           |||||

m769      LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
           130      140      150      160      170      180

a769.pep   190      200      210      220      230      240
           KAENLPFQLMEOVELYRKALRERDAWKVNGGFSVTRHNNINQAPKROQYGKWTFFPKQVDG
           |||||

m769      KAENLPFQLMEOVELYRKALRERDAWKVNGGFSVTRHNNINQAPKROQYGKWTFFPKQVDG
           190      200      210      220      230      240

a769.pep   250      260      270      280      290      300
           TAVNYRLGAEEKWVSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
           |||||

m769      TAVNYRLGAEEKWVSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
           250      260      270      280      290      300

a769.pep   310      320      330      340      350      360
           AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLEKNTRRARSDNTHLOISN
           |||||

m769      AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLEKNTRRARSDNTHLOISN
           310      320      330      340      350      360

a769.pep   370      380      390      400      410      420
           SLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAGWQEWGGGSLSLRLGAAGR
           |||||

m769      SLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAGWQEWGGGSLSLRLGAAGR
           370      380      390      400      410      420

a769.pep   430      440      450      460      470      480
           HYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSDNVFNEYEKN
           |||||

m769      HYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSDNVFNEYEKN
           430      440      450      460      470      480

a769.pep   490
           RAFVEFNKTFX
           |||||

m769      RAFVEFNKTFX
           490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCCG
51  CAGCGCGCAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCGC GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTTCT TTTGACGAAA CCGCGTGCGC CAAACCGAAA
301 GAAGTTTTC AAGCGCGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTTACAGCG
401 ATAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCGACGGG GTGCAAGCCG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTC CAACCCGATA AAAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1  MNRLLLLSAA VLPTACSGSE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKRGTFGA FKSRIQVRYV DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FSGGIPQTDG VQADTSGKLL AGACIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCCG
51  CAGCGCGCAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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1254

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101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGC GTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCTCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

```

m770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKHGASFA FKSQIVRYY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

```

m770/g770 93.5% identity in 186 aa overlap

g770.pep      10      20      30      40      50      60
MNRLLLLSAAVLPTACGSGETDKIGRASTVFNMLGKNDR I EVEGFDDPDVQGVACYISYA
|||||:|||||:|||||:|||||:|||||:|||||:
m770          10      20      30      40      50      60
MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDR I EVEGFDDPDVQGVACYISYA

g770.pep      70      80      90      100     110     120
KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKKEVFKRGTGFQFVSRQIVRYY
|||||:|||||:|||||:|||||:|||||:|||||:
m770          70      80      90      100     110     120
KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKKEVFKHGASFAFKSRQIVRYY

g770.pep     130      140      150      160      170      180
DPKRKAFAFYLVSVDKIVQGSFKNSLSAVSCFGSGIPQTDGVQADTSGKLLAGACIIISNPI
|||||:|||||:|||||:|||||:|||||:|||||:
m770         130      140      150      160      170      180
DPKRKTFAFYLVSVDKIIQGSFKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI

g770.pep      KNPDKRX
               :| ||||
m770          ENLDKRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

```

a770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51 CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGC GTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

```

a770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRK*
101 EVFKHGASFA FKSQIVRYY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC

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1255

151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPDKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
a770.pep	MNRL	LLLSAAVLLTACGSGETDKIGRASTVFN	ILGKNDR	IEVEGFDDPDVQGVAC	YISYA	
m770	MNRL	LLLSAAVLLTACGSGETDKIGRASTVFN	ILGKNDR	IEVEGFDDPDVQGVAC	YISYA	
	10	20	30	40	50	60
	70	80	90	100	110	120
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDE	TAVRKPK	KEVFKHGASFAFKSRQIV	RY		
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDE	TAVRKPK	KEVFKHGASFAFKSRQIV	RY		
	70	80	90	100	110	120
	130	140	150	160	170	180
a770.pep	DPKRKTFAYLVYSDKIIQGS	PKNSLSAVSCF	GGGIPQTDGVQADTSGNLLAGACMISNPI			
m770	DPKRKTFAYLVYSDKIIQGS	PKNSLSAVSCF	GGGIPQTDGVQADTSGNLLAGACMISNPI			
	130	140	150	160	170	180
a770.pep	ENPDKRX					
m770	ENLDKRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

1	ATGGATTAT	TATCGGTTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTGGC
51	GGTGTGACG	ATGCTGCTT	TGGCGGCAGT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCACCTT	CACGCCCGAA	AACATCCGCA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACCC	ACCGGAAAT	CTCGTTTGAT	GCGGATATAC	GGCGCAGGCT
201	TCTGCCCCGC	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	ACGGCGGCGG	GGTCGCCGTT	TCCGTCAAAG	AAACCAAAT	CGGATTGAGC
301	TGGAATAACC	TGTGGTCGGA	TCGGATACAG	GTTGAAAAAT	GGGTGGTTTC
351	GGGTGCGGAT	CTTGCCCTGA	CGCGCGACAG	AAACGGCGCT	TGGAACATCC
401	AAGACCTGTT	CGACGGCGCG	AAACACTCCG	CCTCAGTCAA	CCGCATTATC
451	GTCGAAACA	GCACCGTCCG	CCTCAATTTT	CTGCAGCAAC	AGCTTATCCT
501	GAAGGAAATC	AGCCTCAACC	TGCAATCCCC	CGATTCTGCG	GGGCAGCAGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGAGAG	AGCTGTCCGT	CCCGTGGAAA
601	AGCAGGGGGC	TGTTCTTTTC	AGACGGCATC	GGCAGGCCCG	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATCACCATT
701	CCACCACCGG	CAGCCCTTCT	GTCGCTTCA	ACGCCGGCGG	AGCGGATGCC
751	GCCGGCCTCG	GCCTGCGTGC	AGACACTTCC	TCCGCAACC	TCCACCTGAC
801	CGCGCAATC	CCCGCACTGG	CACTCAAAAA	CAACAGCATC	AAAACCGGCA
851	CGGTCAACGG	CACGTTTACC	GCCGGCGGCG	AATATGCCCG	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAAC	ACCGCGCCTT	CAAAACCAAT
1001	TCTCCCTCGG	CTCGCCGTTG	GTTTGAGTTC	GGGACAACGG	GCTGGACGCC
1051	CGCGCCTGAC	ACATATCGAC	CCTTCAGGAT	ACCGTCGACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCATA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	ACCGTTGCC
1201	GCAAAATTCA	AATATACGCG	GGAAGGCCGA	CCGCACCTCG	AAGCCGCCGC
1251	CGCGCTGCAA	AAATTAACCC	TCGCCCCCTA	TCTTGACGAA	TTTCGGCAAC
1301	AAAACGGCAA	AATATTCCCC	GACATCTCG	GCAGGCTGTC	CGGCAACGTC
1351	GAGGCACACC	TCAAAATCGG	CAGCATCCAA	CTCCCCGGCT	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGACCATATC	GCGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGCGCG	CATCAGCATC
1501	GCCCAACACC	GTCCCGCCAC	TTACCGCCTG	CAACAGAAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	TGCGGTCATC	GACCTGACCG	CAAGCGCGCA	AAACCGCAA
1651	CAGCTTATCC	GCTCGCTGCA	AGGCAGCCTG	TCGCTGAATA	TTTCCAACGG
1701	CGCGTGGCAC	GGCATCGATA	TGGACAGCAT	TTTAAAAAAC	GGCCTTTCCG

1256

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1751 GGAAAAATCTC GGGCAGCACA CCCTTCTACC GATTACACGCT CAACAGCGAA
1801 ATTTTCAGACG GCATCAGCCG CCACATCGAT ACCGAACTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CCTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCCGATTA
2001 CGGCAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
3051 TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

```

g771.pep
1 MDLLSVFHKY RLKYAVAVLT MLLLAAVGLH ASVYRTFTPE NIRSRLQOSI
51 ANTHRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVVETKIGLS
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSAFVNRRI
151 VDNSTVRLNF LQQQLILKEI SLNLQSPDSS GQQFESSGIL VWRKLFVPWK
201 SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALKNNIS KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGSLSI PNLQWNNAEL NGTFDRQPV
401 AKFKYTREGA PHLEAAAAAQ KLNLAAPYLDE FROQNGKIFP DILGRISGNV
451 EAHKIGISIQ LPGLQLDDME TYLHADKDHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLASGENRK
551 QLIRSLOQSL SLNISNGAWH GIDMDSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHID TELFSDSLYV TSNGYTNLDT QELSEDVLIR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDTLLE QWQWLKPREP
701 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

```

m771.seq
1 ATGGATTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGCTGACG ATACTGCTTT TGGCGGCGAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCTGAA AACATCCGCA GCCGCTACA ACAAGCATT
151 GCACACACAC ACCGAAAAAT CTCGTTTGAT GCGGACATTC AGCGCAGGCT
201 CCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCGTACCATT ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAAAC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGGCGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
401 AAGACCTGAT CGACAGCCAA AACGCCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAAACA GCACCGTCCG CCTCAATTTC CTGCAGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTGCTCG GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCCTTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTGCGTGGA CGGACACGGC ATTACCATT
701 CCACCCACCG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCGGCGCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAAAAT CCCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTTACC GCCGGCGGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGGG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACC TGAAAAATCG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAGTGC AGGGCTTTAC GCGGCGCATA CCGAAGGCGG CATCAGCATC
1501 CCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1551 CCAAAATCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTTCAT GACCTGACCG CGGGCGGCGA AACCCGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCAAACGG
1701 TGATATGGAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAAATGTC CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTACAG
1801 CTCAACAGCG AAATTCGAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACCAGCAA CGCTTACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCGGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTTC CGCAAAGAGA
2051 AACAGAAAAA CCTCGAAGAC ACCCTGCTGG AACATGGCA GTGGCTCAAA
2101 CCTAAAGAAC CGTA

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1257

This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

m771.pep
 1 MDLLSVFHKY RLKYAVAVLT ILLAAVGLH ASVYRTFTPE NIRSRLQQSI
 51 ANTHRKISFD ADIQRLLPR PTVILKNLTI TEPGGDOTAV SVQETKIGLS
 101 WKNLWSDQIQ IEKVVVSSAE LALTRDGKGV WNIQDLDSQ KRQASVNRII
 151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
 201 SRGLFLSNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
 251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNNNAEL NGTFDRQTVA
 401 AKFRYTHEDA PHLEAAVALQ KLNLPYLDD VRQQNGKIFP DTLAKLSGDI
 451 EAHKIGKGVQ LPGLQLDDME TYLHADKGGH ALSRFKSGLY GGHTEGGISI
 501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
 551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTFFHFT
 601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
 651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
 701 PKPE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

m771/g771	90.3% identity in 704 aa overlap
	10 20 30 40 50 60
g771.pep	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLQQSIANTHRKISFD
m771	MDLLSVFHKYRLKYAVAVLTILLLAAVGLHASVYRTFTPENIRSRLQQSIANTHRKISFD
	10 20 30 40 50 60
	70 80 90 100 110 120
g771.pep	ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVSGAD
m771	ADIQRLLPRPTVILKNLTITEPDGQTAHSVQETKIGLSWKNLWSDQIEKWVSSAE
	70 80 90 100 110 120
	130 140 150 160 170 180
g771.pep	LALTRDRNGAWNIDLFDAKHSASVNRIIVENSTVRLNFLQQQLILKEISLNLQSPDSS
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNLQSPDSS
	130 140 150 160 170 180
	190 200 210 220 230 240
g771.pep	GQPFESSGILVWRKLSVPWKSRLFLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS
m771	GQPFESSGILVWGKLSVPWKSRLFLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS
	190 200 210 220 230 240
	250 260 270 280 290 300
g771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVMGTFTAGGEYARWDG
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
	250 260 270 280 290 300
	310 320 330 340 350 360
g771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPVWSRDGLDAPRLHISTLQD
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
	310 320 330 340 350 360
	370 380 390 400 410 420
g771.pep	TVDRLPQPRFISRLDGSLSIPNLQNNNAELNGTFDRQPVAAKFYKTREGAPHLEAAALQ
m771	TVNRLPQPRFISRLDGSLSVNLQNNNAELNGTFDRQTVAAKFYTHEDAPHLEAAVALQ
	370 380 390 400 410 420
	430 440 450 460 470 480
g771.pep	KLNLPYLDDVRQQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDH
m771	KLNLPYLDDVRQQNGKIFPDTLAKLSGDI EAHKIGKVQLPGLQLDDMETYLHADKGH

1258

	430	440	450	460	470	480
g771.pep	490	500	510	520	530	540
	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQLLDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQLLDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
g771.pep	550	560	570	580	590	
	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG---STPFYRFT					
m771	DLTAGGETRKLIRSLQGSLSLNISNGAWHGIDMNLKNGISGKTADNAAPSTPFHRT					
	550	560	570	580	590	600
g771.pep	600	610	620	630	640	650
	LNSEISDGISRHHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
g771.pep	660	670	680	690	700	
	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPXX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

```

a771.seq
1  ATGGATTAT  TATCGGTCTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTAGC
51  CGTGTGACG  ATACTGCTTT  TGGCGGCAAT  CGGGCTGCAC  GCTTCCGTAT
101  ATCGCATCTT  CACACCTGAA  AACATCCGAA  GCGCGCTCCA  ACAAAGCATT
151  GCCCATACGC  ACCGAAAAAT  CTCGTTGAT  GCGGATATAC  AGCGCAGGCT
201  TTTGCCCCGG  CCGACCGTCA  TCCTGAAAAA  CCTGACCAT  ACCGAACCCG
251  GCGGCGACCG  GACTGCCGTT  TCCGTCCAAG  AAACCAAAAT  CGGATTGAGC
301  TGGAAAAACC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351  GAGTCGCGAA  CTTGCCCTGA  CGCGCGACGG  GAAAGGTGTT  TGGAAACATCC
401  AAGACCTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATTATC
451  GTCGAAAAAC  GCACCGTCCG  CCTCAATTTC  CTGCAGGAAC  AGCTTATCCT
501  GAAGGAAATC  AACCTCAACC  TGCAATCCCC  CGATTCTGTC  GGGCAGCCGT
551  TTGAAAGTTC  GGGCATACTG  GTTTGGGGAA  AGCTGTCCGT  CCCGTGGAAA
601  AGCAGGGGGC  TGTTCCTTTC  AGACGGCATC  GGCACGCCCA  AAATCTCACC
651  GTTCCCATTT  GAAGCTTCCA  CTTGCTGGA  CGGACACGGC  ATTACCATTT
701  CCACCACCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751  GCCGCGCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801  CGCCCAAAAT  CCTACGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851  CCGTCAACGG  CGCATTTACC  GCCGGCGGCG  AATATGCCCA  ATGGGACGGT
901  TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGCGATCG  CCAACATCGG
951  CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001  TCTCCCTCAA  TTCGCCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGCG
1051  CCGCGCCTGT  ATGTATCGAC  CCTTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101  ACCCGTTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151  AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCGCCA  AACCCTTGCC
1201  GCGAAATTCA  GATACACACA  TGAAGACGCA  CGCATCTGG  AAGCCGCCGT
1251  CGCACTGCAA  AAATTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301  AAAACGGCAA  AATATTTCCC  GACACCCTCG  CCAAGCTGTC  CGGCGACATC
1351  GAGGCGCACC  TGAAATCCGG  AAAAGTCCAA  CTTCCCGGCC  TGCAACTGGA
1401  CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGGCCATATC  GCGCTCAGCC
1451  GTTTCAAGTC  AGGGCTTTAC  GCGGGCCATA  CCGAAGGCGG  CATCAGCATC
1501  GCCAACACCC  GTCCCGCCAC  TTACCGCCTG  CAACAGAATG  CAAGCAACAT
1551  CCAAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601  GCAACGGCGA  CGCGGTCATC  GACCTGACCG  CGGGCGGCGA  AACCAGAAAA
1651  GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGTAAATA  TTTCCAACGG
1701  TGCATGGCAG  GGTATCGACA  TGGACAATAT  CCTGAAAAAC  GGCATTTTCG
1751  GCAAAACTGC  CGACAATGCC  GCACCCAGCA  CACCTTCCA  CCGATTACG
1801  CTCACAGCG  AAATTTCAGA  CGGCATCAGC  CGGCACATCG  ATACCGAACT
1851  CTTCTCCGAC  AGCCTCTATG  TTACCGAGCA  CGGCTATACC  AATCTGGATA
1901  CTGAGGAATT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CCATCCGAAA
1951  AACAAACCGA  TTCCCTGAA  AATCACCAGG  ACGGTGGACA  AACCCTCCAT
2001  TACCGTCGAT  TACGGCAGGC  TGACCGGCGG  CATCAATTCC  CGCAAAGAGA
2051  AACAGAAAT  CCTCGAAGAC  ACCCTGCTGG  AACATGGCA  GTGGCTCAA
2101  CCTAAAGAAC  CGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1259

a771.pep

```

1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQOSI
51 AHTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
101 WKNLWSDQIQ IEKVVVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
401 AKFRYTHEDA PHLEAAVALQ KNLNTPYLDD VRQONGKIFP DTLAKLSGDI
451 EAHKIGKVQ LPGLQLDDME TYLHADKCHI ALSRFKSGLY GGHTEGGSI
501 ANTRPATYRL QONASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRT
601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGIN RKEKQKILED TLEQKJWLK
701 PKEP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

	10	20	30	40	50	60
a771.pep	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPE	NIRSRLQOSIAHTHRKISFD				
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPE	NIRSRLQOSIAHTHRKISFD				
	70	80	90	100	110	120
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLS	WKNLWSDQIQIEKVVVSSAE				
m771	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLS	WKNLWSDQIQIEKVVVSSAE				
	130	140	150	160	170	180
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLN	FLQEQLILKEINLNLQSPDSS				
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLN	FLQEQLILKEINLNLQSPDSS				
	190	200	210	220	230	240
a771.pep	GQPFESSGILVWGKLSVPWKSRLGLFLSDGIGTPKISPFH	EASTSLDGHGITISTTGSPS				
m771	GQPFESSGILVWGKLSVPWKSRLGLFLSDGIGTPKISPFH	EASTSLDGHGITISTTGSPS				
	250	260	270	280	290	300
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTALARNNSI	KIETVNGAFTAGGEYAQWDG				
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALARNNSI	KIETVNGAFTAGGEYARWDG				
	310	320	330	340	350	360
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPL	VWTENKGLDAPRLYVSTLQD				
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPL	VWTENKGLDAPRLYVSTLQD				
	370	380	390	400	410	420
a771.pep	TVNRLPQPRFISRLDGSLSV PNLQNWNAELNGTFDRQT	VAAKFRYTHEDAPHLEAAVALQ				
m771	TVNRLPQPRFISRLDGSLSV PNLQNWNAELNGTFDRQT	VAAKFRYTHEDAPHLEAAVALQ				
	430	440	450	460	470	480
a771.pep	KNLNTPYLDDVRQONGKIFPDTLAKLSGIDIEAHLKIGKV	QLPGLQLDDMETYLHADKCHI				
m771	KNLNTPYLDDVRQONGKIFPDTLAKLSGIDIEAHLKIGKV	QLPGLQLDDMETYLHADKCHI				

1260

	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKEIIRSLQGSLSLNISNGAWHGIDMDNLIKNGISGKTADNAAPSTPFHRFT					
m771	DLTAGGETRKEIIRSLQGSLSLNISNGAWHGIDMDNLIKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

g772.seq

1	GTGTTCCGCC	CGGTCTTGCG	GACTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGTCGGCAAG	TTCTTTCAGG	TTGTTGCGTA	TGGTTTTCGC	GCGTTGGCGG
101	AAGGCGAGTT	TCACCAAGTT	GGCGAAATGA	TCGAAATCGT	CCGCCTTGCC
151	GATACGGTGT	TTACCCGGAA	TCATGCGCAC	CACTGCGGAA	TCGATTTTCG
201	GCGCGGGATC	GAACGATTCG	GGCGGCACGT	CAATCAGCAG	CTCCATATCG
251	AAAAAATATT	GCAGCATCAC	ACCCAAGCGA	CGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATGCGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCATAT
351	CGCGGACATC	GTCCGCTACC	TCCGCCAGTT	TGAACAAAAG	CGGCGTGGAG
401	ATGTTATACG	GCAGGTTCGC	GACGATTTTC	TTTTTGCCCTG	AGATGCCGTT
451	GAAATCAAAC	TGCAACACGT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTACAGCGG	CATACGATGT	CGCGGTCCAT	TTCCGACAACG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATTG	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCC	GATAATCCGC	GTGTCTTGCA	AAAAATTCTG	CCCGAAACGC
701	TTGCGGGCTT	TGTGTTCTTT	CATCGTGTGT	CCTCTTCGGT	TGAAACCCCG
751	CCCTTTAGGG	CGGCAGGATC	AGACTCTGTT	TGGCGGGGCG	GTAACCCCTT
801	CCAAATCAGG	ACGACACATA	GGGCGGTGCT	TTATGTGTCT	TCCTGTGTGT
851	TGGAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTCGGC	ATTGTAA

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

g772.pep

1	VFETVLRTDA	DCLQIIVVGK	FFQVVAYGFA	ALAEGEFHQF	GEMIEIVRLA
51	DTVFHRNHAA	HCGIDFRRGI	ERFGRHVNQQ	LHTEKILQHH	TQATVVVAER
101	RGNHALDHFF	LQHKVHIGDI	VRHLRQFEQK	RRGDVIRQVA	DDFLFA*DAV
151	EIKLQHVAFV	NHQFIRKQR	FQTAYDVAVD	FDNVQAVQLF	RQRFNGRCQT
201	RADFNHDIIR	LRAHGVDNIA	DNPRVLQKIL	PETLAGFVFF	HRVSSSVETP
251	PFRAAGSDSV	WAGRNPFQIR	TTHRAVLVYS	SCVLEHKCVY	SIRLSMAL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

m772.seq

1	ATGTTCCGCC	CGGTCTTGCG	GATTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGCCTGCAAG	CTCTTTCAGA	TTGTTGCGTA	TGGTTTTCGC	GCGTTGGTGG
101	AAGGCGAGTT	TCACCAAGTT	GGCGAAATGC	TCGAAATCGT	CCGCCTTGCC
151	GATGCGGTGT	TTACCCGGAA	TCATACGGAC	GACGGCGGAA	TCCACTTTTCG
201	GCGCAGGGTC	GAACGATTCG	GGCGGTACGT	CAATCAGCAT	TTCCATATCG
251	AAAAAATATT	GCAGCATCAC	GCCCAAGCGG	CGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATACGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCATAT
351	CGACGACATC	GTCCGCCACC	TCCGCCAGCT	TGAACAAAAG	CGGTGTGGAA
401	ATGTTGTACG	GGAGGTTCGC	GACGATTTTC	TTTTTGCCCTG	CGATGCCGTT
451	GAAATCAAAC	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTACAGCGG	CATACGATGT	CGCGGTCCAT	TTCCGACAACG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATCG	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCT	GATAATCCGC	GTGTCTTGCA	AAAAATTCTG	CCCGAAACGC

1261

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701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTAATGTGTC TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

```

m772.pep
1  MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GKMLEIVRLA
51  DAVFHRNHTD DGGIHFRRRV ERFGRYVNHQ FHIEKILQHH AQAADVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEQK RCGNVVREVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RADFNHDIIR LRAHGVNDIA DNPRVLQKIL PETLAGVFVF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLVYS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

```

m772/g772      85.2% identity in 298 aa overlap

              10      20      30      40      50      60
g772.pep      VFGTVLRTDADCLQIIVVGKFFQVVAYGFAALAEGEFHQFGEMIEIVRLADTVFHRNHAAH
              : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m772           MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD
              10      20      30      40      50      60

              70      80      90      100     110     120
g772.pep      HCGTDFRRGIERFGRHVNQQLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI
              : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m772           DGGIHFRRRVVERFGRYVNHQFHIEKILQHHAQAADVVAFRGNHTLDHFFLQHKVHIDDI
              70      80      90      100     110     120

              130     140     150     160     170     180
g772.pep      VRHLRQFEQRRGDVIRQVADDFLFXDAVEIKLQHVAFVNHQFIRKRQRQFQTAYDVAVD
              : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m772           VRHLRQLEQKRCGNVVREVAADDFLACDAVEIKLQYIAFVNHQFIRKRQRQFQTAYDVAVD
              130     140     150     160     170     180

              190     200     210     220     230     240
g772.pep      FDNVQAVQLFRQRFGNCRQTRADFNHDIIRLRAHGVNDIADNPRVLQKILPETLAGVFVF
              : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m772           FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVNDIADNPRVLQKILPETLAGVFVF
              190     200     210     220     230     240

              250     260     270     280     290     299
g772.pep      HRVSSSVETPPFRAAGSDSVWAGRNPFQIRTTTHRAVLVSSCVLEHKCVYSIRLMSALX
              : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m772           HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLVSSCVLKHKCVYSIRLMSALX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

```

a772.seq
1  ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTCGC GCGTTGGTGG
101 AAGGCGAGTT TCACGAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTCG
201 GCGCGGGGTC GAACGATTCG GCGGCGACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGCAGCATA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTTGCC GACGATTTTC TTTTTCCTG CGATGCCSTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATAACGATG CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTT CGCCAAAGGT TCGGTAAATCG CCGCCAAACC
601 CGGACCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAAATCTG CCCGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTAATGTGTC TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

1262

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
1  MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GEMLEIVRLA
51  DTVFHRNHAD DGRIHFRRGV ERFGRHVNQH FHIEILQHH AQAAVVVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNNVVGQVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNHDII RLAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

```
m772/a772    95.6% identity in 298 aa overlap

              10      20      30      40      50      60
a772.pep      MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD
              |||
m772           MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD
              10      20      30      40      50      60

              70      80      90      100     110     120
a772.pep      DGRIHFRRGVVERFGRHVNQHFHIEILQHHAQAAVVVAFRRGNHTIDHFFLQHKVHIDDI
              |||
m772           DGGIHFRRRVVERFGRYVNQHFHIEIKILOHHAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI
              70      80      90      100     110     120

              130     140     150     160     170     180
a772.pep      VRHLRQLEQKRRGNVVGQVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD
              |||
m772           VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD
              130     140     150     160     170     180

              190     200     210     220     230     240
a772.pep      FDNVQAVQLFRQRFGNRRQRTDFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF
              |||
m772           FDNVQAVQLFRQRFGNRRQRTADFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF
              190     200     210     220     230     240

              250     260     270     280     290     299
a772.pep      HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX
              |||
m772           HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX
              250     260     270     280     290
```

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
1  ATGGGATTGG GTGCAACGAC TTTTGTCCGT TCGGGTGCTA TAGGCGGAGG
51  TCTGTGCACT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTAGT ATCTGATGCG AAAAATCTAG
251 CCGTATGGGG ATTGGAAACG CTGATTACGC GCAAATTGGG AAAGTTGGCA
301 ACGGGTGTGA AAAGTTCCCT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCTGTGCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGGCTT GTCTGCCAAT
451 GCAAGGTAC CTAAAAATTT TAAAAATTT GATTATTTTG ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AAAGTCTGGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAAGTGTGG TAGATATGG CAAAAGTCAA
751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA
```

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
1  MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSRQL
51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
101 TGVKTSLTPK TADVQRNLS QSEVGKWK GIEGQMPWE DYVGKGLSAN
151 ARLPKNFKTF DYFDRGTGTA ISAKTLDQT TARLSKPEQL YSTMKGVIDK
201 TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEYGKSQ
251 NITVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAAGT
201 GGAATGTGTA AACGGGAAAG TCAAAGCATT GGAGCATAACG AAAATACACC
251 CTTCCGGCAG GACATACGTC CAAAACTCG ACGACCGCAA ATTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTGGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA AACTATCAA AACGGCAGGT
401 TTTCTGCCGC AGCGCCTTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGGAACGTG GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCAACCGCG CCCGAAGTCA TATTCAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GCGCGAGCCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701 TACGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRITYV QKLDRLKLE
101 HYLNTEGGSA SAHTVETAQN LYNQALKHYQ NGRFSAAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEVIFKIGEC
201 QYRLQOKDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC
51  CTGTGCTTCC GTTTCACCCG TTCCGGCAGG CAGCCAAACC GAAATGTCTGA
101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAAGT
201 GGAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT
251 CTTCCGGCAG GGCATACGTC CAAAACTCG ACGACCGCAA GTTGAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTGCAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA AACTATAAAA AGCGGCAAGT
401 TTTCTGCCGC TGCTCCCTG TTGAAGGCG CGGACGGAGG CGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCAACCGCG CCTGAAGCCA TGTTCAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GCGCGAGCCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701 TCGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDRLKLE
101 HYLNTEGGSA SAHTVETAQN LYNQALKHYK SGKFSAAASL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEAMFKIGEC
201 QYRLQOKDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFI	IWLSVSASCASVLPV	PEGSRT	EMPTQENASDGI	PYPVPTLQDR	LDYLEGKI
m774	MKIKLPLFI	IWLSVSASCASVSPV	PAGSQTEMSTRE	NASDGI	PYPVPTLQDR	LDYLEGKI
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVEM	LNGKVKALEHTKI	HFEGRTYVQK	LDDRKLKEHYL	NTEGGSASA	HTVETAQN
m774	VRLSNEVET	LNGKVKALEHAK	THSSGRAYVQ	KLDDRKLKEHYL	NTEGGSASA	HTVETAQN
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHY	QNGRFSAAAALL	KGADGGDGG	SIAQRSMYLL	LQSRARMGNC	ESVIEIGGRY
m774	LYNQALKHY	KSGRFSAAAALL	KGADGGDGG	SIAQRSMYLL	LQSRARMGNC	ESVIEIGGRY
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPT	APEVIFKIGEC	QYRLQOKDI	ARATWRS	LIQTYPGSPA	AKRAAAVVRKRX
m774	ANRFKDSPT	APEAMFKIGEC	QYRLQOKDI	ARATWRS	LIQTYPGSPA	AKRAAAVVRKRX
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

```

1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCCG TATCCGCCGC
51  CTGTTCTTCC CCTGTTTCCC GCAATATTCA GGATATGCGG CTCGAACCGC
101 AGGCAGAGGC AGGTAGTTCG GACGCTATTC CCTATCCCGT TCCCACCTCG
151 CAAGACCGTT TGGATTATCT GGAAGGCACA CTCGTCCGCC TGTCGAACGA
201 AGTGGAAACC TTAAACGGCA AAGTCAAAGC ACTGGAGCAT GCGAAAACAC
251 ACCCTTCCAG CAGGGCATA C GTCCAAAAC TCGACGACCG CAAGTTGAAA
301 GAGCATTACC TCAATACCGA AGGCGGCAGC GCATCCGCAC ATACCGTCSA
351 AACCCGACAA AACCTCTACA ATCAGGCACT CAAACACTAT AAAAGCGGCA
401 GGTTTCTGCG CGCTGCCTCC CTGTTGAAAG GCGCGGACGG AGGCGACGGC
451 GGCAGCATCG CGCAACGCAG TATGTACCTG TTGCTGCAAA GCAGGGCGCG
501 TATGGGCAAC TCGGAATCCG TCATCGAAAT CGGAGGGCGT TACGCCAACCC
551 GTTTCAAAGA CAGCCCAACC GCGCCTGAAG CCATGTTCAA AATCGGCGAA
601 TGCCAATACA GGCTTCAGCA AAAAGACATT GCAAGGGCGA CTTGGCGCAG
651 CCTGATACAG ACCTATCCCG GCAGCCCGGC GGCAAAACGC GCCGCCGAG
701 CCGTGCACAA ACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

```

1  MKTKLPLFII WLSVSAACSS PVSRIQDMR LEPQAEAGSS DAIPYPVPTL
51  QDRLDYLEGT LVRLSNEVET LNGKVKALEH AKTHPSSRAY VQKDDRKLK
101  EHYLNTGEGS ASAHTVETAQ NLYNQALKHY KSGRFSAAAS LLKGADGGDG
151  GSIAQRSMYL LLQSRARMGN CESVIEIGGR YANRFKDSPT APEAMFKIGE
201  CQYRLQOKDI ARATWRS LIQ TYPGSPA AKR AAAAVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFII	WLSVSAACSSPVS	RNIQDMRLEPQ	AEAGSSDAIPY	PVPTLQDR	LDYLEGT
m774	MKIKLPLFI	IWLSVSASCAS-V	SPVPAGSQTEM	STRENASDGI	PYPVPTLQDR	LDYLEGK
	10	20	30	40	50	

1265

		70	80	90	100	110	120
a774.pep		LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLD	DRKLKEHYLNT	EGGSSASAHTVETAQ			
m774		IVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD	DRKLKEHYLNT	EGGSSASAHTVETAQ			
	60	70	80	90	100	110	
		130	140	150	160	170	180
a774.pep		NLYNQALKHYKSGRFSAAASLLKGADGGDGG	SSIAQRSMYLL	LLQSRARMGNC	ESVIEIGGR		
m774		NLYNQALKHYKSGKFSAAASLLKGADGGDGG	SSIAQRSMYLL	LLQSRARMGNC	ESVIEIGGR		
	120	130	140	150	160	170	
		190	200	210	220	230	239
a774.pep		YANRFKDSPTAPEAMFKIGECQYRLQQDIARAT	WRS	LIQTYPGSPAAK	RAAAAVRKRX		
m774		YANRFKDSPTAPEAMFKIGECQYRLQQDIARAT	WRS	LIQTYPGSPAAK	RAAAAVRKRX		
	180	190	200	210	220	230	

q790.seq not found vet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2671>:

```
m790.seq
1 ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51 ACGTTTCGGT CATCGTGCCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGCTGTG TATCACTGCG CTTAAACATG GAAACCAAAC CTGTTTCGAG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGCA CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT CGTGAACACG CGTGTAAACG GTATGACCAA CCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGC CAGGTTCAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCCA TACGACCATC AACTAACATG
401 ATACGCATAC GCACAACACG ACGGATCCG ATGGCAAAGC AGCTTCGATG
451 AGGCTCACAC CCGTCTCCTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGG
501 CCGTACAGGC AAATCAGCGG GCAGTTTCGA CCTGTTTGCT TCGGTGgTCG
551 CCCCCTCGCA GTACACGTTT CCGCTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGAGA CTTGCTGGTG GTCGAGCCGC GTATGTGCCC
651 TGCGGACGAA ACATCTCGAG TGATTGAACT GTCCGACAAG CCGCTGTGTCG
701 TCGCGCACCT TGTATTCGAT ATGCGGGCA GGA TGCTGAT TATTCAGAGC
751 GGCAGGCCGT GCAAGCCTT TGACGTTCCC GAAGGCAGCA CGATTTTAGG
801 TGTGGTGCTG GAGTCAAAAA ACGGTTTATG TCCGCGGCAC AGGCAAGAAg
851 GCGTGTTGAT TCGGATTACC GGCCTGATG GTGGGACGGT TGGTATGATg
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAATCAGC
951 CGTATGCTTT CTCGATTTTT GCGAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCTGGTGGC AAATCCGAAC AACCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

m790.p	pep	1	51	101	151	201	251	301
	MARRSKTFEE	AAAEVEERFG	HRGIKLVEFE	GTAKPCVINC	PKHGNQTCSR			
	YSNMFGSSW	GCPCSGNEQA	AKAGIATLRK	NHIAEMLKQ	AVTGMTKQER			
	ITTQAYNEMT	KSVAGANSIV	LNDVQGDTTI	NNHHTHTNNH	SDADGKALSM			
	RLTPRPLLSD	RQAAAFARTG	KLTFSGFDLFA	SVVAPSVQTF	AVAMPDTSMS			
	PVIEKGDLIV	VEPRMCPADE	DIALIELSDK	RLVVAHLVID	IAGRMLIYQT			
	GRPSEAFDLP	EGSTILGVLV	ESKNGLCPPI	RQEGVLIRIT	APDVVTWGMII			
	SASKTSCTRP	TAAKSAVCF	LRKWOATRG	PKTRSNNRNP	NA*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

a790.seq

1	ATGGCAAGAA	GGTCAAAAAC	ATTGGAAGAA	GCTGCTGCTG	AGGTTGAGGA
51	ACGTTTCGGT	CATCGTGGCA	TTAAGTTGGT	CGAGTTTGAG	GGTACAGCCA
101	AGCCGTGTGT	AATCAACTGC	CCTAAACATG	GAACACCAAC	CTGTTTCGAGG
151	TACTCCAATA	TGTTCAATGC	AAGTAGCTGG	GSTTGGCCCT	CTTGTGGTAA
201	TGAGCAAGCT	GCAAAAGCCG	GATATAGCGAC	CCTTAGGAAG	AATCAATATAG
251	CGTTAGAAAT	GCTGAAACAG	GCTGTAAACG	GTATGACCAA	GCAAGAGCGC
301	ATCAGCAGCG	AGCTGCTACAA	TGAGATGACC	AAATCCGTGG	CAGGTTCAAA
351	CAGCATAATC	CTTAACGATG	TCCAAGGCCA	TACGACCATC	AACAACCATC
401	ATACGCATAC	GCACAACCCAC	AGCGATGCCG	ACGGCAAAAG	ACTGTCGATG
451	AGGCTCACAC	CCCGCTCTTT	GTGTCAGAC	CGTCAGCGCG	CGCCTTTCCG
501	CCGTACAGCG	AAACTCAGG	CGAGTTTCGA	CCTGTTTGCT	TCGGTGGTGC
551	CCCTTTCACA	ATATACGTTT	CCGGTTGCCA	TGCCCGAC	GTCCATGTCG
601	CCGGTTATCG	AAAAGGGGGA	TTTGCTGGTG	GTCCGAGCCG	GTATGCGCGT
651	TGCGGACGAA	GACATCGTAT	TGATGTAATC	GTCGCGAAG	CGCGTGCTGC
701	TCGCGGACCT	TGTTATCGAT	ATTGCGGGCA	GGATGCTGAT	TTATCATGAC

1266

```

751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGTCT GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGGTGTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTTCGATTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCSSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITQAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTHNN SDADGKALSM
151 RLTPRPLLSR RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

```

a790/m790    98.2% identity in 342 aa overlap

      10      20      30      40      50      60
a790.pep  MARRSKTFEEAAAEVEERFGHRGIKLVFEGTAKPCVINC PKHGNQTCSSRYSNMFIGSSW
          |||
m790      MARRSKTFEEAAAEVEERFGHRGIKLVFEGTAKPCVINC PKHGNQTCSSRYSNMFIGSSW
          |||

      10      20      30      40      50      60
a790.pep  MARRSKTFEEAAAEVEERFGHRGIKLVFEGTAKPCVINC PKHGNQTCSSRYSNMFIGSSW
          |||
m790      MARRSKTFEEAAAEVEERFGHRGIKLVFEGTAKPCVINC PKHGNQTCSSRYSNMFIGSSW
          |||

      70      80      90     100     110     120
a790.pep  GCPCSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER ITTQAYNEMTKSVAGSNSII
          |||
m790      GCPCSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER ITTQAYNEMTKSVAGSNSIV
          |||

      70      80      90     100     110     120
a790.pep  GCPCSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER ITTQAYNEMTKSVAGSNSII
          |||
m790      GCPCSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER ITTQAYNEMTKSVAGSNSIV
          |||

      130     140     150     160     170     180
a790.pep  LNDVQGDTTI NNHHTHTHNN SDADGKALSM RLTPRPLLSR RQAAAFARTG KLTGSFDLFA
          |||
m790      LNDVQGDTTI NNHHTHTHNN SDADGKALSM RLTPRPLLSR RQAAAFARTG KLTGSFDLFA
          |||

      130     140     150     160     170     180
a790.pep  LNDVQGDTTI NNHHTHTHNN SDADGKALSM RLTPRPLLSR RQAAAFARTG KLTGSFDLFA
          |||
m790      LNDVQGDTTI NNHHTHTHNN SDADGKALSM RLTPRPLLSR RQAAAFARTG KLTGSFDLFA
          |||

      190     200     210     220     230     240
a790.pep  SVVAPSQYTF AVAMPDTSMS PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID
          |||
m790      SVVAPSQYTF AVAMPDTSMS PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID
          |||

      190     200     210     220     230     240
a790.pep  SVVAPSQYTF AVAMPDTSMS PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID
          |||
m790      SVVAPSQYTF AVAMPDTSMS PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID
          |||

      250     260     270     280     290     300
a790.pep  IAGRMLIYQT GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
          |||
m790      IAGRMLIYQT GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
          |||

      250     260     270     280     290     300
a790.pep  IAGRMLIYQT GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
          |||
m790      IAGRMLIYQT GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
          |||

      310     320     330     340
a790.pep  SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
          |||
m790      SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
          |||

      310     320     330     340
a790.pep  SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
          |||
m790      SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
          |||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

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g791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTAAGTTGTTT
51  TGGTTTGTGT TTTGGTTTTT GTGTATTTGG AGTGGGTCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCGT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GAGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGCAATT TACAAAAATC GGCGATTTCC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGTG GCGCGCGCTG CCGTCGGCAA
351 TGTCTGTGCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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1267

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401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAACT GCATTATGAG CGGTTTGTTC GGAAAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCGATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGCGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCCCGCC GTTGTGTTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTATAC AGCTGCCCGG CGGCAGGCGG GTTGCCTTGG
1151 ACAGGCGCGC CTTGGGTTT CGCGCCCGAG CGGTTCGATA TGAGAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAT GATGCGCCGA TTCCCTGCC GGGGAAAGGG
1501 CCGAAGCGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GGCGGAGGCA TATAGTGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGCG ACGTGATCGA TAAGATTTAT
1801 GACAGAGACG GCAGTTGCG CGCCCAAATG CAACCTTTGG TGGCAGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAACG ACAATAAAGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGTACGG CGGTACGATT
2101 CGCGTGCCGG TTTGGTGGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

```

g791. pep
1  MVNYYSAMIK KILTTCEGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLOH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWGV ARAAVGNVVS GSVQSGASTI TQOVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLQG RAYGFASAAQ IYFNKNVRDL
201 TLAEAAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFVYTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDEV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIIRRAV IRVKNNGGRW AVVQEP LLQ ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPKGG
501 PNGSVWTPKN SDGRYSGYIT LROALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQ QPLVAGQNAF QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRDIDAGKTG TTNDNKDAWF VGFPNDVITA VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKQGGK MKMPEGVVSS NGEYMKERM VTDPLMLDN
751 SGIAPQPSRR AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791. seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51  TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACCTGCCG CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGGAATT TACAAAAATC GGCATTTCCT
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGTG CCCCAGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

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1268

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451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCAGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCGCTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAACT GCATTACGAG CGGTTTGTTT GGAAAAATCGA
801 TCAGAGTGCG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACCGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGGGAAGAA TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTGCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGCTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCGCGG CGGTCAATAA TGAAAAAATG
1201 GGGGAGGACC GTATCCGCGG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGCGGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACACGCA AAACATTCAA TCGTGCCCTT CAGTCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CGCGCTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCCG GGGGAAGGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAA ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCTGC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATAAGG GTTCTTCCG ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTTCGG CGCCCAATG CAACCTTTGG TGGCTGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCCTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTACGACG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCGCTAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GGCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

m791.pep

```

1 MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYLNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHOKVATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMVA VVLDVTKKKK VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNNGRW AVVQEP LLOG ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVVSS NGEYYMKERM VTDPLTLDN
751 SGIAPQPSRR AKEDDGGAEE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

g791/m791 97.3% identity in 805 aa overlap

```

          10      20      30      40      50      60
g791.pep  MVNYYSAMIKKILTTFCGLFFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m791      MVNYYSAMIKKILTTFCGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          10      20      30      40      50      60

          70      80      90     100     110     120
g791.pep  SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m791      SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
          70      80      90     100     110     120

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1269

	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPGKAPSAYNPINPERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPGKAPSAYNPINPERAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVP					
m791	RADHQQVATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVP					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIIRGAVIRVKNNGRW					
m791	VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIIRGAVIRVKNNGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQEPPLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPPLQGALGSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWFGFNPDVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGQKGK					
m791	TTNDNKDAWFGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGQKGK					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVVSSNGEYYMKERMVTDPLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVVSSNGEYYMKERMVTDPLMLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```

1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51  TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAGTCCCGT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGGAAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGGAATT TACAAAAATC GGGCATTTCC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCTTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC AATAAGAATG CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAAGTAA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAGT GCATTACGAG CGGTTTGTTC GGAAAAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CCGCGCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCGAGC GCTACCGCGG TGCGGAAATC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CCGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAAAAAATG
1201 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAAC ...
1251 CCGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGTTTT
1301 CGCTGGATGC AAAAACCAGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACACAGC AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GGCAGGAGCA TATAGCGTAT
1751 TTGCGAACCG CGGATATAGG GTTCTTTCGC ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTGG TGGCCGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TCGGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGACC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CCGCGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```

1  MVNYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWG ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSESV EETVSQYLSG
351 LYTVDKMMPA VVLDVTRKKK VVIQLPGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGVAQQYIR
551 RFGRFSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVVSS NGEYMKERM VTDPLGLTDN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

a791/m791 99.9% identity in 805 aa overlap

10

20

30

40

50

60

1271

a791.pep	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
m791	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPVNPRAKLROKYILNNMLE
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPVNPRAKLROKYILNNMLE
	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFVYTTV
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFVYTTV
	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
	RADHQKVATEALRKALRNFDRGSSYRGAENYIDLSKSEDEETVSQYLSGLYTVDKMVPA
m791	RADHQKVATEALRKALRNFDRGSSYRGAENYIDLSKSEDEETVSQYLSGLYTVDKMVPA
	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
	VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
m791	VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
	AVVQPEPLLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
m791	AVVQPEPLLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
	KGMTASTVVNDAPISLPKGKPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI
m791	KGMTASTVVNDAPISLPKGKPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI
	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
	GVGYAQQYIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
m791	GVGYAQQYIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
	DRDGRLAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
m791	DRDGRLAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
	TTNDNKDAWVFGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAPVWVDYMRFALKGKQKGK
m791	TTNDNKDAWVFGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAPVWVDYMRFALKGKQKGK
	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
	MKMPEGVSSNGEYYMKERMVTDPLGLDLSNGIAPQPSRRAKEDDGGAAEGGRJAADDEV
m791	MKMPEGVSSNGEYYMKERMVTDPLGLDLSNGIAPQPSRRAKEDDGGAAEGGRJAADDEV

1272

```

              730      740      750      760      770      780
              790      800
a791.pep      RQDMQETPVLPSENTGSKQQQLDSLFX
              |||||
m791          RQDMQETPVLPSENTGSKQQQLDSLFX
              790      800

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

```

g792.seq
1  ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTTACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGTTGC TTCCGAAGAT GTCCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAA
401 GGGAAAGAGG GGCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAAC
451 AGGATTTTCG AACTGTATTT AAATCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAAACCG GCcgcaGACC
551 TGACcAAACA GCAGgcggcG aaactgacgg tactcgtccc cgcgccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcattgggtt cggc^aatta ccccaagcg aaacggactg
701 attgttcag atatggaat gccgcctgaa ctggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

```

g792.pep
1  MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKPP AADLTQQA KLTVLVPAPF
201 YYSDFPKSKR LRNKTNIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

```

m792.seq
1  ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTGC
251 CGGCGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAA
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTTAC CGACAAAGAC
451 AGGATTTTTT AACTGTATTT AAATCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCGCGTCCC GGTATTTTA TCAAATACCC GCCGCCAAGC
551 TGACCAAAACA GCAGGCGGCA AAATGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CCGCAACA AAACCAATAT
651 CGTGCTCAA CGCATGGGT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

```

m792.pep
1  MFRIIKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQAIR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQA KLTARVPAPL
201 YYADHPKSKR LRNKTNIVLK RMGSAELPES DTD*

```

g792 / m792 90.4% identity in 230 aa overlap

```

              10      20      30      40      50      60
g792.pep      MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR
              |||||
m792          MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMPMKQFEQEGRDVALDYR
              10      20      30      40      50      60

              70      80      90      100     110     120
g792.pep      WVPYNRISTNLKKALIASDVRFAGHGGFDGDGIQNAIRNRNSGEVKAGGSTISQQLAK

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1273

```

m792      100 200 300 400 500 600 700 800 900 1000
          WMPYKRISTNLKKALIASEDARFAGHGGFDFWGGIQNAIRNRNNSGKVKAGGSTISQQLAK
          70      80      90      100     110     120

g792.pep  130      140      150      160      170      180
          NLFLNESRNYLRKGEEAAITAMMEAVTDKNRIFELYLNSIEWHYGVFGAEAAASRYFYKRP
          |||||:::||||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
m792      130      140      150      160      170      180
          NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNKIEWHYGVFGAEAAASRYFYQIP
          190      200      210      220      230      240

g792.pep  AADLTQQAAKLTVLVPAFFYYSDHPKSKRLRNKNTNIVLRRMGSANYPHAKRTDCSRYGN
          || |||||::: ||:::||:|||||:::|||||:::|||||:::
m792      AAKLTQQAAKLTARVPAPLYADHPKSKRLRNKNTNIVLKRMGSAELPESDIDX
          190      200      210      220      230

g792.pep  AAXTGVRTAYVFWDLX
          250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2685>:

```
a792.seq
1      ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51     CTTTTTCAAT GCGTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101    CGCCCCATCG GACTGCGTTT ATGTGCGATG GGATGAACGA GTTTGAACAG
151    GAAGGTCGCG ATGTGCGACT GGATTACCGC TGGATGCCCT ACAAAAGCAT
201    TTCCACCAAC CTGAAAAAAG CCGTGATTGC TTCGGAAGAT GCCGCTTTTCG
251    CGGGGACGCG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301    AACCGGAACA CGGGCAAAAT GAGGGCGGGC GGCTCGACCA TCAGCGACCA
351    GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401    GCGAAGAAGC AGGCTATTACC GCGATGATGG AAGCCGTTCAC CGACAAGAAGC
451    AGGATTTTTT AACTGTATTT AAACCTCAAT GAATGGGCAT ACGCGCTTTT
501    CGGCGCGGAA GCGCGTCTCC GGTATTTTTT TCAATAACCC GCCGCGAAGC
551    TGACCAAAAC CAGGGCGGCA AAACGTACGG CGCGCGTCCC CGCCCGCTC
601    TACTACGCGC ACCATCGCGA AAGCAAAACG CTCGCAACA AAACCAATAT
651    CGTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701    GA
```

This corresponds to the amino acid sequence <SEQ ID 2686; ORF 792.a>:

a792.pep

1	MFRIIKWLIA	LPVGIFIFFN	AYVYGNIIYT	RAVAPHRTAF	MSMRMKQFEQ
51	EGRDVALDYR	WMPYKRSTN	LKKALIASED	ARFAGHGDFD	WGGIQNAIRRR
101	NRNSGKVKAG	GSTISQQLAK	NLFLNESRSY	IRKGEEAAIT	AMMEAVTDKDD
151	RIFELYLNSI	EWHYGVFGAE	AASRYFYQIP	AAKLTKQQA	KLTRVPPAPL
201	YYADHPKSKR	LRNKNTIVLRL	RMGSAELPES	DTD*	

m792/a792 99.6% identity in 233 aa overlap

	10	20	30	40	50	60
a792.pep	MFRIIKWLI	ALPVGIF	IFFNAYVY	GNII	TYRAVAPH	RHTAFMSMRMKQFEQGRDVALDYR
m792	MFRIIKWLI	ALPVGIF	IFFNAYVY	GNII	TYRAVAPH	RHTAFMSMRMKQFEQGRDVALDYR
	10	20	30	40	50	60
	70	80	90	100	110	120
a792.pep	WMPYKRIST	NLKKALIA	SEDARFAG	HGGFDWGG	IQNAIRNR	NSGKVKAGGSTISQQLAK
m792	WMPYKRIST	NLKKALIA	SEDARFAG	HGGFDWGG	IQNAIRNR	NSGKVKAGGSTISQQLAK
	70	80	90	100	110	120
	130	140	150	160	170	180
a792.pep	NLFLNESRS	YIRKGEEA	AITAMMEAV	TDKDRIFE	LYLNSIEW	HYGVFGAEAAASRYFYQIP
m792	NLFLNESRS	YIRKGEEA	AITAMMEAV	TDKDRIFE	LYLNSIEW	HYGVFGAEAAASRYFYQIP
	130	140	150	160	170	180
	190	200	210	220	230	
a792.pep	AAKLTKQQA	AKLTARVP	APLYYADH	PKSKRLRN	KTNIVLRR	MGSaelPESDtdX
m792	AAKLTKQQA	AKLTARVP	APLYYADH	PKSKRLRN	KTNIVLRR	MGSaelPESDtdX
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2687>:

g793.seq

1274

```

1  ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATGGCGGT CTTGTTTGCC TGTCTGATTG CCCGCGGGCT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACCTTGTA TTTGAAAAAG AATTAAAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGACACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTTGTTTTG CGGGACCGGC AGGGC^ATAT
651 TTGGACAGC TTGGACTCCC CGCGCAATAA AGCACCGCAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTGCAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGACCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCTGGTTCG GCAATCAAAC CGTTCGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAAATCGGA CCGTCTCCCG TGCGCGATGA TACCCATGTT
1051 TACCCCTCTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCA. ^GTCCG
1101 CACAAGCAAA CTGTCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGGCATCGGT GTGCGTATGC ACTCGGGCTT TCCGGGGGAA
1201 ACTGCAGGTT TGTGAGAAA TTGGCGCAGG TGCGGGCCCA TCGAACAGGC
1251 GACGATGTCT TTCGGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 GCGCCTATAC CGCACTGACG CACGACGGCG TTTTGCTGCG GCTCAGCTTT
1351 GAGAAGCAGG CGGTTGCGCC GCAAGGCAAA CGCATATTCA AAGAATCGAC
1401 CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGGCGGCA
1451 CCGGTACGGC GGGTGCGGTG GACGGTTTCG ATGTCGGCGC TAAACCGGC
1501 ACGGCGCGCA AGTTCGTCAA CCGGCGTTAT GCCGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGCCC CCGCCAAAAA CCCCCTGTGT ATTGTGGCGG
1601 TAACCATCGA CGAACCGACT GCCCACGGCT ATTACGGCGG CGTAGTGGCA
1651 GGGCCGCCCT TCAAAAAAAT TATGGGCGGC AGCCTGAACA TCTTGGGCAT
1701 TTCCCGGACC AAGCCACTGA CCGCGCAGC CGTCAAAACA CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

```

g793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAMAVLFA CLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQA LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 DMKEMPSSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYF MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 YGEDGAEVVL RDRQGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPQ RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
351 YPSLDVRGIM QKSSNVGTSK LSARFGAEM YDFYHELIG VMMHSGFPGE
401 TAGLLRNWRR WRPIEQATMS FGYGLQLSL QLARAYTALT HDGVLLPLSF
451 EKQAVAPQK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFVDVGAKTG
501 TARKFVNTRY ADNKHVATFI GFAPAKNPRV IVAVTIDEPT AHGYGVGVVA
551 GPPFKIMGG SLNILGISPT KPLTAAAVKT PS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

```

m793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAA GCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACCTTGTA TTTGAAAAAG AATTAAAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGACACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTGCAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA

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1275

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1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTGGGCAC
1101 AAGCAAACCTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTCC GGGCGAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGGCGGG TCGGTGGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCCGT TTTGCCCCCG CCAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTT
1701 CCGGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

m793.pep

```

1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF LMAIAVLFA GLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQT LPATRGTVSD RRGAVLALSA PTESLFAVFK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYPMGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRRG RADSEQRRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPKYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNRRW RPIEQATMSF GYGLQLSLQ LARAYTALH DGVLLPVSE
451 KQAVAPQGR IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYVGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAVKTP S*

```

g793/m793 98.5% identity in 582 aa overlap

	10	20	30	40	50	60
g793.pep	MLIKSEYKPRMLPKKEEQVKKPMTSNGRISFVLMAMAVLFACLIARGLYLQTVTYNFKLEQ					
m793	MLIKSEYKPRMLPKKEEQVKKPMTSNGRISFVLMAMAVLFACLIARGLYLQTVTYNFKLEQ					
	10	20	30	40	50	60
g793.pep	GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVFKDMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVFKDMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
g793.pep	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
m793	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
	130	140	150	160	170	180
g793.pep	FTDIDGKGQEGLELSLEDSLYGEDGAEVVLDRQGNIVDSLDSPRNKAPQNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLYGEDGAEVVLDRQGNIVDSLDSPRNKAPQNGKDIILSLD					
	190	200	210	220	230	240
g793.pep	QRIQTLAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRRGRADSEQRRNR					
m793	QRIQTLAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRRGRADSEQRRNR					
	250	260	270	280	290	300
g793.pep	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKYKIGPSPVRDTHVYPSLDVRGIM					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKYKIGPSPVRDTHVYPSLDVRGIM					
	310	320	330	340	350	360
g793.pep	QKSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS					
m793	QKSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS					
	370	380	390	400	410	420
g793.pep	QKSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS					
m793	QKSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS					
	360	370	380	390	400	410

1276

	430	440	450	460	470	480
g793.pep	FGYGLQLSLLQLARAYTAL	THDGVLLPLSFEKQAVAPQ	GKRIFKESTAREVRNLM	SVTE		
m793	FGYGLQLSLLQLARAYTAL	THDGVLLPLSFEKQAVAPQ	GKRIFKESTAREVRNLM	SVTE		
	420	430	440	450	460	470
	490	500	510	520	530	540
g793.pep	PGGTGTAGAVDGF	DVGAKTG	TARKFVN	GRYADNKH	VATFIGFAPAKN	PRVIVAVTIDEPT
m793	PGGTGTAGAVDGF	DVGAKTG	TARKFVN	GRYADNKH	IATFIGFAPAKN	PRVIVAVTIDEPT
	480	490	500	510	520	530
	550	560	570	580		
g793.pep	AHGYYG	GGVVAGPP	FKKIMG	SLNILGIS	PTKPLTAA	AVKTPSX
m793	AHGYYG	GGVVAGPP	FKKIMG	SLNILGIS	PTKPLTAA	AVKTPSX
	540	550	560	570	580	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

a793.seq

```

1   ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCTTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGACAAACC GGATTGTGCG
201 GACTCAAAAC TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AATGCCCCTC TGCCGCACAA TTGGAACGCC TGTCGAGCT
351 TGTCGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTTA CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACCTTGTA TTTGAAAAG AAT'AAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGT'TTGGAAC TTTGCGTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTGG CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 AGCATCATCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TCCACAAGG CGGTGGAATA CCATCAGGCA AAAGCCGGA CCGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTCC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCAGGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCT TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTCC GGGCGAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGCTTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGCGCTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAAACG ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGGCGGG TCGGTGGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTGCCCCCG CCAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGCGCT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCGGACCAAG CCACTGACCG CCGCAGCCGT CAAACACCG TCTTAA

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This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

a793.pep

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1   MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLK QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYF MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEEVL RDRQGNIVDS LDSPRNKAPK NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPQ RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTOPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRRW RPIEQATMSF GYGLQLSLLQ LARAYTALH DGVLLPVSE
451 KQAVAPQGKR IFKESTAREV RNLMVSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYYGGVVAG
551 PPFFKIMGGS LNILGISPTK PLTAAAVKTP S*

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a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLOTVTYNFLKEQ					
m793	10	20	30	40	50	60
	MLIKSEYKPRMLPKKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLOTVTYNFLKEQ					
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
a793.pep	130	140	150	160	170	180
	PVDVLRNKLEQKGKFSIWIQRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
m793	130	140	150	160	170	180
	PVDVLRNKLEQKGKFSIWIQRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLELSLEDLSLHGEDGAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793	190	200	210	220	230	240
	FTDIDGKGQEGLELSLEDLSLHGEDGAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
a793.pep	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAKAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAKAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR					
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
m793	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMDFYHELGI GVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMDFYHELGI GVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
a793.pep	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALTDGVLLPVSFQAVAPQGKRIFKESTAREVRNLMVSVTEP					
m793	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALTDGVLLPVSFQAVAPQGKRIFKESTAREVRNLMVSVTEP					
a793.pep	490	500	510	520	530	540
	GGTGTAGAVDGFVVGAKTGARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	490	500	510	520	530	540
	GGTGTAGAVDGFVVGAKTGARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
a793.pep	550	560	570	580		
	HGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
m793	550	560	570	580		
	HGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcgtttca ATCATTTCAT AATGGTAACG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGTCC GCCGCCCGG CGTTCCTACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTCACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCGG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTGT ATTGGGCGGG CAGCGGCAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 CAAAGGCATC CGCAATATCA CGGGGCGCCT GATGCTCGAC CACAGCCTGT

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1278

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551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAAATCC GACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTCCGTCAA AAAACTGATG CGCGCATCTT TTTGCGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCGAAATG TTGGAAACGG CTTATTTTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCGCG GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCGCGCGGC
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

```

g794.pep
1  VRFNHFIMVT IIIYVISPAN KPVRPRPVPT YPALPYNCFF YVTDSPMNF
51  KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHR'
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLT GNLYWALSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRMLD HSLWGEVSGP DHFEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVMFMA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILD MNKRSDNLIA
351 RSVFLKLGGD GKLPAVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMAQM LETAYFSPFA QDFIDTLPIA GTDGLLRNRF KQSGGLLRLE
451 TGTINNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVAKNIISGG
501 DGWLDALMC KERRA*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

```

m794.seq
1  GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGCCC GCGGCCACAG CGTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGGTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAC
351 CTTGGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTAT ATTTGGGCGG CAGCGGCGAC
451 CCGGTTTTCA ATCAGGAAAA CCTGCTTGAT GCTCAAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTTGCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCCG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGCCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCGAAATG TTGGAAACGG CTTATTTTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACCTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCGCG GCGGTTTCCC
1451 TGCTGCCGAG CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGCGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

```

m794.pep
1  VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51  KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV

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1279

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101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLD AOKQLREOGI LNTIGHLMLD HSLWGEVGSF DFEADSGSP
201 FMTPPNPTML SAGVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSNTLK LRGNIPECL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSDNLIA
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLK
451 TGTLLNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISG
501 DGWLDKLMC KERRA*

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g794/m794 95.5% identity in 515 aa overlap

	10	20	30	40	50	60
g794.pep	VRFNHFMVT	IIIVISPA	NKPVRRPG	VPTYPALP	YNCFFYVT	DSPMNFPKTAASLLLLL
m794	VRLNHFMIA	IIIVISPA	NKPARRHVS	PTYPALP	YNCFFYVTD	LPNMNFPKTAASLLLLL
	10	20	30	40	50	60
g794.pep	ASLAHA	LDTGRI	PQNEIA	VYVQEL	DSGKVI	IDHRAGIPVNPASTMKLVTAFAAFKTFGS
m794	ASLAHA	LDTGRI	PQNEIA	VYVQEL	DSGKVI	IDHRSDVPVNPASTMKLVTAFAAFKTFGS
	70	80	90	100	110	120
g794.pep	NYRWATEF	KSNGTV	NDGTLD	GNLYWAG	SGDPVFN	QENLLAVQKQLRLKGI
m794	NYRWATEF	KSNGTV	NDGTLD	GNLYWAG	SGDPVFN	QENLLDAQKQLREQGI
	130	140	150	160	170	180
g794.pep	HSLWGEV	GSFDPH	FEADSG	SPFMT	PPNPTML	SAGVMVRAERNAAGSTDILTDPPLPHIFA
m794	HSLWGEV	GSFDPH	FEADSG	SPFMT	PPNPTML	SAGVMVRAERNAAGSTDILTDPPLPHIFA
	190	200	210	220	230	240
g794.pep	QNNLKITA	SQAACP	SVKKLM	RASFS	GNLTKL	RGNIPECLGKPVGVRMFALDELIRQSFT
m794	QNNLKITA	SQAACP	SVKKLM	RASFS	DNLTKL	RGNIPECLGKPVGVRMFALDELIRQSFT
	250	260	270	280	290	300
g794.pep	NRWLLGG	GRISD	GIGIAD	TPEGAQ	TLAVAH	SKPMKEILTMNKRSDNLIARSVFLKLG
m794	NHWLLGG	GRISD	GIGIAD	TPEGAQ	TLAVAH	AKPMKEILTMNKRSDNLIARSVFLKLG
	310	320	330	340	350	360
g794.pep	GKLPVSE	QAASAV	RRELAV	SGIDVA	DLVLE	NGSGLSRKERV
m794	GKLPVSE	QAASAV	RRELAV	SGIDVA	DLVLE	NGSGLSRKERV
	370	380	390	400	410	420
g794.pep	QDFIDTL	PIAGT	DGTLRN	RFKQSG	GGLRLK	TGTLNNVRALAGYWLGDKPM
m794	QDFIDTL	PIAGT	DGTLRN	RFKQSG	GGLRLK	TGTLNNVRALAGYWLGDKPM
	430	440	450	460	470	480
g794.pep	AVSLLPD	LDNFVA	KNIISG	GDGWL	DAKLM	CKERRAX
m794	AVSLLPD	LDNFVA	KNIISG	GDGWL	DAKLM	CKERRAX
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

```

a794.seq
1 GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTGCGATTG CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGCTC

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1280

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301 AACCCCGCCT CCACAATGAA ACTCGTTAQC GCGTTTGCCG CCTTCAAAAC
351 CTTGGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCC AAGCCGACAG CGGTTCCGCC
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCTCCCAA
751 GCTGCCTGCC CTTTCGATCAA AAAACTGATG CGTGCACTTT TTTCCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCGG GATGTTCCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CCGACGGATT TCAGACGGCA TCGGCAATC
951 CGACACGGCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCAAAATCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGCGCAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCA GCGTCTGCCG TCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCCGA TTTGTTTTCG GAAACCGTT CAGGCTCTGC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGGCAATG TTGGAACGG CTTATTTTCA
1251 CCCGTTTGCA CAAGATTTC TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCGCG GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTCG AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

a794.pep

```

1 VRLNHFIMIA IIIYVISPA KPARRHVPT YPALPYNCF YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLA VQRQLREQGI RNITGHLMLD HSLWGEVGSF DDFEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILD MNKRSNLI
351 RSVFLKLGGD GKLPAVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMAQM LETAYFSPFA QDFIDTLPIA GTDGLLRNF KQSGGLLRK
451 TGTNNVRAL AGYWLGDKPM AVVVIINSGR AVSLPDLN FVANNIISGG
501 DGWLDALMC KERRA*

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a794/m794 98.6% identity in 515 aa overlap

	10	20	30	40	50	60
a794.pep	VRLNHFIMIA	IIIYVISPA	KPARRHVPT	YPALPYNCF	YVTDLPMNFP	KTAASLLLLL
m794	VRLNHFIMIA	IIIYVISPA	KPARRHVPT	YPALPYNCF	YVTDLPMNFP	KTAASLLLLL
	10	20	30	40	50	60
a794.pep	ASLAHALDT	GRIPONEIA	VYVQELDS	GVIIIDHR	SDVPVNP	PASTMKLV
m794	ASLAHALDT	GRIPONEIA	VYVQELDS	GVIIIDHR	SDVPVNP	PASTMKLV
	70	80	90	100	110	120
a794.pep	ASLAHALDT	GRIPONEIA	VYVQELDS	GVIIIDHR	SDVPVNP	PASTMKLV
m794	ASLAHALDT	GRIPONEIA	VYVQELDS	GVIIIDHR	SDVPVNP	PASTMKLV
	130	140	150	160	170	180
a794.pep	NYRWATEFK	SNGTVNDG	LDGNLYWA	GSGDPVF	NQENLLA	VQRQLREQ
m794	NYRWATEFK	SNGTVNDG	LDGNLYWA	GSGDPVF	NQENLLA	VQRQLREQ
	190	200	210	220	230	240
a794.pep	HSLWGEVGS	PDDFEADSG	SPFMTPPN	PTMLSAGM	VVMVRAE	RNAADSTD
m794	HSLWGEVGS	PDDFEADSG	SPFMTPPN	PTMLSAGM	VVMVRAE	RNAAGSTD
	250	260	270	280	290	300
a794.pep	QNNLKITAS	QAACPSIK	KLMRASFS	DNTLKR	GNIPESCL	GKPVGVRM
m794	QNNLKITAS	QAACPSIK	KLMRASFS	DNTLKR	GNIPESCL	GKPVGVRM
	310	320	330	340	350	360
a794.pep	NHWLLGGGR	ISDGIGIS	DTPGAQTL	AVHSHKPM	KEILDMNK	RSNLIARS
m794	NHWLLGGGR	ISDGIGIS	DTPGAQTL	AVHSHKPM	KEILDMNK	RSNLIARS

1281

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|||||
m794      NHWLLGGGRISDGIGIADTPEGAQTL...HAKPMKEILTDMNKRSDNLIARSVFLKLGGD
          310      320      330      340      350      360

          370      380      390      400      410      420
a794.pep   GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMM AQMLETAYFSPFA
          |||||
m794      GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMM AQMLETAYFSPFA
          370      380      390      400      410      420

          430      440      450      460      470      480
a794.pep   QDFIDTLPIAGTDGTLRNRFKQSGGLRLKTGT LNNVRALAGYWLGD KPM AVVV IINSGR
          |||||
m794      QDFIDTLPIAGTDGTLRNRFKQSGGLRLKTGT LNNVRALAGYWLGD KPM AVVV IINSGR
          430      440      450      460      470      480

          490      500      510
a794.pep   AVSLPDLDNFVANNIISGGDGWLD AKLMCKERRAX
          |||||
m794      AVSLPDLDNFVANNIISGGDGWLD AKLMCKERRAX
          490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2699>:

```

g900.seq
1   ATGccgTCTG AAATGCCGTC TGAAACGTGG CAGGCGGAGG TTCGGACGGC
51  ATTGGGTTTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
101 AACAAATTCGC GCGCTTCTTT GCGCGCTTTT TGC GCGcctg cctGCAAAAT
151 CTCTTCGATT TGCGAAGGAT TAGAGGTCAA TGCGTTGTAG CGTTCGCGCA
201 GTTCTGCCAA TTCGGCGTTG ATTTTCGCCG CCGAAAAGTTT TTTCGCCTCG
251 CCCC AAGCCA AGCCGTCGGC AAGCATTTGC GTAAATTCCG CCGTTTCAGA
301 CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
351 GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
401 TTTTGGGTTT TTTTGTCTGT TTCCCAAAGC GGAATGGTAT TGCCGTAGGA
451 TTTGGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTCG ACGTTTTCGT
501 CGATTTTCAC TTCGGGCagg GTGaagagtt cTTGGAaacc gtgggtgaag
551 cggccggcAa tgtcgcgcgc cATTcgacg tgttgGATTT GGTGCGGCCC
601 GACGGGGACT TCGTTGGCGT TGAACATCAA AATGTCGGCA GTCATCAGAA
651 TCGGATAACT GAACAAACCC ATTTCCACAC CGAAATCGGG GTCTTCCTGC
701 CCGTTTTCGG CATTGCTTG AACGGCGGCT TGTAGGCGT GGGCGCGGTT
751 CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
801 CTTCGGGAAT GTCGCTTTGG CGTAGAAGG TGGTGCCTC GGGGTCGAGT
851 CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tgGGTGGATT GGTGAATCAT
901 CTCCTGCTCG TGGCATTGTA TGATGCCGTG GTAATCGGCG AGGAAGAGGA
951 AGGATTCGCT ATCGGGGTTT TGCGCCGCGC GGACGGCGGG GCGGATGGCG
1001 CCGACGTAGT TGCCAGATG CGGGGTGCCG GTGGTGGTTA CGCCGGTCAG
1051 AACTCGTTTT TTGCTCATAA AAATGTCCTT ACGGCAGCAA TGCCGTCTGA
1101 AAGGGAAaA. gatgcgCCGA TTATACCCGA TTGCCACAT ACATCCAGCC
1151 GacaACagaC TTTTCCATAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng>:

```

g900.pep
1   MPSEMPSETW QAEVRTALGL FQRADADRIA YFIQQFARFF ARFLRACLQN
51  LFDLRRIRGQ CVVAFAPFCQ FGVDPRRRKF FRLAPSQAVG KHLRKFRRFR
101 RRGEFIDFK QRAFVGLFRL ARLFHVGNDF VDRFLGFFV FPKRNGIAVG
151 FGHFASVQTD QEFDFVDFH FGQGEFLET VGEAAGNVAR HFDVLDLVAP
201 DGDFVGVVEHQ NVGSHQNRIT EQTHFHT EIG VFLPVFRIGL NGGFVGVGAV
251 HQTLGGDAGQ NPVQLHHFGN VALAVEGGAL GVESAGKPSG GNGLGGLVNH
301 LLLVAFDDAV VIGEEEGFG IGVLRADGG ADGADVVAQM RGAGGGYAGQ
351 NSFFAHKNVL TAAMPSEREK DAPIIPDLPH TSSRQOTFPY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

```

m900.seq
1   ATGCCGTCTG AAACGCGGCA GGCGGAGGTT CGGACGGCAT CGGGTTTCATT
51  TCAACGGGCG GATGcCGACC GCATcGg.TA CTTTGTCCAA TAATTCGCGT
101 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTCGATTTG

```

```
m900.pep
1  MPSETRQAEV RTASGFSQRA DADRIXYFVQ *FACFFTRFR RACLQNLFDL
51  RRVGGQLVVA FARFGFEGVD FRQKFFGFT PRQAVGKFR KFRHFRRRGE
101 GFVDFKQWAF VGLFRLRLRF HIGDDFVDRF LGFFVVFPR NGVAVGFGHF
151 ASVQTDQEFDF VIDFHFHGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVHQHNGS HQNRITQTH FHTEIRVFLP VFCLHGGF VGMGAVHQT
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGNGNL GGLVNHLRLV
301 AFDDTVVIGE EEEFGFIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QQTFFPY*
```

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

		10	20	30	40	50		
m900.pep		MPSETRQAEVRTASGSFQRADADRIGYFVQXFACFFTRFRRACLQNLFDLRRVGQG						
			: :		:	:		
g900		MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGQ						
		10	20	30	40	50	60	
	60	70	80	90	100	110		
m900.pep	LVVAFARFGEGVDFFRRQKFFGFTPRQAVGKHFRKFHRRRRGEGFVDFKWQAFVGLFRL							
	:	:	:					
g900	CVVAFAQCFCQGVDFRRRKFFRLAPSQAVGKHLRKFRFRRRRGEGFIDFKQRAFVGLFRL							
	70	80	90	100	110	120		
	120	130	140	150	160	170		
m900.pep	ARLFHIGDDFVDRFLGFFVVFPKRNGVAVGGFHGFASFVQTDEQFDVFIDFHFGQGEETPEA							
	:		:		:	:		
g900	ARLFHVGNDFVDRFLGFFVVFPKRNGIAGVGGFHGFASFVQTDEQFDVFVDFHFHGQGEETLET							
	130	140	150	160	170	180		
	180	190	200	210	220	230		
m900.pep	VVEAAGDVARHFDVLDDLVPDGHFVGVGHEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICL							
g900	VGEAAGNVARHFDVLDDLVPDGHFVGVGHEHQNVGSHQNRITEQTHFHTIEIGVFLPVFRIGL							
	190	200	210	220	230	240		

```

      240      250      260      270      280      290
m900.pep HGGFVGMGAVHQTLGSDAGQNPNVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH
          :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g900      NGGFVGVGAVHQTLGGDAGQNPNVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH
          250      260      270      280      290      300

      300      310      320      330      340      350
m900.pep LRLVAFDDTVVIGEEEEFGFIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVL
          | |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g900      LLLVAFDDAVVIGEEEEFGIGVLRRADGGADGADVVAQMRGAGGGYAGQNSFFAHKNVL
          310      320      330      340      350      360

      360      370      380
m900.pep AASMPSEREKDVPIIPDLPTSSRQQTFFPYX
          :|:|||||:|||||:|||||:|||||
g900      TAAMPSEREKDAPIIPDLPTSSRQQTFFPYX
          370      380      390

```

a900.seq	(partial)						
1	GAGGTTTCGGA	CGGCATTGGG	TTTATTTCAA	CGGGCGGATA	CCGACCCGAT		
51	CACGCTACTTT	GCCCAATAAT	TCGGTGCTT	CTTTACGGCG	TTTTTGCGCG		
101	CTGCGCTGCA	AAATCTCTTC	GATTTCGGAA	GGGTCGGCGG	TCAGCTCGTT		
151	GTAGCGTTTCG	CGCGGTTTCG	CGAGTTCGGC	GTTGATTTTC	GCCGCCAAAA		
201	GTTTTTTTTCG	CTCGGCCCAA	GCCAAGCCGT	CGGCAAGCAT	TTTCGTAAAT		
251	TCTGCGGTTT	CAGACGGCGT	GCGAAGAGCT	TTGTAGATT	CAAAACGAGG		
301	GCTTTCGTCG	GGCTTCTTCG	GCTCGCCCGG	CTCTTTCATA	TTGGTGATGA		
351	TTTTGTGTAC	CGATTTTTCG	GTTTTTTTGT	CGTTTTCCCA	AAGCGGAATG		
401	GTGTTGCCGT	AGGATTTCGA	TTCTTTGCGT	CCGTCCAAAC	CAACCCAGAG		
451	TTTCGACGTT	TGCTCGATT	TCACTTCCGG	CAGTGTGAAG	AGTTCACCGA		
501	AGCGGTGGTT	GAAACGGCCG	GCAATATCCC	GTCGCATTTC	AACGTTGTTG		
551	ATTTGGTTCG	GACCGACTGG	AACTTCATGG	GCATTGAACA	TGAGAATGTC		
601	GGCAGTCATG	AGGATAGGGT	AGCTGTACAA	ACCTGATTCC	ACGCCGAAAT		
651	CGGGGCTCTC	CTGCCCGTTT	TCCGCAATTG	CTCGCACGGC	GGCTTTGTAG		
701	CGGTGGGCGC	GGTTTCATCA	ACCCTTGGCG	GTGATGCAGG	TCAGAATCCA		
751	GTTCAATTCC	ATCACTTCGG	GAATGTCGCT	TTGACGGTAG	AAGGTGGTGC		
801	GCTCGGGGTC	GAGTCCGCAG	GCAAGCCAA	TGGCGGCAC	GGCTTGGGTG		
851	GATTGGTGAA	TCATCTCCGG	CTCGTGCCAT	TTGATGATAC	CGTGGTAATC		
901	GGCGAGGAAG	AGCAAGGATT	CGGTATCAGG	GTTTTGCGCC	CGCGGCAGCG		
951	CGGGGCGGAT	AGCACCGACG	TAGTTGCCCA	GATGCGGGAT	GCCGGTGGTG		
1001	GTTACGCGCG	TCAGAACTCG	TTTTTTGCTC	ATAAAAAATG	CCTTGGCGCA		
1051	TCAATTCCGT	CTGAAAGGGA	AAAGATGCGC	CCGATTATAC	CCGATTTGCC		
1101	ACCTACATCC	AGCCGACAAC	AGACTTTTCC	ATATTAA			

```

a900.pep (partial)
  1 EVRTALGLFQ RADTDRITYF AQ*FACFFTR FLRACLQNLF DLRRVGGQLV
  51 VAFARFGEFG VDFRRQKFFL LAPSQAVGKH FRKFCRFRRR GESFVDFKQR
101 VAEVGLLRFG LFHIGDDFVD RFLGFFVFP KRNGVAVGFG HFASVQTNQE
151 FDFVDFHFHG QCEEFPAAVV EAAGNIACHF NVLDLVATDW NFMGIEHENV
201 GSHEDRVAVQ THFHAELGVF LPVFRICLHG GFVGVGAVHQ TLGGDAGQNP
251 VQFHHFGNVA LVTEGGALGV ESAGKPSGGN GLGLVNHILR LVAFDDTVVI
301 GEEEEFGFIR LTREADGGAD STDVVAQMRD AGGGYAGQNS FFAHKNVLAA
351 SMPSEREKDA PIIPDLPTS SRQOTFPY*

```

```

      10      20      30      40      50      60
m900.pép  MPSETRQAEVRTASGSFQRADADRIXVFVOXFACFFTRFRRACLQNLFDLRRVGGQLVVA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a 900      EVRTALGLFQRADTDRIITYFAQXFACFFTRFLRACLQNLFDLRRVGGQLVVA
            10      20      30      40      50

      70      80      90      100     110     120

```

1284

```

m900.pep    FARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRFRRRGEGFVDFKQWAFVGLFRLARLF
|||||
a900        FARFGEFGVDFRRQKFFCLAPSQAVGKHFRKFCRFRRRGESFVDFKQRAFVGLLRLARLF
          60          70          80          90          100         110

          130          140          150          160          170         180
m900.pep    HIGDDFVDRFLGFFVVPKRNQVAVGFGHFASVQTDQEFDFVDFHFGQGEFFPEAVVEA
|||||
a900        HIGDDFVDRFLGFFVVPKRNQVAVGFGHFASVQTNQEFDFVDFHFGQCEFFPEAVVEA
          120         130         140         150         160         170

          190          200          210          220          230         240
m900.pep    AGDVARHFDVLDLVAPDGHFVGVHQNIGSHQNRITEQTHFHTAIRVFLPVFCICLHGGF
|||||
a900        AGNIACHFNVLDLVATDWNFMGIEHENVGSHEDRVAVQTHFAEIGVFLPVFRICLHGGF
          180         190         200         210         220         230

          250          260          270          280          290         300
m900.pep    VGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNHLRLV
|||||
a900        VGVGAVHQTLGGDAGQNPVQFHHFGNVALTVEGGALGVESAGKPSGGNGLGGLVNHLRLV
          240         250         260         270         280         290

          310          320          330          340          350         360
m900.pep    AFDDTVVIGEEEEFGFIEVLRRADGGADGVVAQMRDAGGGYAGQNSFFAHKNVLAASM
|||||
a900        AFDDTVVIGEEEEFGFIRVLRRADGGADSTDVVAQMRDAGGGYAGQNSFFAHKNVLAASM
          300         310         320         330         340         350

          370          380
m900.pep    PSEREKDVPIIPDLPPTSSRQQTFPYX
|||||
a900        PSEREKDAPIIPDLPPTSSRQQTFPYX
          360          370

```

g901.seq not found yet

g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

```

m901.seq
1  ATGCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCTTTT CCATCACATT
51  GGCTGCCGGT TTGTTTACCG TATTakGyAG TGGCTTGGTG ATGTTTCCA
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTTG GTTTGGCGTT TGCCGGCGGT
151 GCGATGGTAT ATGTTTCCCT GACGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
251 CATTTTGGC CGGATGGGC GCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTT CAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
401 CGCACAATT CCCGAAGGC TTGGCGACGT TTTTGCCAC ATTGGAAAAT
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGTTTA TTTTGCCACC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTGGGG
601 GCGGCTTTGG GCTATTGGT TTTGCAGCCG TTTTGTGCG CT3CCGTGTT
651 TGGTTCGTA TTCCGCGTGA TAGCCGGTGT GATGGTGT TGGCGTTGG
701 ACGAGCTGnt GCCGCTGCC AAACGCTATT CAGACGCCA TGAAACCGTT
751 TACGCGCTGA CAACGGGTAT GCGGTGATT GCCGTAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

```

m901.pep
1  MPDFSMSNLA VAFSITLAAG LFTVLXSLV MFSKTPNPRV LSFGLAFAGG
51  AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP

```


1285

```

101 NPHETLDAQD PSFOESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
201 AALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELXPAA KRYSDGHETV
251 YGLTTGMAVI AVSLVLFHF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

```

a901.seq
  1 ATGCCCGATT TTTCGATGTC CAATTGGGCC GTTGCCCTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTTCCA
101 AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTTGGCATT TGCCGGCGGT
151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTGGCGCG GCGACCATGG
251 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACCTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
401 CGCACAAATT CCCCGAAGGC TTGGCGACGT TTTTGGCCAC ATGGGAAAT
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGGCCAC CGCAGCCGTA
551 AGAAAACGCT GTGGCGGTGT CTGCTATCCG GCTTGGCCGA GCCGTTGGGG
601 GCGGCTTTGG GCTATTGGT TTTGCAGCCG TTTTGTGCG CTGCCGTGTT
651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTTT TTGGCGTTGG
701 ACGAGCTGCT GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAACCGTT
751 TACGGCCTGA CAATGGGCAT GCGGTGATT GCCGTAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

```

a901.pep
  1 MPDFMSNLAVAFSITLAAGLFTVLGSLV MFSKTPNPRV LSFGLAFAGG
 51 AMVYVSLTEI FSKSSEAF AEIYDKDHAF AAATMAFLAGM GGIALIDRLVP
101 NPHETLDAQD PSFOESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
201 AALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
251 YGLTMGMAVI AVSLVLFHF*

```

m901/a901 98.9% identity in 269 aa overlap

m901.pep	10	20	30	40	50	60
	MPDFMSNLAVAFSITLAAGLFTVLXSGLV MFSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
a901	MPDFMSNLAVAFSITLAAGLFTVLGSGLV MFSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
	10	20	30	40	50	60
m901.pep	70	80	90	100	110	120
	FSKSSEAF AEIYDKDHAF AAATMAFLAGM GGIALIDRLVP NPHETLDAQD PSFOESKRRH					
a901	FSKSSEAF AEIYDKDHAF AAATMAFLAGM GGIALIDRLVP NPHETLDAQD PSFOESKRRH					
	70	80	90	100	110	120
m901.pep	130	140	150	160	170	180
	IARVGMMAAF AITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
a901	IARVGMMAAF AITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
	130	140	150	160	170	180
m901.pep	190	200	210	220	230	240
	RSRKKTVWAC LLSGLAEPLGAALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELXPAA					
a901	RSRKKTVWAC LLSGLAEPLGAALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELLPAA					
	190	200	210	220	230	240
m901.pep	250	260	270			
	KRYSDGHETV YGLTTGMAVI AVSLVLFHF					
a901	KRYSDGHETV YGLTMGMAVI AVSLVLFHF					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

```

g902.seq
1  ATGCCGTCGG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCCTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTTGATTTC
151 ACGCCGCGCC TGTTCCGCGT CCGGCATTTT GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GCGCGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGCCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTgcggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTGGT CTGGGcgatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TGCGTGcgcG CGcgcccggtg aacggcaaGg
551 gcggcaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgtcgtcg tgccaaccca AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCTGc
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTTcttgg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgcg
801 catCCGCCAT CtggttcggGG TCGTGCCGG CAATCTGCAC tttAACGATC
851 CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCCT
901 GAGCGTCGGA TCGCTGGCCA GCATTTCGCA CACCGCCCAA CCTGCGCCAA
951 ACGCCCGACA GAGCGGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCga TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

```

g902.pep
1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQN GGSAPCQTQG
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAIF GDFDGGQVL
201 IVVVPQTGF EGNFYARRLD HRLQNGGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDDLPE SDVVTRRIRH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

```

m902.seq
1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATT TGGCGGTAGG
51  CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCTG ATTGCGCCGC CGCACTGTCC AAGCGTTGA TTTCACGACG
151 TgTCTgTTCG CCGTcGGGCA TTTCTGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGCG GTGTCGCCGT AAAACGCGTG TATGGCGCGG
251 ATGTGTTTCA AAATAGCGGC GCGCATTTCT GCCAAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTCCGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGGCGGC GGTGTTGTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTCGCGT TGACCCAGAC
451 CGGGATGTTC AGACGGCATT TGGTTTCGGC GATGAGTTCT TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCCTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTCCGGCAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGCAATCT GCACGGCAAC AATGCCGCCCT
851 TCATCGCAA AATCGCTGCG GTGCAAGGT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

m902.pep
 1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
 51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQCQTQGRR
 101 QNTVFGIMFQ IAEEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
 151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAIFGD FGDDGQVLMV
 201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV
 251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
 301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRCDCGVVDK IAADVHNGSA
 351 FQKSTPLYIF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng)
 from *N. gonorrhoeae*:

m902/g902

m902.pep	10	20	30	40	50
	LHFQRIIKCS	EGIWAVGARPT	TVGFFGKSFK	ITCKHVVLRR	RTVQAVDFTT
g902	10	20	30	40	50
	MPSEPERRHGNTAL	PFPIAARPT	TVGFGSKP	FKITGKCVLRR	RIVQAVDFTT
m902.pep	60	70	80	90	100
	VDVPAYVFACDA	HTGGVAVKRV	YGADVQNSG	GAFQCQTQGR	RQNTVFGIMFQ
g902	60	70	80	90	100
	ADVPAYVFACDA	HTDGLTIKRV	HGADVQNGG	SAFCQTQGR	RXNAVFGIMLQ
m902.pep	120	130	140	150	160
	LRAAPYHNAVGG	LFEGLGFL	RRSNVAVD	PDPRDVTAF	GGDEFVTRFA
g902	120	130	140	150	160
	LRAAPYHNAVGG	LFEGLGFL	RRSNVAVD	PDPRDVTAF	GGDEFVTRFA
m902.pep	180	190	200	210	220
	DGKGGDAI	FGDFGDDG	QVLMVVPT	QTGFEGNGY	ACRTDDGFQ
g902	180	190	200	210	220
	NGKGGNAI	FGDFGDDG	QVLMVVPT	QTGFEGNGY	ARRLDHRLQ
m902.pep	240	250	260	270	280
	DIADFFSGTA	HVDVDKLR	PKADVVT	TRGIRHLL	RIASGNLH
g902	240	250	260	270	280
	DVAHFLGGA	AHIDVDDL	RPESDV	VTTRIRH	LFVGAAGN
m902.pep	300	310	320	330	340
	ERRVAGQHFA	HRPTCAK	ISAKSAER	FVGNARH	RRKCDGV
g902	300	310	320	330	340
	ERRIAGQHFA	HRPTCAK	RPTAAEG	FVGNARH	RRKCDGV
m902.pep	360				
	IFX				
g902	360				
	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

1 TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATT GGGCGGTAGG
 51 CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTCAAG ATAACCTGCA

1288

```

101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCAGGACG
151 TGTCTGTTCG CCGTCGGGCA TTTCGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAACTCA AGGCAGGCGG
301 TAAAAACACG TGTTCGGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTGTTGTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAGGTA ATGTCGCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTTCGGTG CGCGTGCCTC CGTGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCCGCGCCTT
651 TGACCACCGC CTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACCC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCTT
851 TCATCGGCAA AATCGCTCGC GTGCAAGTTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAAGT
1001 GCGATGGGGT TGTGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

a902.pep

```

1 LHFQRIIKCS EGIWAVGARPTVGFFGKSFK ITCKHVVLRRTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGRR
101 *NTVFGVMFQ IAEEPRSAIR AAPYHNAVCG GLFEDGLGFL RRGNVAVDPP
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGGNAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSCTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFHR PTCAKISAKS AERFVGNAHR RRCDCGVVDK AADVHNGSA
351 FOKSTPLYIF *

```

m902/a902 94.7% identity in 360 aa overlap

	10	20	30	40	50	60
m902.pep	LHFQRIIKCS	EGIWAVGARPT	TVGFFGKSFK	ITCKHVVLRRT	TVQAVDFTT	CLFAVGHFVD
a902	LHFQRIIKCS	EGIWAVGARPT	TVGFFGKSFK	ITCKHVVLRRT	TVQAVDFTT	CLFAVGHFVD
	10	20	30	40	50	60
	70	80	90	100	110	120
m902.pep	VPAYVFACDA	HTGGVAVKRV	YGADVQNSG	GAFCQTQGR	RQNTVFGIM	FQIAEEPRPALR
a902	VPAYVFACDA	HTGGVAVKRV	HGSDVVQNSG	GTFCQTQGR	RXNTVFGVM	FQIAEEPRSAIR
	70	80	90	100	110	120
	130	140	150	160	170	180
m902.pep	AAPYHNAVGG	LFEDGLGFL	RRSNVAVDP	DRDVTAFG	FGDEFVTR	FAFVHLRTRASVDG
a902	AAPYHNAVCG	LFEDGLGFL	RRGNVAVDP	DRDVTAFG	FGNQVVSRA	FAFVHLRARASVDG
	130	140	150	160	170	180
	190	200	210	220	230	240
m902.pep	KGGDAAIFG	DFGDDGQV	LMVVVPTQT	GFEGNGYAC	RDDGFQNG	GNQRLVLHQRATGLDI
a902	KGGNAIFG	DFGDDGQV	LMVVVPTQT	GFEGNGYAR	RFDRHLQNG	GNQRLVLHQRATGLDI
	190	200	210	220	230	240
	250	260	270	280	290	300
m902.pep	ADFFSGTAHV	DVDKLRPKAD	VVTRGIRHLL	RIASGNLHGN	NAAFIGKIAA	VQGFSSISER
a902	ADFFSGTAHV	DVDKLRPKAD	VVTRGIRHLL	RIASGNLHGN	NAAFIGKIAA	VQGFSSISER
	250	260	270	280	290	300
	310	320	330	340	350	360
m902.pep	RVAGQHFHR	PTCAKISAKS	AERFVGNAHR	RRCDCGVVDK	IAADVHNGSA	FOKSTPLYIF

1289

```

a902      |||||
          RVAGQHFHAHRPTCAKISASAEERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTFLYIF
          310      320      330      340      350      360

m902.pep   X
          |
a902       X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
51 TCCTATTCTT GAGGTGGAaT TGGTGGGTGA aGaaacggct aAATTCCGgt
101 tTGCCTCcaa ccaTGCCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAatcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCGGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAAccctga tgccggGCTA TctgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTT CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTTGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGTAAC GTCTGTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTCGG CTTCAACCGC CTGTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAAC TGCTGTACAAC GGCGTAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTGCGAGTA CGGCAGATTT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAACAGC TATTTGCTTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCGCTA ACATCGCAAG ACAAAGTGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTTAAA
1351 CCAGGCCATC AGCTTTATCT TGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGTTTATCGG GCCAAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA TATATTTACC
1501 GGCCGTGCAT TGAAAAAGCC cgaatatttt cAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51 LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAFO NKFPTRSNDL LNLRLDLEQL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHKKEGCSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQAVSG LSEVYDYGK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRE TKS YIDDAEL TVQRRKTTGW LAELSHKGYI GRSTADFLKL
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGKY WRNDLSWQFK
451 PGHQLYLGLD VGHVSGQSAK WLSGQTLAQT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKWTGFG VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAAATGT
51 CCGTTTCGAG CAACCATTGG AGAAGAACAA TTATGCTCTG AGTGAAGATG
101 AAACACCGTG TACTCGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

1	MQRQOHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTV
51	RKFSFLPSVL	MKETAFKTM	CLGSNNLSRL	QKAAQILIV	RGYLTSQAI
101	QPQNMDSGIL	KLRVSAGEIG	DIRYEKRDG	KSAEGSISAF	NNKFPLYRNM
151	ILNLRDVEQG	LENLRRLSVP	KTDQIIPSE	EFGKSDLOIK	WHQNKPIRFS
201	IGIDDAGGKT	TKGYQGNVAL	SFDNPLGLSD	LFYVSYGRGL	AHKTDLTDAT
251	GTETESGSRV	YSVHYSVPVK	KWLFSFNHMG	HRYHEATEGY	SVNYDYNGKQ
301	YQSSLA AERM	LWRNRLHKTS	VGMKLWTRQT	YKYIDDAEIE	VQRRRSAGWE
351	AELRHAYRLN	RWQLDGKLSY	KRGTMGRQSM	PAPEENGDI	LPGTSRMKII
401	TASLDAAAPF	XLGQOQFFYA	TAIQAQWNT	PLVAQDKLSI	GSRYTVRGGLD
451	GEQSLFAGER	FWYQNTLTWY	FHPNQHFYLG	ADYGRVSGES	AOYVSGKQLM
501	GAUVGFRRGH	KVGMGFAYDL	FAGKPLHKPK	GFOTTNTVYG	FNLNYSF*

Homology with a predicted ORF from *N. gonorrhoeae*

m903/g903

	10	20	30	40	50	60
m903.pep	MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYSISLDDKTVRKFSFLPSVL					
			:	:	:	:
g903			MATQVGGSNDSEASPCFPPISEVELVGEETAKFRFALNHA			
			10	20	30	
	70	80	90	100	110	120
m903.pep	MKETAFKTGMCLGSNNLSRLQKAAQQLIVRGYLTSAIIQPQNMDSGILKLRSAGEIG					
	:	:	:	:	:	:
g903	LCQTHFVSGKCLHAGDINQIMSLAQNALICRGYTTRILAAPDLNSGKLQLTLMPGYL					
	40	50	60	70	80	90

1291

	130	140	150	160	170	180
m903.pep	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRDVEQGLNLRRLPSVKTDIQIIPSE					
g903	SIRIDRSNDQTHAGRIAAFQNKFPTRNDLLNLRDLEQGLNLRRLPSVKTDIQIIPSE					
	100	110	120	130	140	150
	190	200	210	220	230	
m903.pep	EE-GKSDLQIKWQNK-PIRFSIGIDTAGGKTTGKYQGNVALSFDNPLGLSDFVSYGR					
g903	REPNSQSDVVQWRXRLLPYCVSVGMDNSGSEATGKYQGNITFSADNPFGLSDMFYVNYGR					
	160	170	180	190	200	210
	240	250	260	270	280	290
m903.pep	GLAHKTDLDATGTETESGSRYSVHYSPVKKWLFSPNHNHRYHEATEGYSVNYDYG					
g903	SIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAFNHNHRYHQAVSGLSEVYDYG					
	220	230	240	250	260	270
	300	310	320	330	340	350
m903.pep	KQYQSSLAERMLWRNRLHKTSSVGKMLWTRQTYKIDDAEIEVQRRRSAGWEAELRHAY					
g903	KSYNTDFGFNRLLYRDAKRKTYLSVKLWTRTKSYIDDAELTVQRRKTTGWLAELSHKGY					
	280	290	300	310	320	330
	360	370	380	390	400	410
m903.pep	LNRWQLDGKLSYKRGTMGRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQOFF					
g903	IGRSTADFKLKYKHGTGMKDALARPEEAFGE---GTSRMKIWTASADVNTPFQIGKQLFA					
	340	350	360	370	380	390
	420	430	440	450	460	470
m903.pep	YATAIQAWNKTPPLVAQDKLSIGSRYTTRGFDGEQSLFGERGFYQNTLTWYFHPNHQFY					
g903	YDTSVHAQWNKTPPLTSQDKLAIGGHHTVRGFDGEMSLPAERGWYWRNLDLWQFKPGHQLY					
	400	410	420	430	440	450
	480	490	500	510	520	530
m903.pep	LGADYGRVSGESAQYVSGKQLMGAVVGFGRGHKVGGMFAYDLFAGKPLHKPKGFQTTNTV					
g903	LGADVGHVSGSAKWLSGQTLAGTAIGRQIKLGGNLHYDIFTGRALKKPEYFQTKKWV					
	460	470	480	490	500	510
	540					
m903.pep	YGFNLNYSFX					
g903	TGFQVGYSFX					
	520					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2719>:

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTAACTG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATGG	AGAAGAACA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTCTTCC	TTCTGTGCTC	ATGAAAGAAA	CAGCTTTTAA
201	AACGGGATG	TGTTAGGTT	CCAATAATT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGGCTACC	TCACTTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTC	GGGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGGCAGTAT	TAGTGCATTC	AATAACAAAT	TTCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TTCGCGATGT	AGAGCAGGGC	TTGGAAAACC	TGCGTCGTTT
501	GCCGAGTGTT	AAAACAGATA	TTCAGATTAT	ACCGTCCGAA	GAAGAAGGCA
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTCAGT

1292

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601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTGCGTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTATG
701 TTTCATATGG ACGCGGTTTG GTGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAAT ACGATTACAA CCGCAACAAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCCGGAT TGGATGCAGC GGCCCCGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATT CAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTTGAT
1351 GGGAGACAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTGCGCGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903.pep

```

1 MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTA
51 RKFSFLPSVL MKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NKFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGFSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNGKQ
301 YQSSLAERMLWRNRFHKT VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRAYLN RWQLDGKLSY KRGTMQRQSM PAPEENGGGT IPGTSRMKII
401 TAGLDAAAPF MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTXXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTNTVYV FNLNYSF*

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m903/a903 98.4% identity in 547 aa overlap

	10	20	30	40	50	60
m903.pep	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTV	RKFSFLPSVL
a903	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTAR	KFSFLPSVL
	10	20	30	40	50	60
m903.pep	MKETAFKTM	CLGSNNLSRL	QKAAQQILIV	RGYLTSQAI	QPQNMDSGIL	KLRVSAGEIG
a903	MKETAFKTM	CLGSNNLSRL	QKAAQQILIV	RGYLTSQAI	QPQNMDSGIL	KLRVSAGEIG
	70	80	90	100	110	120
m903.pep	DIRYEEKRDG	KSAEGSISAF	NKFPLYRNK	ILNLRDVEQ	LENLRLPSV	KTDIQUIPSE
a903	DIRYEEKRDG	KSAEGSISAF	NKFPLYRNK	ILNLRDVEQ	LENLRLPSV	KTDIQUIPSE
	130	140	150	160	170	180
m903.pep	EEGKSDLQIK	WQONKPIRFS	IGIDDAGGKT	TGKYQGNVAL	SFDNPLGLSD	LFYVSYGRGL
a903	EEGKSDLQIK	WQONKPIRFS	IGIDDAGGKT	TGKYQGNVAL	SFDNPLGLSD	LFYVSYGRGL
	190	200	210	220	230	240
m903.pep	AHKTDLTDAT	GTETESGSR	SVHYSVPVK	KWLFSFNHNG	HRHYHEATEG	SVNYDYNGKQ
a903	VHKTDLTDAT	GTETESGSR	SVHYSVPVK	KWLFSFNHNG	HRHYHEATEG	SVNYDYNGKQ
	250	260	270	280	290	300
m903.pep	AHKTDLTDAT	GTETESGSR	SVHYSVPVK	KWLFSFNHNG	HRHYHEATEG	SVNYDYNGKQ
a903	VHKTDLTDAT	GTETESGSR	SVHYSVPVK	KWLFSFNHNG	HRHYHEATEG	SVNYDYNGKQ

1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKTSGVMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
a903	YQSSLAERMLWRNRFHKTSGVMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIIITASLDAAAPFXLGKQOFFYA					
a903	RWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIIITAGLDAAAPFMLGKQOFFYA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

```

g904.seq
1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGCGCG GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAAAT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGGCCTT CAAACAGCAG TTTTTCGCGG TTTTGTGTTT
651 TTTCGTTCAA CACGCGggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGTCGCT
901 GCCGATTTG CCTTTGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCCCAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAGGAT ACCGTCGGA ATCAGGCGCA AAATGGTTTT TTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

```

g904.pep
1  MMQHNRFFAV GAGGDDGDRR AADFFNPFI CFGRQCVV AFHADSRFAP

```

1294

```

51 AGHGFVNRF A GFHRIARTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
101 HTGNAVDLDG AFQGGGIKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS RAGETVGRGN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRSR
251 VMQVLELDVV IGKDG IQFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFARCF AGLVERDVVR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGNDNART DEAIQS FVQD TARNQAQNGF FAADDQGMAR IVAALEAHDA
401 AGFFRQPVND FTFTLVAPLC ADYNYIFSHS HITYRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

```

m904.seq
1 ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCGgTG GAGACGATGG
51 CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCG
101 TTTTCGGGCA ATGCGCCGTA GTCCTTCACG CCGAAAGTGG ATTTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTCACACC GCATCGGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC ATAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TAGTAATACA
301 CATAACGGAA ATGCCGTTGA TTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCTTCTG CCAAACCTAC GCCTACTTCG TCGAACCAATT CGGTGCGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC TGCGCCCGCC
551 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTGCCG. ACT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCGG TTTTGTGTTT
651 TCTCGTTCAA CACGCGGAC ACCTCGGTAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTAA CCGGCTCGGC
751 ATTGTGCAGA TGTTCAGTT GGACATTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTyTCA GGATGCAGCA AATCGGCGGC GCGAATGCGC
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CTTTGGCCGC GCG.ATcTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAAACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACCAcGCC
1201 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTAsT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

```

m904.pep
1 MMQHNRRFFSV GAGGDDGDRR AADFFNPFI CPGVFGQCAV VLHAESGFAP
51 AGHGFVNRLA GFHRIARTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVSAFCQTY AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS CARQTVGRGN EGISAVVDVQ
201 QRTLRAFQKQ FFAVFVFLVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRLG
251 IVQMLQLDIV IGKDG IQFFT QFXRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAXIF AGLVERDVVR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMR IVAALEAHHA
401 AGFFRQPVND FTFTLVAPLC ADXYNIFSHS HITYRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

```

m904/g904
10 20 30 40 50 60
m904.pep MMQHNRRFFSVGAGGDDGDRRAADFFNPFI CPGVFGQCAVVLHAESGFAPAGHGFVNRLA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g904 MMQHNRRFFAVGAGGDDGDRRAADFFNPFI CPGIGRQCVVAFHADSRFAPAGHGFVNRF
10 20 30 40 50 60
70 80 90 100 110 120

```

1295

m904 . pep	GFHRIGTARQDVGFAAVGFQFIADADIDGFNAVHYIEFSNTHGTGNAVLDGAFQGGGIKPA
g904	GFHRIRTARQDVGFAAAWQFVADADIDGFNAVHYIEFGNAHTGNAVLDGAFQGGGIKPA
	70 80 90 100 110 120
m904 . pep	AAACASGYRTEFVS AFCQTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
g904	AAARAAGYRTEFVSALRQTCAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
	130 140 150 160 170 180
m904 . pep	CARQTVGRGNEGISAVVDVQORTLRAFQKQFFAVFVFLVQHAGHVGHNHRRNARRDFFDNR
g904	RAGETVGRGNEGVS AVVDVQORTLRAFQKQFFAVFVFFVQHAGHVGHNHRRNARRDFFDNR
	190 200 210 220 230 240
m904 . pep	HHVFRFNRLGIVQMLQLDIVIGKDG IQFFTQFXRMQ QIGGANGAACHFVFVGRADAAAGR
g904	HHVFRFNRS GVMQVLELDV VIGKDG IQFFTQFFRMQ QIGGANGAACHFVFVGRADAAAGR
	250 260 270 280 290 300
m904 . pep	ADFAFAARI FAGLVERDVVRQDQRAGR RDFQTA FDV FHACRVQLVDF AQGGFGGDDNART
g904	ADFAFAARC FAGLVERDVVRQDQRAGR RDFQTA FDV FHACRVQLVDF AQGGFGGDDNART
	310 320 330 340 350 360
m904 . pep	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVA ALEAHHAAGFFRQPVNDF TFLVAPLC
g904	DEAIQSFVQDTARNQAQNGFFAADNQGMARIVA ALEAHDAAGFFRQPVNDF TFLVAPLC
	370 380 390 400 410 420
m904 . pep	ADXYNIFSHSHITYRYX
g904	ADYYNIFSHSHITYRYX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

```

1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTG GAGACGATGG
51  CGACCGGCGC ACCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGTA ATGCGTCGTA GCTTTTCACG CCGAAAGTGG ATTTCGCTCCA
151 ACCGGGCATG GTTTCGTAAA TCGGCTTGCA GGCTTCTACC GCATCAGAGC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATACA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCCGCAT
351 CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTTC TG CCAAACCTGC TCCGACTTCG TCGAACAATT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGGCCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGGCAGTTGG ACGAAGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCGG TTTTGTGTTT
651 TTTCGTCAA CACGCGGGAC ACGTCGATAA TCATCGGCGT AATGCGCGGC
701 GCGACTTTT CGATAACCGC CATCACGTCT TCCGCTTTCA CCGACTCGGC
751 ATTGTGCAGA TGTTGCAGTT GGACGTTGTA ATAAGCAAAG ACGGCATCCA
801 GTTTTTCACG CAGTTTTCAT GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGTCGCT
901 GCCGATTTG CCTTTGCCGC GCGATGCTTC TCGGCTTGG TCGAGCGCGA

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1296

```

951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCGAACG GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTGCGCGCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCG CCTTGAAGC GCACCACGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

a904.pep

```

1 MMQHNRRFAV GAGGDDGDRR TADFFNPFQI CFGIGF*CVV AFHAESGFAP
51 TGHGFVNRLA GFYRIRAA*Q DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVDLDG AFQGGGIKP* AAACASGYRT EFVSAFCQIC SDFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFHRLG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQQIGG ANGAACHEVF VGRADAAAGR
301 ADFAFARCF SGLVERDVIR QDQRAGRRDF QTAFDVFHAC RVQLVDFACQ
351 GFGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMTR IVAALEAHHA
401 SGFFRQPVND FTFTLVAPLC ADYNYIFSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

m904.pep	10	20	30	40	50	60
	MMQHNRRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA					
a904	10	20	30	40	50	60
	MMQHNRRFFAVGAGGDDGDRRTADFFNPFQICFGIGRXCVAFAHAESGFAPTGHGFVNRLA					
m904.pep	70	80	90	100	110	120
	GFHRIGTARQDVGFAAVGGQFIADADIDGFNAVHYIEFSNTHGNAVDLDGAFQGGGIKPA					
a904	70	80	90	100	110	120
	GFYRIRAAQDVGFAAVGGQFVADADIDGFNAVHYIEFGNTHGNAVDLDGAFQGGGIKPA					
m904.pep	130	140	150	160	170	180
	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRYARACRS					
a904	130	140	150	160	170	180
	AAACASGYRTEFVSAFCQTCSDFEQFGRERARTDARGIGFDDAQNI IQHLRAYARACRS					
m904.pep	190	200	210	220	230	240
	CARQTVGRGNEGISAVVDVQQRITLRAFQKQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR					
a904	190	200	210	220	230	240
	RAGEAVGRSNEGVSAVVDVQQRITLRAFQKQFFAVFVFFVQHAGHVGNHRRNARRDFFDNR					
m904.pep	250	260	270	280	290	300
	HHVFRFNRLGIVQMLQLDIVIGKDGIOFFTQFXRMQQIGGANGAACHEVFVGRADAAAGR					
a904	250	260	270	280	290	300
	HHVFRFHRLGIVQMLQLDVVISKDGIOFFTQFFRMQQIGGANGAACHEVFVGRADAAAGR					
m904.pep	310	320	330	340	350	360
	ADFAFAAXIFAGLVERDVVRQDQRAGRRDFQTAFDVFHACRVQLVDFACQGGFGDDNART					
a904	310	320	330	340	350	360
	ADFAFAARCFSGLVERDVIRQDQRAGRRDFQTAFDVFHACRVQLVDFACQGGFGDDNART					
m904.pep	370	380	390	400	410	420
	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
a904	370	380	390	400	410	420
	DEAVQTFMQDAARNQAQNGFFAADNQGMTRIVAALAHHASGFFRQPVNDFTFTLVAPLC					

1297

```

m904.pep      ADXYNIFSHSHITYRYX
               || ||||| |||| |||
a904          ADYYNIFSHSHITXRYX
               430

```

```

g906.seq      not found yet
g906.pep      not found yet

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101 TGAATAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFGG FKPWPDAAS FWELKNYANP YPGSASAALD
51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGcaAC GCCGCCGCCT
51 GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101 CGCAACGTGA AGAAACGCTt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTTCGACA ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGCA AGATTCGTCC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAOREETL ADDVASVMRS
51 SVGSVNPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51 GTTGTGTGCC GCCGGTGCCT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGCA AGGTTCTGTC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTAT GCCGTTkTGG AAAAActACA TCGGCAAACC GGCGCACAAc
451 CTGTTTCGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MRKPTDTLPV NLQRRRLCA AGALLSPLA HAGAOREETL ADDVASVMRS
51 SVGSVNPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVGA RGLMQVMPXW XNYIGKPAHN

```

1298

151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907.pep	MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQR	EETLADDVASVMR	SSVGSVNP	PRL		
m907	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQR	EETLADDVASVMR	SSVGSVNP	PRL		
	10	20	30	40	50	60
	70	80	90	100	110	120
g907.pep	VFDNPKEGERWLSAMSARLARFVPEDEGERRLLVNIQYESSRAGLDTQIVLGLIEVESGY					
m907	VFDNPKEGERWLSAMSARLARFVPEEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	70	80	90	100	110	120
g907.pep	RARIIS					
m907	RQYAIISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

```

1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGCAAC GCCGCCGCCCT
51  ATTGTGTGCT GCCGCGCGCG TGTGCTCAG CCCGCTGGCA CAAGCCGGCG
101 CGCAACGTGA AGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGC
151 TCTGTCGGCA GCATAAATCC GCCGAGGCTG GTGTTTCGACA ATCCGAAAGA
201 GGGCGAGCGT TGGCTGTCCG CGATGTCTGC TCGGTTGGCA AGGTTCTGTC
251 CCGATGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTAT GCCGTTTTGG AAAAATACA TCGGCAAACC GGCGCACAAC
451 CTGTTTCGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCACTC GCCCGTTTTA
551 ACGGTAGCCT CGGCAGCAAT AAATATCCGA ACGCCGTTTT GGC GCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

```

1  MKKPTDTLPV NLQRRRLCA AGALLSPLA QAGAQR EETL ADDVASVMRS
51  SVGSINPPRL VFDNPKEGER WLSAMSARLA RFVPDEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAIISGVA RGLMQVMPFW KNYIGKPAHN
151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

```

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQR	EETLADDVASVMR	SSVGSVNP	PRL		
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAQR	EETLADDVASVMR	SSVGSINP	PERL		
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
a907	VFDNPKEGERWLSAMSARLARFVPEEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

1299

	70	80	90	100	110	120										
	130	140	150	160	170	180										
m907.pep	RQY	AIS	GVG	ARGL	MQV	MPXW	KNYIGK	PAH	NLFD	IRTN	LRYG	CTIL	RHYR	NLEK	GNIV	RAL
a907	RQY	AIS	GVG	ARGL	MQV	MPFW	KNYIGK	PAH	NLFD	IRTN	LRYG	CTIL	RHYR	NLEK	GNIV	RAL
	130	140	150	160	170	180										
	190	200														
m907.pep	ARF	NSL	GSN	KYP	NAVL	GAW	RNR	WQWR	X							
a907	ARF	NSL	GSN	KYP	NAVL	GAW	RNR	WQWR	X							
	190	200														

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1   ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAGT CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTTAT
151 CAAAACGGTC CGCATTTAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatT TTagcttcgc tgaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1   MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF DGEVEADESYF GGQRKGKGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIVYDCY RSYDVLVDSE FSHFSFAETS
151 FSYQSQTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1   ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAAC
51  GTTTGTCACA GGTGTAAGT CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAC CCTGACAGCA TTTTATATAC GCATTGTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1   MRKSRLSRYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMF DGEVEADESYF GGQRKGKGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIFYDCY RSYDVLVDRE FSHFSFAETS
151 FSYQSQTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng)

from *N. gonorrhoeae*:

g908/m908

	10	20	30	40	50	60
g908.pep	MXKSRLSRYK	QNKLIGLFV	AGVTARTAAEL	VGINKNTAAY	DFHRLRLLIY	QNGPHLEMF

m908	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNTAAYYFHRRLRLLIYQNSPHLEMF
	10 20 30 40 50 60
g908.pep	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNTQTATLFPPIIREQVK
m908	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNTQTATLFPPIIREQVK
	70 80 90 100 110 120
g908.pep	PDSIVYTD CYRSYDVL DVSEF SHFSFAETSFSYQSQHTFCRRTTKPYX
m908	PDSIFYTD CYRSYDVL DVREFSHFSFAETSFSYQSQHTFCRRTTKPYX
	130 140 150 160

```

a908.seq
1  ATGAGAAAAA  GTCGTCTAAG  CCAGTATAAA  CAAAATAAAC  TCATTGAGCT
51  ATTTGTCGCA  GGTGTAACCT  CAAGAACCGG  AGCAGAGTAT  GTAGGCGTTA
101 ATAAAAATAC  CGCAGCCTAT  TATTTTCATC  GTTTACAGTT  ACTTATTTAT
151 CAAAACAGTC  CGCATTTGGA  AATGTTTGAT  GGCGAAGTAG  AAGCAGATGA
201 AAGTTATTTT  GCGGGAACA  GCAAAGGCAA  ACGCGGTCCG  GGTGCTGCCG
251 GTAAAGTCGC  CGTATTCGGT  CTTTGTGAAG  GAAATGGTAA  GGTTTATACG
301 GTTACAGTAC  CGAATACTAC  AACCCTACT  TTATTTCTTA  TTATCCGTGA
351 ACAAGTGAAA  CCTGACAGCA  TTGTTTATAC  GGATTGTTAT  CGTAGCTATG
401 ATGTATTAGA  TGTGCGCGAA  TTTAGCCATT  TTAGCTTCGC  TGAAACTTCG
451 TTTTCGTATC  AATCACAGCA  CACATTTTGC  CGAACGACAA  AACCATATTA
501 A

```

```
a908.pep
  1  MRKSRLSQYK QNKLIELFVA GVTARTAAEL VGVNKNTAAY YFHLRLLIY
51  QNSPHLEMFQ GEVEADESYK GGQRKGKGRG GAAGKVAVFG LLKRNKGVYT
101 VTPVNTQTAT LFPIIREQYK PDSIVYTDY RSYDVLVDRE FSHFSFAETS
151 FSYSOHTFC RTTKPY*
```

	10	20	30	40	50	60
m908.pep	MRKSRLSQYKQXKLI	ELFVTGTARTAAELV	GVNKNNTAAYYFHR	LRLLIYQNSPHLE	MFD	
a908	MRKSRLSQYKQKLI	ELFVAGVTARTAAEL	GVNKNNTAAYYFHR	LRLLIYQNSPHLE	MFD	
	10	20	30	40	50	60
	70	80	90	100	110	120
m908.pep	GEVEADESYFGGQR	KGRGRGAAGKVAV	FGLLRNGKVYTV	TVPTQTATLFPI	IREQVK	
a908	GEVEADESYFGGQR	KGRGRGAAGKVAV	FGLLRNGKVYTV	TVPTQTATLFPI	IREQVK	
	70	80	90	100	110	120
	130	140	150	160		
m908.pep	PDSIFYTDCYRSYD	VLDVREFSHFSFA	ETSFYSQSQHTF	CRRTTKPYX		
a908	PDSIVYTDYRSYD	VLDVREFSHFSFA	ETSFYSQSQHTF	CRRTTKPYX		
	130	140	150	160		

```
g909.seq (partial)
      1  atgcgtaaaa ccgtacttat cCTgaccatc tccgccgcc ttttgcggg
     51  ctgcacatgG gaaacttatac aagacggcag cggcaaaacc gccgtccgtg
    101  caaaatgttc caccggcacg ccgctgtgtt gcacaagacg gcgcgcctca
```


1301

```

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg
201 caaccaaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa
301 acgggggagg ggaagcgatc ggcgagg..

```

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

```

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
51 KKVDCDEYGG ERRAVLNRQK RGKPTRRAA TLGKPSFRAR DGGGRVNRAE
101 TGEKRSAR..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

```

1 ATGCGTAAAA CCTTCCTCTT CTGACCGCT GCCGCCGCC TTTGTGCGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AACCAAAGTT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

```

1 MRKTFLEFLTA AAALLSGCAW ETYQDGNgKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDGNgKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		:	:	:	:	: : :
g909	MRKTVLILTI	SAALLSGCTW	ETYQDGSgKT	AVRAKSTGT	PLCWQDGRGS	KKVDCDEYGG
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLPNQT	GNNADEEHRQ	HWQKPKFQNR	X		
	:	: :	: :			
g909	ERRAVLRNQK	RGKPTRRAA	TLGKPSFRAR	DGGGRVNRAE	TGEKRSAR	
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

```

1 ATGCGTAAAA CCTTCCTTAT CTGATGACT GCCGCCGCC TTTGTGCGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AGCCCAAATT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

```

1 MRKTFILILT AAALLSGCAW ETYQDGNgKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDGNgKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		:	:	:	:	: : :
a909	MRKTFILILT	AAALLSGCAW	ETYQDGNgKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
	10	20	30	40	50	60

1302

	70	80	90
m909.pep	ERHAVLPNQ	TGNNADEEHRQHWQKPKFQNRX	
a909	ERHAVLPNQ	TGNNADEEHRQHWQKPKFQNRX	
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAAACAGC CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.pep
1  MKKLLLAADV SLSAAAAFAG DSAERQIYGD PHFEQNRKA VKMLEQRGYQ
51  VYDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
g910.pep	MKKLLLAADVSLNAATAFAG	DSAE	RQIYGD	PHFEQNR	KAVKMLEQRGYQ	VYDVDADDYW
m910	MKKLLLAADVSLSAAAAFAG	DSAE	RQIYGD	PHFEQNR	KAVKMLEQRGYQ	VYDVDADDHW
	10	20	30	40	50	60
	70	80	90			
g910.pep	GKPVLEVEAY	KDGREYDIVL	SYPDLKIIKEQLDRX			
m910	GKPVLEVEAY	KDGREYDIVL	SYPDLKIIKEQLDRX			
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAAACAGC CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```

a910.pep

```

1303

```

1 MKKLLLVAVV SLAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
51 VHDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

m910/a910 95.7% identity in 94 aa overlap

```

              10      20      30      40      50      60
m910.pep      MKKLLLAHVVSLSAAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVVDVDADDHW
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a910           MKKLLLVAVVSLAATAFAGDSAERQIYGDPIYFEQNRTKAVKMLEQRGYQVHDVDADDHW
              10      20      30      40      50      60

              70      80      90
m910.pep      GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a910           GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

```

g911.seq
1 ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCTTGATCGG
51 CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCGGGC GGCGCGGCGT
101 TCGGCGGTTT GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTTGATTT GGACGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
351 CGGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCACTT
401 CTGCAATGGT TCTGAAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC
451 GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcag aAtaa

```

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

```

g911.pep
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNAEGGNAE KAAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

```

m911.seq
1 ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG
51 CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTT GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTT GGACGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCACTT
401 CTGCAATGGT TCTGAAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

```

m911.pep
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

```

              10      20      30      40      50      60

```

1304

```

g911.pep      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
              |||||
m911          MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
              10      20      30      40      50      60

              70      80      90      100     110     120
g911.pep      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              |||||
m911          SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              70      80      90      100     110     120

              130     140     150     160
g911.pep      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              |||||
m911          ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1   ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGA CTGTTTCG TCCTGATTGG
51  CGCGCGGCGC GTTGCCCTTC TCGCTTTCCG CGTGGCCGCG GGTGCGCGCT
101 TCGGCGGTTC GGACAAACTT TACGCCGTTT ATGCCGATTG CGGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTG GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCACTT
401 CTGCAATGGT TCTGAAAAAC CTTATCGGCA AATTATGACG GAGTTTGGCC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1   MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAGFGSDKT YAVYADFGDI
51  GGLKVNAPVK  SAGVLVGRVG AIGLDPKSYQ ARVRDLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

m911.pep      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
              |||||
a911          MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
              10      20      30      40      50      60

              70      80      90      100     110     120
m911.pep      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              |||||
a911          SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              70      80      90      100     110     120

              130     140     150     160
m911.pep      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              |||||
a911          ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1   gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTGTACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

1305

```

151 CGCCCAAAAG CCGAAGCCTA TCGGGTTCCC TATTTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG TACCGCGTCC GACGCGCAAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTCAA AAACGCGACC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAGGGCGGCA AGGAAATCGT CGTCCGTGCC GAAGTCGGCA
401 TCCCCGGTCA GAAGCCCGTC AATATGGACT TTACCACCTA CCAAAGCGGC
451 GGCAAATAC GTACCTACAA CGTCGCCATC GAAGGCACGA GCCTGGTTAC
501 CGTGATCCGC AACCAATTCG GCGAAATCAT CAAAGCCAAA GGCATCGACG
551 GGCTGATTGC CGAGTTGAAA GCCAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2760; ORF 912.ng>:

```

g912.pep
1 VKKSSFISAL GIGILSIGMA FASPADAVGQ IRONATQVLT ILKSGDAASA
51 RPKAEAYAVP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYS
101 GTMLKFKNAT VNVKDNPIVN KKGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTYR NQFGEI IKAK GIDGLIAELK AKNGGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2761>:

```

m912.seq
1 ATGAAAAAAT CCTCCCTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
51 CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAGCCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA ACGCGCATGC CAACACCGCT
151 CGCCCAAAAG CCGAAGCCTA TCGGATTCCC TATTTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAATATAC GTACCTACAA CGTCGCCATC GAAGGCACGA GCCTGGTTAC
501 CGTGATCCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGGTGGACG
551 GACTGATTGC CGAGTTGAAA GCCAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:

```

m912.pep
1 MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRONATQVLS ILKNGDANTA
51 RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYS
101 GTMLKLKNAN VNVKDNPIVN KKGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYR NQFGEI IKAK GVDGLIAELK AKNGGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

```

g912/m912
          10      20      30      40      50      60
g912.pep VKKSSFISALGIGILSIGMAFASPADAVGQIRONATQVLTILKSGDAASARPKAEAYAVP
          :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m912      MKKSSLISALGIGILSIGMAFAAPADAVSQIRONATQVLSILKNGDANTARQKAEAYAIP
          10      20      30      40      50      60

          70      80      90     100     110     120
g912.pep YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKFKNATVNVKDNPIVN
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m912      YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN
          70      80      90     100     110     120

          130     140     150     160     170     180
g912.pep KKGKEIVVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTYVRNQFGEI IKAK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m912      KKGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYVRNQFGEI IKAK
          130     140     150     160     170     180

          190
g912.pep GIDGLIAELKAKNGGKX

```

1306

```

      |||||
m912  GVDGLIAELKAKNGGKX
      190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

```

a912.seq
1  ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
51  CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAACCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
151 CGCCAAAAAG CCGAAGCCTA TCGGATTCCC TATTTGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGCGCGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAATACCG GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGGTGGACG
551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

```

a912.pep
1  MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA
51  RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTL LIR TYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPSQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYR NQFGEI IKAK GVDGLIAELK AKNGSK*

```

m912/a912 98.0% identity in 196 aa overlap

```

      10      20      30      40      50      60
m912.pep  MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNATQVLSILKSGDANTARQKAEAYAIP
      10      20      30      40      50      60

      70      80      90      100     110     120
m912.pep  YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTL LIR TYS GTMLKLKNANVNVKDNPIVN
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTL LIR TYS GTMLKLKNANVNVKDNPIVN
      70      80      90      100     110     120

      130     140     150     160     170     180
m912.pep  KGGKEIIVRAE VGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEI IKAK
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      KGGKEIIVRAE VGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEI IKAK
      130     140     150     160     170     180

      190
m912.pep  GVDGLIAELKAKNGGKX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      GVDGLIAELKAKNGSKX
      190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

```

g913.seq
1  atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCAGAAACCC GCCCGGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCGCGCGT
201 GTCCAATTTT TTTAACAACC TGCGCGACGT GGTCAAGTTT GGCAGCAATA
251 TCTTGGCTTT GGACatCAAA cgcgcAAGcg aAGACtctg CCGcgtcggc
301 atCAATACCA CCTTCGGTTT GGcgcGGCTC ATTGATATTG CCGGcgcGGg
351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctgGAAAAa cagcaATTAT TTCGTgttgc CCGtcttagg cccgctccac

```

g913.pap

m913.seq

m913 . pep

g913/m913

	10	20	30	40	50	60
g913.pep	MKKTAYAILLLIGFASAPAF	AE	TRPADP	YEGYNRAVSKFNDQADRYIF	FAPAARGYRKVTP	
	:					:
m913	MKKTAYAFLLLLIGFASAPAF	AE	TRPADP	YEGYNRAVFKFNDQADRYIF	FAPAARGYRKVAP	
	10	20	30	40	50	60
	70	80	90	100	110	120
g913.pep	KPVRAGVSNFFNNLRDVVS	FGSNILRLDI	KRASEDLVRVGINTT	FGLGGLIDI	AGAGGVP	
m913	KPVRAGVSNFFNNLCDVVS	FGSNILRLDI	KRASEDLVRVGINTT	FGLGGLIDI	AGAGGIP	
	70	80	90	100	110	120

1308

	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWKNSNYFVL	PVLGPSTVRDALGTGITSVYPPKNIVFHT	PAGRWGTT			
m913	DNKNTLGDTFASWGWKNSNYFVL	PVLGPSTVRDALGTGITSVYSPKNIVFRT	PVGRWGTT			
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAVSTREGLLDLTD	SLDEAAIDKYSYTRDLYMKVRARQT	GATPAEGTEDNIDID	DEL		
	::					
m913	AVSAVSTREGLLDLTD	SLDEAAIDKYSYTRDLYMKVRARQT	GATPAEGTEDNIDI	--DEL		
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPAVHEDSVSETQAEAA	AGEAETQPGTQPX				
m913	VESAETGAAETAVQEDSVSETQAEAA	AGEAETQPGTQPX				
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

```

a913.seq
1  ATGAAAAAAA CCGCCTATGC CTTCTCCTG CTGATCGGGT TCGCTTCGCG
51  CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCTT
151 GCGCGCGCGC GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCAAGTTC GGCAGCAATA
251 TCTTGCGCTT AGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGT
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCCACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCTTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCCGTATCCG
551 CCGTCAGTAC CCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

```

a913.pep
1  MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVEKEN DQADRYIFAP
51  AARGYRKVAP KPVRAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLVPLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDLSDE
201 AADKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*

```

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVEKEN	DQADRYIFAP	AARGYRKVAP
a913	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVEKEN	DQADRYIFAP	AARGYRKVAP
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVRAGVSNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG	INTTFGLGGL	IDIAGAGGIP
a913	KPVRAGVSNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG	INTTFGLGGL	IDIAGAGGIP
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTF	ASWGWKNSNY	FVLVPLGPST	VRDALGTGIT	SVYSPKNIVF	RTPVGRWGTT
a913	DNKNTLGDTF	ASWGWKNSNY	FVLVPLGPST	VRDALGTGIT	SVYSPKNIVF	RTPVGRWGTT

1309

	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgcttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTC TGCCGATTCTG
451 taggcttCGA CGATTTTTT CACCAGAGGA TGCCGGACAA CGTCTTCGCG
501 GGTGAAGGTA TGGAAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAG TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTTGT TCGGGCGTGg tgTtttGcgC TTCGTGAGG ATGATGTATG
701 CGCCGTTGAg cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAFAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLW
201 SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCGTAGG CTTGACGAT TTTTGCACC AAAGGATGCC GGACAACGTC
501 TTCGCCGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTAATCCC GATTTGATGT TTTTGGGCAG GTCGATTGTC
601 CTGGTGTGCG CGTAATGAC GGCTTTCGCG CCGAAGCCGA TGCGGGTCAG
651 GAACATTTTC ATTTGTTCCG GCGTGGTGTT TTGCGCTTCG TCAGGATGTA
701 TGTATGCGCC GTTGAGCGTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCRKFDXCI GWTDKETDTD TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

1310

151 DSXASTIFCT KGCRTTSSPV KVKYSPSTL CSFSRASFPN DLMFLGRSIW
 201 LVSPVMTAFA PKPMVRNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng)
 from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMP	AFADRISDLEARLAQ	LEHRVAVLESGGNT	VKIDLFGSNSTMYVC		
m914	MKKCILGILTACAAMP	AFADRIGDLEARLAQ	LEHRVAVLESGGNT	VKIDLFGSNSTMYVC		
	10	20	30	40	50	60
g914.pep	SVTPFQKTFEASDR	NEGVARQKVRQACN	RETSAMFCGDEAIRC	RKFDXCIGWTDKETD	T-	
m914	SVTPFQKTFEASDR	NEGVARQKVRQACN	RETSAMFCEDEAIRC	RKFDXCIGWTDKETD	TD	
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDR	NEGVARQKVRQACN	RETSAMFCGDEAIRC	RKFDXCIGWTDKETD	T-	
m914	SVTPFQKTFEASDR	NEGVARQKVRQACN	RETSAMFCEDEAIRC	RKFDXCIGWTDKETD	TD	
	70	80	90	100	110	120
g914.pep	-ELGFRLCFSLPDF	PCIGFQTALEQCSC	SADXSASTIFCTRGC	RTTSSPVKVKYSPAT	P	
m914	TELGFRICFSLPDF	PCIGFQTALEQCSC	SADXSASTIFCTKGC	RTTSSPVKVKYSPST	L	
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSLPDF	PCIGFQTALEQCSC	SADXSASTIFCTRGC	RTTSSPVKVKYSPAT	P	
m914	TELGFRICFSLPDF	PCIGFQTALEQCSC	SADXSASTIFCTKGC	RTTSSPVKVKYSPST	L	
	130	140	150	160	170	180
g914.pep	CSFSRASFPNDLM	FLGRSIWLVS	PVMTAFAPKPMVRN	IFICSGVVFCASSR	MMYAPLSV	
m914	CSFSRASFPNDLM	FLGRSIWLVS	PVMTAFAPKPMVRN	IFICSGVVFCASSR	MMYAPLSV	
	180	190	200	210	220	230
g914.pep	CSFSRASFPNDLM	FLGRSIWLVS	PVMTAFAPKPMVRN	IFICSGVVFCASSR	MMYAPLSV	
m914	CSFSRASFPNDLM	FLGRSIWLVS	PVMTAFAPKPMVRN	IFICSGVVFCASSR	MMYAPLSV	
	190	200	210	220	230	240
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

1	ATGAAAAAAT	GTATTTTGGG	CATTTTGACC	GCGTGTGCCG	CCATGCCTGC
51	ATTTGCCGAC	AGAATCGGCG	ATTTGGAAGC	ACGTCTGGCG	CAGTTGGAAC
101	ACCGTGTCGC	CGTATTGGAA	AGCGGCAGCA	ATACCGTCAA	AATCGACCTT
151	TTCGGTTCAA	ATTCCACCAT	GTATGTATGC	AGCGTTACGC	CTTTTCAGAA
201	GACGTTTGAG	GCAAGCGATC	GGAATGAAGG	CGTGGCGCGG	CAGAAAGTGC
251	GTCAGGCGTG	CAACCGCGAA	ACTTCGGCAA	TGTTTTCGCA	AGATGAGGCA
301	ATCCGATGCA	GAAAATTCGA	TTGATGTATC	GGTTGGACGG	ATAAAGAAAC
351	GGATACGGAG	CTTGGCTTCC	GTATCTGTTT	TTCTCTGCCC	GATTTTCCAT
401	GCATCGGGTT	TCAGACGGCA	TTGGAATGTC	AGTCGTGTTC	TGCCGATTCG
451	TAGGCTTCGA	CGATTTTTTG	CACCAAAGGA	TGCCGGACAA	CGTCTTCGCC
501	GGTAAAGGTG	TGGAAATACA	GCCCTTCCAC	GCCGTGCAGT	TTCTCACGCG
551	CATCTTTTAA	TCCCATTGTT	ATGTTTTTGG	GCAGGTCGAT	TTGGCTGGTG
601	TCGCCGGTAA	TGACGGCTTT	CGCGCCGAAG	CCGATGCGGG	TCAGGAACAT
651	TTTCATTTGT	TCGGGCGTGG	TGTTTTGCGC	TTCTGCGAGG	ATGATGTATG
701	CGCCGTTGAG	CGTCTGCCG	CGCATATAG		

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

1	MKKCILGILT	ACAAMP	AFAD	RIGDLEARLA	QLEHRVAVLE	SGSNTVKIDL
51	FGSNSTMYVC	SVTPFQKTFE	ASDRNEGVAR	QKVRQACNRE	TSAMFCEDEA	
101	IRCRKFD*CI	GWTDKETDTE	LGFRICFSLP	DFPCIGFQTA	LECQSCSADS	
151	*ASTIFCTKG	CRTTSSPVKV	WKYSPSTPCS	FSRASFPND	MFLGRSIWLV	
201	SPVMTAFAPK	PMVRNIFIC	SGVVFCASSR	MMYAPLSVLP	RI*	

1311

m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914.pep	MKKCILGILTACAAMP	AFADRIGDLEARLAQ	LEHRVAVLESGGNTV	KIDLF	GSNSTMYVC	
a914	MKKCILGILTACAAMP	AFADRIGDLEARLAQ	LEHRVAVLESGSNTV	KIDLF	GSNSTMYVC	
	70	80	90	100	110	120
m914.pep	SVTPFQKTFEASDR	NEGVARQKVRQACN	RETSAMFCEDEAIR	CRKFDXCIGWTD	KETD	TD
a914	SVTPFQKTFEASDR	NEGVARQKVRQACN	RETSAMFCEDEAIR	CRKFDXCIGWTD	KETD	--
	130	140	150	160	170	180
m914.pep	TELGFRICFSLP	DFPCIGFQTALE	CQSCSAD	SXASTIFCTK	GCRTTSSP	VKVWYSPSTL
a914	TELGFRICFSLP	DFPCIGFQTALE	CQSCSAD	SXASTIFCTK	GCRTTSSP	VKVWYSPSTP
	190	200	210	220	230	240
m914.pep	CSFSRASFPDLM	FLGRSIWLVSP	VMTAFAPKPM	VRNIFICSG	VVFCASSR	MMYAPLSV
a914	CSFSRASFPDLM	FLGRSIWLVSP	VMTAFAPKPM	VRNIFICSG	VVFCASSR	MMYAPLSV
	180	190	200	210	220	230
m914.pep	LPRIX					
a914	LPRIX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915.seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gTTTCGCCT TAAGTGCCTG
51  CCGGCagcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915.pep

```

1  MKKTLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915.seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGC.tg
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCcCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG

```

1312

451 GTTGTGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

```
m915.pep
  1 MKKTLLAIVA VSALSXCRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDGGK
151 VVGFDMPDT YIFK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

```
m915/g915

      10      20      30      40      50      60
m915.pep MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||
g915      MKKTLLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||

      70      80      90     100     110     120
m915.pep DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
          |||||
g915      DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWIDAKKAFYVIDS
          |||||

     130     140     150     160
m915.pep GFIGGMAEDALPFGNKEQA EKFAKDGGKVVGFDMPDTYIFKX
          |||||
g915      GFIGGMAEDALPFGNKEQA EKFAKDGGKVVGFDMPDAYIFKX
          |||||

     130     140     150     160
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

```
a915.seq
  1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
101 GTTCGGTCCG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG
451 GTTGTGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

```
a915.pep
  1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDGGK
151 VVGFDMPDT YIFK*
```

m915/a915 99.4% identity in 164 aa overlap

```
      10      20      30      40      50      60
m915.pep MKKTLLAIVAVSALSXCRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||
a915      MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||

      70      80      90     100     110     120
m915.pep DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
          |||||
a915      DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
          |||||
```

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDDMPDTYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc t3cttgacgc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCCG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
501 GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACATAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GGCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCCTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGGACACAAA
901 TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTTG ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCCTAT CCGGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNQ IKVTYDVYDS DETLESKVLV GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDQWDLV FNPEYTFKLK QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDLNIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCTT GGCCGTCCTG ACTGCTTTGC TGCTTGACAG
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACATAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

```

```
m917.pep
1  MTKHLPLAVL  TALLLAACGG  SDKPPAEKPA  PAENQNVLK*  YNWSEYVDPE
51  TVADFEKKNQ  IKVTYDVVDS  DETLESKULT  GKSGYDIVAP  SNAFVGRQIK
101 AGAYQKIDKS  LIPNYQHLPN  EMMRLMDGVD  PGHEYAVPFY  WGTNTFAINT
151 ERVKKALGTD  KLPDNQWDLV  FDPEYTSKLK  QCGISYLSA  AEIYPMVLNY
201 LGKNPNSSNT  EDIREATALL  KKNRPNIKRF  TSSGFIDDLA  RGDTCVTIGF
251 GGDNLIAKRR  AEEAGGKEKI  RVMPKPEGVG  IWVDSFVIPK  DAKNVANAHK
301 YINFLLDPEV  SAKNGNFVTV  APSSKPAREL  MEDEFKNDNT  IFTTEEDLKN
351 SFIMVPIQPA  ALKFMVRQWQ  DVKAGK*
```

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLAACGGS	DKPPAEKPAPAENQNV	LKIYNWSEYVDPETVAD	FEKKN		
	:					
g917	MVKHLPLAVLTALLAACGGS	DKPPAEKPAPAENQNV	LKIYNWSEYVDPETVAD	FEKKN		
	10	20	30	40	50	60
	70	80	90	100	110	120
m917.pep	IKVTYDVYDSDETLES	SKVLTGKSGYDIVAP	SNAFVGRQIKAGAYQ	KIDKSLIPNYKHLNP		
g917	IKVTYDVYDSDETLES	SKVLTGKSGYDIVAP	SNAFVGRQIKAGAYQ	KIDKSLIPNYKHLNP		
	70	80	90	100	110	120
	130	140	150	160	170	180
m917.pep	EMMRLMDGVDPGHEYA	VPFYWG	TNTFAINTERVKKAL	GTDKLPD	NQWDLV	FDPEYTSKLK
g917	EMMRLMDGVDPDHEYA	VPFYWG	TNTFAINTERVKKAL	GTDKLPD	NQWDLV	FNPEYTFKLK
	130	140	150	160	170	180
	190	200	210	220	230	240
m917.pep	QCGISYLD	SAAEIYPMVLN	YLGNPNSSNT	EDIREATALLKKNRPN	IKRFTSSG	FIDDLA
g917	QCGISYLD	SAAEIYPMVLN	YLGNPNSSNT	EDIREATALLKKNRPN	IKRFTSSG	FIDDLA
	190	200	210	220	230	240
	250	260	270	280	290	300
m917.pep	RGDTCVTIGFGGDLN	IAKRRAE	EAGGKEKIRVMMPKE	GVGIWVDSFV	IPKDAKNVANA	HK
g917	RGDTCVTIGFGGDLN	IAKRRAE	EAGGKEKIRVMMPKE	GVGIWVDSFV	IPKDAKNVANA	HK
	250	260	270	280	290	300
	310	320	330	340	350	360
m917.pep	YINDFLDPEVSAKNGN	FVITYAPSSK	PARELMEDEFKNDNT	IFPTEEDLKNSFIM	VP	IQPA
g917	YINDFLDPEVSAKNGN	FVITYAPSSK	PARDLMEDEFKNDNT	IFPSGEDLKNSFIM	VP	PIRPA
	310	320	330	340	350	360

1315

```

m917.pep    ALKFMVRQWQDVKAGKX
            |||||
g917         ALKFMVRQWQDVKAGKX
            370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

```

a917.seq
1  ATGACCAAAC ATCTGCCCTT GCGCGTCTG ACTGCTTTGC TGCTTGACAGC
51 GTGCGGCGGT TCGGACAAAC CGCTGCCGA AAAACCGGCG CCGGGCGGAAA
101 ACCGAAACGT ATTGAAATTT TACAACCTGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCTGT
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATGCCCA ATTATAAACCA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GCTACGGAC AAGCTGCCGG ACAACCACTG
501 GGATTGCGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATCGCGGA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GGCGGCGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAAATC CGCGTGATGA TGCCCAAGA GGGCGTGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCTTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCACTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

```

a917.pep
1  MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
51 TVADFEKKNQ IKVTYDVYDS DETLESKVLK GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDEEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

m917/a917    99.7% identity in 376 aa overlap

          10      20      30      40      50      60
m917.pep    MTKHLPLAVLTALLLAACGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNQ
            |||||
a917         MTKHLPLAVLTALLLAACGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKKNQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m917.pep    IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP
            |||||
a917         IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP
          70      80      90      100     110     120

          130     140     150     160     170     180
m917.pep    EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLG
            |||||
a917         EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLG
          130     140     150     160     170     180

          190     200     210     220     230     240
m917.pep    QCGISYLSAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA
            |||||

```

1316

```

a917      QCGISYLDAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTCVTIGFGGDLNIAKRRAEAEAGGKEKIRVMPKPEGVGIWVDSFVI PKDAKNVANAHK
           |||||
a917      RGDTCVTIGFGGDLNIAKRRAEAEAGGKEKIRVMPKPEGVGIWVDSFVI PKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           |||||
a917      YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWQDVKAGKY
           |||||
a917      ALKFMVRQWQDVKAGKY
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAGca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATT TGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTCACGC cgtGGCagg tgcaggcaAC GGAAGcCTTG
401 CaggtaaggT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCGGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCGG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGGAANAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCCG ACCTCTCCCG ATTCCCACAT ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCGcgcTT GACGGCAAag cccCATCCT CggttaagcC
751 GAagaccCcg tgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCTT
801 GAAAACCCcg tccggcaaat acatCCGCAT cggTaagcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TCGGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA GCCTGGCGCA ATCGACCGGC ACTACATTAC
1101 CTGGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCCAAG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

```

g919.pep
1  MKKHLRLSAL YGIAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELPFMH IQSGSRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAGS GNEGPVGALG
351 TPLMGEYAGA IDRHYTELGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QXTTGYVWQL LPNGMKPEYR P*

```


	10	20	30	40	50	60
m919.pep	MKKYLFRAALYGIAAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
	: :					
g919	MKKHLLRSALYGIAAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER					
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER					
	70	80	90	100	110	120

	130	140	150	160	170	180
m919.pep	YFTPQWVAGNGSLAGTVTGYEYEPVLKGD	DRRTAQARFPIYGIPDDFISVPLPAGLRSGKA				
			:		:	
g919	YFTPQWVAGNGSLAGTVTGYEYEPVLKGD	GRRTERARFPIYGIPDDFISVPLPAGLRGGKN				
	130	140	150	160	170	180
m919.pep	LVRIRQGTGKNSGTIDNTGGTHTADLSRFPITARTTA	IKGRFEGSRFLPYHTRNQINGGAL				
			:			
g919	LVRIRQGTGKNSGTIDNAGGTHADLSRFPITARTTA	IKGRFEGSRFLPYHTRNQINGGAL				
	190	200	210	220	230	240
m919.pep	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIR	IGYADKNEHPYVSIGRYMADKGYL				
g919	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIR	IGYADKNEHPYVSIGRYMADKGYL				
	250	260	270	280	290	300
m919.pep	KLGTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFREL	AGSSNDGPVGALGTPLMGEYAGA				
			:			
g919	KLGTSMQGIKAYMRNPQRLAEVLGQNPSYIFFREL	AGSGNEGPVGALGTPLMGEYAGA				
	310	320	330	340	350	360
m919.pep	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTG	SAIKGAVRVDPYFWGYGDEAGELAGK				
			:			
g919	IDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTG	SAIKGAVRVDPYFWGYGDEAGELAGK				
	370	380	390	400	410	420
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
g919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1 ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGCAATCG CGCGCCCAT
51 CCTCGCCGCG TGCCAAAGCA AGAGCATCCA AACCTTTCGG CAACCCGCACA
101 CATCCGTCAT CAACGCCCGG AGACGGCCGA TCGGCATCCC GACCCCGCCG
151 GGAACGACGG TCGGCGGCGG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGCGGG CTGAAATCCC CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT CTGAAAAATT GCCAAGGCTG GCAGGATGTG
301 TCGGCCCAAG CCTTTCAAAC CCCCGTCCAT TCGGTCAGG AAAACAGTT
351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACAGCAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 TCCGTCGCC TCGCCTGCGG GTTTCGGGAG CGGAAAAGCC TTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGCGGCACA
601 CATACGCCCG ACCTCTCCCA ATTCCCATCT ACTCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCGCCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGTGCGGCTT GACGGCAAAG CCCCGATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG CTGCGGCAAT ACATCGCAT CGGCTATGCC GAGCAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGG AGACCTCGAT GCAGGGCATC AAAGCCTATA TGACGACAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCCG CGCACTGGGC
1051 ACGCCGCTGA TGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCTTATTTTG TCGCCACCAG CCATCCGGTT ACCCGCAAA

```

```

1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

1  MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51  GTTVGGGGAV YTVVPHLSLP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPQVQVAGN GSLAGTVTGY YEPVLKGGDR
151 RTAQAARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPQR LAEVLGQNP YIFFRELTGS SNGFPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
          10      20      30      40      50      60
m919.pep MKKYLFRALYLGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          |||||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          10      20      30      40      50      60

          70      80      90      100     110     120
m919.pep YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
          |||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
          70      80      90      100     110     120

          130     140     150     160     170     180
m919.pep YFTPQVQVAGNGLAGTVTGYEPVLKGGDRRTAQAARFPIYGIPDDFISVPLPAGLRSGKA
          |||||
a919      YFTPQVQVAGNGLAGTVTGYEPVLKGGDRRTAQAARFPIYGIPDDFISVPLPAGLRSGKA
          130     140     150     160     170     180

          190     200     210     220     230     240
m919.pep LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
          |||||
a919      LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
          190     200     210     220     230     240

          250     260     270     280     290     300
m919.pep DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
          |||||
a919      DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
          250     260     270     280     290     300

          310     320     330     340     350     360
m919.pep KLGQTSMQGIKSYMRQNPQRLAEVLGQNPYSYIFFRELAGSSNDGFPVGALGCTPLMGEYAGA
          |||||
a919      KLGQTSMQGIKAYMQQNPQRLAEVLGQNPYSYIFFRELTGSSNDGFPVGALGCTPLMGEYAGA
          310     320     330     340     350     360

          370     380     390     400     410     420
m919.pep VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          |||||
a919      VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          370     380     390     400     410     420

          430     440
m919.pep QKTTGYVWQLLPNGMKPEYRPX
          |||||
a919      QKTTGYVWQLLPNGMKPEYRPX
          430     440

```

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTCGGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAACTT GGAAATCGTC
301 CCGCTGGACA ATCccgcccga caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtggtc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacggtt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaagtgg acatcatCCC
501 CTTGCgccaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAttttc
551 CCGATcaaaAG CCTGTGccga AAACAggcga ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTaa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEK GK ENMIQRGTYN YQYRSNRPVK DGSYLVTA EY QPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR QANYTTLTTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCACGCC CACCGmGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCCTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAATC GTCCCCTGGA ACAATCCCGC
501 CAACATTAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GTCATTCGCA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEK KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKXK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAI I
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```

1321

201 SDRSKTHXXE AQAFSDSTDD KGEVDIIXLR QGFWKANVEH KTDFFDQSVK
 251 QKQANYSTLT FQIGHSHH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng) from *N. gonorrhoeae*:

g920/m920

g920.pep				10	20	30
				PMQLVTEKGKENMIQRGT	YNYQYRSNR	RPVK
m920	GGEY	LKAD	LG	YGEF	PELEPIAK	DRLHIFSKPMQLVTEKGKENMIQRGT
	40	50	60	70	80	90
g920.pep				40	50	60
	DGSYL	VTA	EYQPTFR	SKNKAG	WKQAGIK	EMPDASYCEQTRMFGKNIVNVGHESADTAII
m920	DGSYL	VIAE	YQPTF	WSKXK	AGWKQAGIK	EMPDASYCEQTRMFGKNIVNVGHESADTAII
	100	110	120	130	140	150
g920.pep				100	110	120
	KPVGQ	NLEI	VPLDNP	ADIVHGX	RFKVRVL	FRGEPLPNATVTATFDGFDTS
m920	KPVGQ	NLEI	VPLDNP	ADIVHGX	RFKVRVL	FRGEPLPNATVTATFDGFDTS
	160	170	180	190	200	210
g920.pep				160	170	180
	QAFSD	TTD	GEGE	VDIIP	LRRQGF	WKA
m920	QAFSD	STDD	KGEVD	IIXLR	QGFWKAN	VEHKTD
	220	230	240	250	260	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2799>:

a920.seq

1	TGAAAGAAAA	CATTGACACT	GCTCGCCGTT	TCCGCCCTAT	TTGCCGCATC
51	CGCCACGCC	CACCGCGTCT	GGGTGCGAAC	CGCCACACG	CACGCGGCG
101	AATACCTTAA	AGCCGACTTG	GGCTACGGCG	AATTTCCCGA	ACTCGAACCC
151	ATCGCCAAAG	ACCGCCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAGGC	AAGGAAAACA	TGATTCAACG	CGGCACATAC	AACTACCACT
251	ACCGAAGCAA	CCGTCCCGTT	AAGGACGGCA	GTTACCTCGT	CATCGCCGAA
301	TATCAGCCTA	CTTCTGGTC	AAAAAACAAA	GCAGGCTGGA	AACAGGCGGG
351	CATCAAAACA	ATGCCTGACG	CAAGCTATTG	CGAACAAACC	CGAATGTTTC
401	GCAAAAACAT	CGTCAACGTC	GGACACGAAA	GCGCGGACAC	CGCCATCATC
451	ACCAAACCGG	TCGGACAAAA	CTTGGAATC	GTCCCGCTGG	ACAATCCCGC
501	CAACATTAC	GTAGGCGAAC	GCTTCAAAGT	CCGCGTCTCT	TTCCGTGGCG
551	AACCGCTGCC	CAATGCCACC	GTTACCGCCA	CCTTTGACGG	CTTCGACACC
601	AGCGACCGCA	GCAAAACGCA	CAAAACCGAA	GCACAGGCTT	TCTCCGACAG
651	CACAGACGAC	AAAGGCGAAG	TGGACATCAT	CCCCTTGCGC	CAAGGCTTCT
701	GGAAGCCAA	TGTCGAACAC	AAAGCCGACT	TCCCCGATCA	AAGCGTGTGC
751	CAAAAACAGG	CGAACTACTC	GACTTTAACC	TTCCAAATCG	GCCATTGCGA
801	CCATTAA				

This corresponds to the amino acid sequence <SEQ ID 2800; ORF 920.a>:

a920.pep

1	*KKTLLTLLAV	SALFAASAH	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDLRLHIFS	KPMQLVTEKG	KENMIQRGT	YNYQYRSNR	RPVK
101	YQPTFWSKNK	AGWKQAGIK	MPDASYCEQT	RMFGKNIVNV	GHESADTAII
151	TKPVGQNLEI	VPLDNPANIH	VGERFKVRVL	FRGEPLPNAT	VTATFDGFD
201	SDRSKTHKTE	AQAFSDSTDD	KGEVDIIP	LRRQGF	WKA
251	QKQANYSTLT	FQIGHSHH*			

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLTLLSVSALFATS	SAHAHRVWVETAHT	HGGEY	LKADLGYGE	FPELEPIAKDRLHIFS	
a920	: :	: :	: :	: :	: :	: :
	10	20	30	40	50	60
m920.pep	KPMQLVTEKGKENMIQ	RGTNYQYRSNRPVKD	GSYLVIAEYQPTFWS	KXKAGWKQAGIKE		
a920	: :	: :	: :	: :	: :	: :
	70	80	90	100	110	120
m920.pep	MPDASYCEQTRMFGKN	IVNVGHESADTAII	ITKPVGQNLEIVPLD	NPANIHVGERFKVRVL		
a920	: :	: :	: :	: :	: :	: :
	130	140	150	160	170	180
m920.pep	FRGEPLPNATVTATFD	GFDTSDRSKTHXEAQ	AFSDSTDDKGEVDII	XLROGFWKANVEH		
a920	: :	: :	: :	: :	: :	: :
	190	200	210	220	230	240
m920.pep	KTDFPDQSVQCQKQAN	YSTLTFQIGHSHHX				
a920	: :	: :	: :	: :	: :	: :
	250	260	269			
m920.pep	KADFPDQSVQCQKQAN	YSTLTFQIGHSHHX				
a920	: :	: :	: :	: :	: :	: :
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCggtt TcCGCACTAT TTGCCACATc
51  cgCaCACCCCC CACCgCGTCT GGGTCGAAAC CgccCACACg cAcgGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGccAAAG ACCgccTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGT AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGCAGCAA CCGTCCCCTC AAAGACGGCA GCTACCTCGT TACCGCCGAA
301 TATCAGCCTA CTTTCCCGTC AAAAAACAAA GCAGGCTGGA AACAGGCTGG
351 CATCAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGTATGTTCTG
401 GTAAAAACAT TGTCAACGTG GGACACGAAA GCGCGGACAC GCCTCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG TAGGCGGAAC GCTTCAAAGT CCGCGTCTG TTCCGTGGCG
551 AACCCTGCTC CAATGCCACC GTTACCGCTA CATTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCCCAAGCCT TCTCCGACAC
651 CACCGACGGC AAGGCGGAAG TGGACATCAT CCCCTTGC GC CAAGGCTTTT
701 GGAAGCGAG TGTGCAATAC AAAGCCGATT TCCCCGATCA AAGCCTGTGC
751 CAAAAACAGG CGAACTACAC AACTTTAACC TTCCAATCG GCCATTCTCA
801 CCATTA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLTLLAV SALFATS AHP HRVWVETAHT HGGEY LKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRTY NYQYRSNRPV KDGSYLVTAE
101 YQPTFRSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDN PANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDTTDG KGEVDIIPLR QGFWKASVEY KADFPDQSLC
251 QKQANYTTLT FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCACGCGC CACCGCGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGAAGCAA CCGTCCCCTT AAGGACGGCA GTTACCTCGT CATCGCCGAA

```

1323

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAGGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCCTGCTC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

m920-1.pep

```

1 MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLIVIAE
101 YQPTFWKSNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFFDQSV
251 QKQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
g920-1	MKKTLTLLAVSALFATSAHPRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m920-1.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLIVIAEYQPTFWKSNKAGWKQAGIKE					
g920-1	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVTAEYQPTFRSKNAGWKQAGIKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m920-1.pep	MPDASYCEQTRMFGKNIVNVGHESADTAII TKPVGQNLLEI VPLDNPANIHVGERFKVRVL					
g920-1	MPDASYCEQTRMFGKNIVNVGHESADTAII TKPVGQNLLEI VPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m920-1.pep	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
g920-1	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDTTDGKGEVDIIPLRQGFWKASVEY					
	190	200	210	220	230	240
	250	260	269			
m920-1.pep	KTDFFDQSVCKQKQANYSTLTFQIGHSHHX					
g920-1	KADFFDQSLCQKQANYTTLTFQIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

a920.seq

```

1 TGAAAGAAAA CATTGACACT GCTCGCCGTT TCGCCCTAT TTGCCGCATC
51 CGCCACAGCC CACCGCGTCT GGTTCGAAAC CGCCACACG CACGCGCGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCGGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCCTGCTC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGGCCAA TGTCGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTGCGA
801 CCATTAA

```

1324

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

```
a920.pep
1  *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVAIE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSV
251 QKQANYSTLT FQIGHSHH*

m920-1/a920 98.9% identity in 267 aa overlap

m920-1.pep      10      20      30      40      50      60
M K K T L T L L A V S A L F A T S A H A H R V W V E T A H T H G G E Y L K A D L G Y G E F P E L E P I A K D R L H I F S
a920            10      20      30      40      50      60
X K K T L T L L A V S A L F A A S A H A H R V W V E T A H T H G G E Y L K A D L G Y G E F P E L E P I A K D R L H I F S

m920-1.pep      70      80      90     100     110     120
K P M Q L V T E K G K E N M I Q R G T Y N Y Q Y R S N R P V K D G S Y L V I A E Y Q P T F W S K N K A G W K Q A G I K E
a920            70      80      90     100     110     120
K P M Q L V T E K G K E N M I Q R G T Y N Y Q Y R S N R P V K D G S Y L V I A E Y Q P T F W S K N K A G W K Q A G I K Q

m920-1.pep      130     140     150     160     170     180
M P D A S Y C E Q T R M F G K N I V N V G H E S A D T A I I T K P V G Q N L E I V P L D N P A N I H V G E R F K V R V L
a920            130     140     150     160     170     180
M P D A S Y C E Q T R M F G K N I V N V G H E S A D T A I I T K P V G Q N L E I V P L D N P A N I H V G E R F K V R V L

m920-1.pep      190     200     210     220     230     240
F R G E P L P N A T V T A T F D G F D T S D R S K T H K T E A Q A F S D S T D D K G E V D I I P L R Q G F W K A N V E H
a920            190     200     210     220     230     240
F R G E P L P N A T V T A T F D G F D T S D R S K T H K T E A Q A F S D S T D D K G E V D I I P L R Q G F W K A N V E H

m920-1.pep      250     260     269
K T D F P D Q S V C Q K Q A N Y S T L T F Q I G H S H H X
a920            250     260
K A D F P D Q S V C Q K Q A N Y S T L T F Q I G H S H H X
```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

```
g921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51  Ccagtctatt tatGtgccca cattgacggA aatccccgTg aatcccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCCTCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGGTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggAA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

```
g921.pep
1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAVD SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMKMQP LK*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

```
m921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCCC CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
```


1325

```

251  ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301  TATGAAATCT ACCTGCGTTC GCGGATAGAC AGCCAGCGGG GCGCAATCAA
351  TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
401  AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
451  TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

```

m921.pep
  1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51  HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101  YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
151  FLMEVMKMQP LK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng) from *N. gonorrhoeae*:

m921/g921

```

              10      20      30      40      50      60
m921.pep  MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD
           |||||
g921      MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPIN' 'TEAPAKGFRLAPSHWADVAKISD
           |||||
              10      20      30      40      50      60

              70      80      90      100     110     120
m921.pep  EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ
           |||||
g921      EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAVDSQRGAINTEQ
           |||||
              70      80      90      100     110     120

              130     140     150     160
m921.pep  SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX
           |||||
g921      SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX
           |||||
              130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

```

a921.seq
  1  ATGAAAAAAT ACCTTATCCC TCTTTCATT GTGGCAGTTC TTTCCGGCTG
 51  CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCGGTG AATCCTATCA
101  ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTCCGCGCT TGCTCTTCG
151  CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201  TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
251  ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301  TATGAAATCT ACCTGCGTTC GCGGATAGAC AGCCAGCGGG GCGCAATCAA
351  TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
401  AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
451  TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

```

a921.pep
  1  MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51  HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101  YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
151  FLMEVMKMQP LK*

```

m921/a921 99.4% identity in 162 aa overlap

```

              10      20      30      40      50      60
m921.pep  MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD
           |||||
a921      MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD
           |||||
              10      20      30      40      50      60

```

1326

	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1  ATGGAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101  CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGCG GTTTGACGCG
151  GCAGCCGTAC CGGTATCCGA CAGCGGTTT GCCGCCAATG CAAATGTCCG
201  CCGTTTGTG GACGATGAAG TCGGAAAGG GGATTTTCC CAGGCGGAAT
251  GGCAGGATTT TTTTGACAAA GCGGCTTACA AGCGGACAT CGTCAAGATt
301  ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtgttcc gCacggGAAa
351  ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaAacc
401  gcgcggttat cgatgatgtg gcgCAAAAt acggcgtGCC TGCCGAGCTT
451  ATCGTGGCGA TTATCGGGAT TGAAACGAAT TACGGCAAAA ATACGGGCAG
501  TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551  GCGCCGGTT TTTCAAAAA GAATTGGTCG AGCTTTTAAA GCTGGCAAAA
601  GAAGAAGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651  GGGTATGCCG CAATTATGC CTTCGAGCTA CCGGAAATGG GCGGTGATT
701  ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
751  gcatcggTTG CCAATTAtat gaagCAGCAC GGTGCGCGA CgggcggtAA
801  AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CAggcAATCA
851  TTGGCGAAAA AACGCCCTG ACGCGACGG TGGCGGATTT GAaggCGTAc
901  ggcacatcc ccggggaaac GCTCGCAGAT GATGAAAAGg cgGTTTGTt
951  CAACTGGAA ACCGCACCCG GCGTGTtTGA ATATTATTG GGCTTGAACA
1001  ATTTTATAC GGTATGGCAG TACAACCACA GCCGGATGTA TGTAACGgcg
1051  gtcaggGACA TTCCAATTC GCTCGCGGC CCGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KESRPAFDA
51  AAVPVSDSGF AANANVRRFV DDEVGKDFS QAEWQDFDK AAYKADIVKI
101  MHRPSTSRPW YVFTGNNGR AKFHGARRFY AENRAIDDV AQKYGVPAEL
151  IVAIIGIETN YGNTGSFRV ADALATLGFY YPRRAGFFQK ELVELLKLAK
201  EEGGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVDVA
251  ASVANVMKQH GWRTGGKMLV SATLAPGADV QAIIGKLTAL TRTVADLKAY
301  GIIPGETLAD DEKAVLFKLE TAPGVFEYYL GLNNFYTVWQ YNHSRMYVTA
351  VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1  ATGAAAAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACCC CCGGGCAAAT GAAGCCCAAG
101  CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGCG GTTTGACGCG
151  GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201  CGCCAATGCA AATGTCCGCC GTTTGTGGA CGATGAAGTC GGGAAAGGGG
251  ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301  GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351  TGTGTTCCGC ACGGGAATT CCGGCAAGGC GAAATTTTCG GCGCGCGGCC
401  GGTTTTATGC GGAACCCG GCGTTATCG ATGATGTGGC GCAAAAATAC
451  GCGGTGCCTG CCGAATTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501  CCGCAAAAAT ACGGGCAGT TCCGTGTGCG GGACGCATTG GCGACCTTAG
551  GCTTTGATTA CCCCCCGCGC GCCGGGTTTT TCCAAAAAGA ATTGGTCGAG

```

m922.ppt

Computer analysis of this amino acid sequence gave the following results:

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

	10	20	30	40	50	60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAAPRAVEMKKESRPAFDAAAVFDAAAVP					
	:					
g922	MEKKRKILPLAICLAALSACTAMEARTPRANEQAAPRADEMKKESRPAFDAA-----AVP					
	10	20	30	40	50	
	70	80	90	100	110	120
m922.pep	VSDSGFAANANVRRFVDDDEVGKGDFSRAEWQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
g922	VSDSGFAANANVRRFVDDDEVGKGDFSQAEWQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
	60	70	80	90	100	110
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
	: : :	:				
g922	TGNSGRAKFHGARRFYAENRAVIDDDVAQKYGVPAELIVAIIGIETNYGKNTGSFRVADAL					
	120	130	140	150	160	170
	190	200	210	220	230	240
m922.pep	ATLGFIDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
g922	ATLGFIDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
	180	190	200	210	220	230
	250	260	270	280	290	300
m922.pep	DGDGHRDIWGNVGDVAASVANYMKQHWRTGGKMLVSATLAPGADVQAIIGEKTALTRTV					
g922	DGDGHRDIWGNVGDVAASVANYMKQHWRTGGKMLVSATLAPGADVQAIIGEKTALTRTV					
	240	250	260	270	280	290
	310	320	330	340	350	360
m922.pep	ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSMRYVTAVRDI					
g922	ADLKAYGIIIPGETLADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSMRYVTAVRDI					

1328

	300	310	320	330	340	350
		370				
m922 . pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922.seq
1  ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCCCGC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCGCCCCGCG GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACGCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAAATT CGGCAAGGC GAAATTTGCG GCGCGCGGCC
401 GGTTTTATGC GGAAAACCGC GCGTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CCGCAAAAT ACGGGCAGTT TCCGTGTGCG GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCG GCGGGTTTT TCCAAAAGA ATTGGTCGAG
601 CTTTAAAGC TGGCAAAAGA AGAAGGCGCG GATGTTTCG CCTTTAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGACG GACATCGGGA CATATGGGCG
751 AATGTTGGCG ATGTCGCGGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGAAAA TACTGGTGTG TGCAACATTG GCGCCGGGTG
851 CGGATGTCA GGCAATCATT GGCGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGA AGGCGTACGG CATCATCCCC GGCGAAGAGC TTGCCGATGA
951 TGAAAAGGCG GTTTTGTTC AACTGGAAAC CGCACCCGCG GTGTTTGAAT
1001 ATTATTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAATCACAGT
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTGCG TTGGCGGCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922. pep
1  MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KKERPAFDA
51  AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDFSRAEW QDFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHGWRT GGKILVSATL APGADVQAI GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922. pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKESRPAFDAAAVFDAAAVP					
	:					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAQAPRADEMKKESRPAFDAAAVFDAAAVP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m922. pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFDKAAYKADIVKIMHRPSTSRPWYVFR					
a922	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFDKAAYKADIVKIMHRPSTSRPWYVFR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m922. pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

1329

```

m922.pep  ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
           190      200      210      220      230      240

           250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEKALTTRTV
           ||||||||||||||||:||||||||||||||:||||||||||||||
a922      DGDGHRDIWGNVGDVAASIANYMKQHGWRTGGKILVSATLAPGADVQAIIGEKALTTRTV
           250      260      270      280      290      300

           310      320      330      340      350      360
m922.pep  ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
           310      320      330      340      350      360

           370
m922.pep  ANSLGGPGLX
           ||||||||
a922      ANSLGGPGLX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCGG
201 CGGTTGGACG GCGGCATACT TGGGTAGTAG GATGTTTCAGG CATAAAACGG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTC GTTCCGCCCG AACTTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRRAVR
51  GKRRRIPEHRL LLPALFGGWT GAYLGSRMFR HKTAKKRFVV LFRLTVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GCGCGGTATT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTAA ACCAGTACGG
351 CGTTGCCTCG CCTTGCCGTA CTATTTGTAC TGTCTGCGGC TTCGTCGCTT
401 TGTCTGATT TTTGTTAATC CACTATAT.T ATTTGTCCC GCCTGAATTT
451 TTCGTAAAC TCGGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCRIR
51  GQRRRIPEHRL LLPALLGGWV GAYFGSMTFK HKTAKKRFVV LFRLTVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HXYFVPPPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

1330

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

	10	20	30	40	50	60
g923 . pep	MKRQAFFKPMACAAFLSAVSLRPLVVGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
m923	MKRQAFFKLMACAAFLSAVSLRPLVVGACYAILSLEYAFALYGIDKRCAIRGQRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100		
g923 . pep	LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFRLLTVSGNVLATCILID-----					
m923	LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			110	120		
g923 . pep	-----YFVPPPELFVKLGQHLX					
m923	PCRTICTVCGFVALSXFLLIHYIYFVPPPEFFVKLGQNTX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923 . seq

```

1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTCTGTGC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CCTTGTTCCG
201 CCGTTGGGCG GCGGCATACT TGGGCAGCAG GATATTCAGG CATAAACGG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCC TCATCCTGAT TTATAGTGA TTAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTA.GCTC AAAGAGAACG ATTCTCTAAG GTGCTGAAGC
401 ACCAAGTGAA TCGGTTCCGT ACTATTTGTA CTGCTGCGG CTTCGTCGCC
451 TTGTCCTGAT TTTTGTTAAT CCACTAT.AT TATTTTGTCC CGCCTGAATT
501 TTTTCGTAATA CTCGGGCAGA ATACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923 . pep

```

1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRRAVR
51  GKRRRIPEHRL LLPALFGGWA GAYLGSRIFR HKTAKKRFVV LFRLLTVSGNV
101 LATLILIIYS LNLNQYGVAS PXAQRERFSK VLKHQVNRFR TICTVCGFVA
151 LS*FLLIHYX YFVPPPEFFVK LGQNT*

```

m923/a923 84.6% identity in 175 aa overlap

	10	20	30	40	50	60
m923 . pep	MKRQAFFKLMACAAFLSAVSLRPLVVGACYAILSLEYAFALYGIDKRCAIRGQRRRIPEHRL					
a923	MKRQAFFKLMACAAFLSAVSLRPLVVGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m923 . pep	LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
a923	LLPALFGGWAGAYLGSRIFRHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			130	140	150	159
m923 . pep	PC-----RTICTVCGFVALSXFLLIHYXYFVPPPEFFVKLGQNTX					
a923	PXAQRERFSKVLKHQVNRFR TICTVCGFVALSXFLLIHYXYFVPPPEFFVKLGQNTX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

```
g925.seq
  1  ATGAAACAAA TGCTTTTGGC cgtcggcgtg ggcGCGGTGT TGGCGGGCTG
 51  CCGCAaggat gcCGGCGGtt acgagggTA TTGGCGCGAA AAGTCGGACA
101  AAAAagaggG CGTGATTGCC GTCAAAAAA AAGGCAATTA CTTCTTAAT
151  AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201  AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251  TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301  ACCGATGCGG CGATGAAGGA CAAATCATC GCCCACCAGA AAAAGTGGCG
351  ACAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401  AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451  GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAATGCA ACGGCAAACC
501  GACATTGTTG TTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

```
g925.pep
  1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
 51  KINVFTGKEE SLLSEKDGA LSINTGIGEI PIKL DDGKE LYVERRRYVK
101  TDAAMDKII AHQKKCGQA QAYLDARNAL PSNQTYYQQRQ AAIEQLKRRF
151  EAEFDELEKE IKCNGKPTLL F*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

```
m925.seq (partial)
  1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
 51  CCGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101  AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TACTTCCTT
      . . . . .
```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

```
m925.pep (partial)
  1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE				
	10	20	30	40	50
g925	ESLLSEKDGALSINTGIGEIPIKLSDDGKELYVERRRYVKTDAAMDKIIAHQKKCGQT				
	60	70	80	90	100
					110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

```
g925-1.seq
  1  ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
 51  CCGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101  AAAAAGAGGG CGTGATTGCC GTCAAAAAA AAGGCAATTA CTTCTTAAT
151  AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201  AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251  TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301  ACCGATGCGG CGATGAAGGA CAAATCATC GCCCACCAGA AAAAGTGGCG
351  ACAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401  AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451  GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAATGCA ACGGCAAACC
501  GACATTGTTG TTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKOMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLH
51  KINVFTGKEE SLLLSEKDG ALSINTGIGE IPIKLSDDGKE ELYVERRRQYV
101 TDAAMKDKII IAHQKKCGQT AQAYLDARNAL PSNQTYYQORQ AAIEQLKRRF
151 EAEFDELEKE IKCNKGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTGTCTGA
201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTCCCGTCAA
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

m925-1.pep..

```

1  MKOMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL
51  NKIHVVVTGKE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRRQYV
101 KTDAAAMKDKI IAHQKKCGQT AQAYRDARNA LPSNQTYYQH LAAIEQLKRR
151 FEAFFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKOMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKHVVVTGKE					
g925-1	MKOMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKH-KGNVFLNKHVVVTGKE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRQYVKTDAAMKDKIIAHQKKCGQT					
g925-1	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYYQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX					
g925-1	AQAYLDARNALPSNQTYYQORQAAIEQLKRRFEAEFDELEKEIKCNKGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

a925-1.seq

```

1  AATAAAATCA ACGTGTTCAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51  AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCGGTCAA
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

a925-1.pep

```

1  NKINVFTGKE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRRQYV
51  KTDAAAMKDKI IAHQKKCGQT AQAYLDARNA LPSNQTYYQH QAAIEQLKRR
101 FEAFFDELEK EIKCNKGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

	10	20	30
a925-1.pep	NKINVFTGKEESMLLSEKDGALSINTGIGE		
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKHVVVTGKEESMLLSEKDGALSINTGIGE		
	30	40	50
	60	70	80
	40	50	60
	70	80	90
	90	100	110

1333

```

a925-1.pep  IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKFCGQTAQAYLDARNALPSNQTYQQH
m925-1      IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKFCGQTAQAYRDARNALPSNQTYQQH
              90      100      110      120      130      140

              100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKNGH-PTLLFX
m925-1      LAAIEQLKRRFEAEFDELEKEIKNGRSPALLX
              150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCCG
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GCGGCGCGCG CCTtaccGCA
401 TCCGTTTACA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcCGACAGT GGGGGGCAag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCCG
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GCGGCGCGCG CCTTACCGCA
401 TCCTGCCCGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAAAC
451 GCGGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTC ACGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCCGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWVGRT
151 ADGGGQVRTL QLNNGNLNI RLVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

              10      20      30      40      50      60
g926.pep  MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
m926      MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              10      20      30      40      50      60

              70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEGETEDLSRQLVGFKLPIQYLHI
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEESAELSRQLVGFKLPIQYLHI
              70      80      90      100     110     120

              130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEOYGTWIGQNCROWGASPNVATE

```

1334

```

m926      |||:||||||| |||||:|:| :|
          WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
          130      140      150      160      170      180

a926.seq
1  ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
101 GCAGTTTCAC GCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAAGTGC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCTGTG GCGGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CCGCAGAACC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA
551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

a926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
151 ADSGGQVRTL QLNNGNLIR LVFTEIGMPS ETETQECCAA RIQ*

```

m926/a926 96.9% identity in 191 aa overlap

```

m926.pep      10      20      30      40      50      60
              MKHTVSASVILLTACAQLPQNNENLWQPS EHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              |||:||||||| |||||:|:| :|
a926           10      20      30      40      50      60
              MKHTVSASVILLTACAQLPQNNENLWQPS EHSFTAEGRLAVKAEGKGSYANFDWTYQ

m926.pep      70      80      90      100     110     120
              PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI
              |||:||||||| |||||:|:| :|
a926           70      80      90      100     110     120
              PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI

m926.pep      130     140     150     160     170     180
              WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
              |||:||||||| |||||:|:| :|
a926           130     140     150     160     170     180
              WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS

m926.pep      190
              ETETPERCAARTRX
              |||:||||
a926           190
              ETETQECCAAARIQX
              190

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

```

g927.seq
1  atgaaaacct acGCACAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
51  CAGCCCcgca GCcgatTcaa accaTCCGTC CGGAcAaAAT GCCCCGCCCA
101 ATACCGAATC cgacGgaaa AACATtaccC TGctcaatgc cTcgtaacgat
151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcggaacATA
201 CCAATCCGAA CACCCCGGCA CATCCGTcAG CATCCAACAA TCCCACGGCG
251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCTACA

```

1335

```

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATA CGGT TACGGTCTGA
551 AAGCCAAACA CGGcaaCGAG CAGGAAGCCC AAAA ACTCGT CGCATCCATC
601 CTCAAAAACA CACCCGTTTT TGAAAACGGC GGACGCGc.C CGCCGCCACC
651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
701 agCcaactac gtCAGCAAAA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

```

g927.pep
  1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
 51 VTRYFYKEYD HLFVGTQYSE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV
101 VTMNQSSDID LLEKKGLVEK GWQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIAKTSN GRYAFLGAY YGLKANNGNE QEAQKLVAI
201 LKNTPVFENG GRXPPPPSH NATSATYSSL LKTKPTTSAK N*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

```

m927.seq
  1 ATGAAAACCT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
 51 CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA
101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTC.ACGC CTCATACGAT
151 GTGGCAGGGG ATTTTACAA AGAATACAAC CCCTTATTTA TCAAAACATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCCAA ACAGATCCGC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
501 CAAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
551 GTCTGAAAAC CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
601 TCCATCCTCA AAAACACCCC CGTTTTTGAA AACGGCGGAC GCKCgCCACC
651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTTGAAAA
701 CGAAGCCAAC TACGTCAGCt AAAAAcTGA

```

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

```

m927.pep
  1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
 51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
101 VTMNQSSDID LLEKKGLVEK GWQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
201 SILKNTPVFE NGGRXPPPPS HNATSATYSS LLKTKPTTSA KN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
m927	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
g927.pep	HLFVGTQYSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	:					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
	130	140	150	160	170	
g927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGNGRYAFLGA					
m927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGNGRYAFLGA					
	130	140	150	160	170	180

1336

	180	190	200	210	220	230
g927.pep	YG YGLKANNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTS					
m927	YG YGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPP-SHNATSATYSSLLKTKPTTS					
		190	200	210	220	230

	240
g927.pep	AKNX
m927	AKNX
	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1   ATGAAAACCT  ACGCACCGGC  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCGA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTCCTT  GTCCGAAAAA  ACAACCCCAA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAACCTCG  GGCAACGSAC  GCTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAC  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTTGAAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1   MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGSSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTPVFE  NGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*

```

m927/a927 99.2% identity in 242 aa overlap

	10	20	30	40	50	60
m927.pep	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
a927	MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60

	70	80	90	100	110	120
m927.pep	PLFIKTYQSEHPGTSVSIQQSHGSSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
a927	PLFIKTYQSEHPGTSVSIQQSHGSSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120

	130	140	150	160	170	180
m927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA					
a927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA					
	130	140	150	160	170	180

	190	200	210	220	230	240
m927.pep	YG YGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA					
a927	YG YGLKTTNGNEQEAQKLVASILKNTPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA					
	190	200	210	220	230	240

1337

```

m927.pep      KNX
              |||
a927          KNX

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq

```

1  ATGAAATTGG GTTCAAAC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTGGT TTGGCACTGC CCGTACccga CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCACT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAacgctggG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GCGCGCATTA TACATCcgat TATGCagtcg attgCcgga GttacggctC
501 caatCCCGCA AAAGGCACag aaggcaagat cggtaAATAT TtggcTTtgg
551 tcaattaTCA TTcCaatCCC attcgcgcg ctAtggctat taCTGcaact
601 gCCCCcaaCC CTTAATCgt caacttgatt gccGaaatTt taggcagtag
651 tttccgtCTT TCttgggggg cgTGGGcgtg ggcaatGCc Gtccccggcg
701 ttatcgccct TTtcgTTATG CCTTTGATTT TATATTTTTT GTATCCGCTT
751 GAAATTAAAG AAACGCCCAA TGCTGttcAA TTGCCAAAG ACCGCTGAG
801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTC CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGTGTAT TGAATTGGGA CGATGTTTGG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGCGC CATTGATTAT GATGGCCGCA
1051 TTTTtaAATA AActcggact gattaaatGG TTCTCCGGAG TGTGGCGGA
1101 AagtgtcggC GGTTTGGGCG TTAGCGGCAC GGCTGCGGCG GTAATCCTCG
1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGCGC ATTTCTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCGGCTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTG TGGAAGTTC
1451 TGGGATATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep

```

1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51  VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMCKY LALVNYHNSP ISSAMAITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASHTAH
401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFSIVIGSIW WKVLGYW*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq

```

1  ATGAAATTGG GTTCAAAC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTGGT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCACT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

```

1338

```

451  GGCGGCATTA  TACATCCGAT  TATGCAGTCG  ATTGCCGGCA  GTTACCGCTC
501  CAATCCCGCA  AAAGGCACAG  AAGGCAAGAT  GGGTAAATAT  TTGGCTTTGG
551  TCAACTATCA  TTCCAATCCC  ATTTCTGTCG  CTATGTTTAT  TACTGCAACT
601  GCCCCAACCC  CTTTAATCGT  CAACTTGATT  GCCGAAAATT  TAGGCAGTAG
651  TTTCCGTCTT  TCTTGGGGGG  CGTGGGCGTG  GGCAATGGCT  GTTCCCGGCG
701  TTATCGCCTT  TTTCTGTTAT  CCTTTGATTT  TATATTTwyT  GTATCCGCCT
751  GAAATTAAAG  AAACGCCCAA  TGCCGTTCAG  TTTGCCAAAG  ACCGTCTGAG
801  GGAGATGGGT  AAAATGTCGG  CAGACGAAAT  CATTATGGCG  GTCATTTTCG
851  GTATCTTGCT  GCTGTGTGG  GCAGATGTTC  CCGCCCTTAT  TACCGGCAAT
901  CACGCTTTTA  GTATCAACGC  CACCGCCACC  GCATTTATCG  GATTAAGCCT
951  GCTTTTGCTT  TCCGGTGTAT  TGACTTGGGA  CGATGTTTGG  AAAGAAAAAA
1001 GCGCGTGCGA  TACGATTATT  TGGTTTGGCG  CATTGATTAT  GATGGCCGCA
1051 TTTTAAATA  AACTCGGACT  GATTAAATGG  TTCTCCGGAG  TGTGGCGGA
1101 AAGTGTGCGC  GGTGTGGGCG  TTAGCGGCAC  GGCTGCGGCG  GTAATCCTCG
1151 TGCTTGCTTA  TATGTATGCG  CATTATATGT  TTGCCAGTAC  TACTGCACAT
1201 ATTACGCTA  TGTTCGGCGC  ATTTTTCGCT  GCTGCCGTTT  CACTGAATGC
1251 CCCGCGATG  CCGACCGCGC  TGATGATGGC  GgCCGCATCC  AACATTATGA
1301 TGACCCTCAC  TCATTATGCG  ACCGGTACTT  CGCCTGTGAT  TTTCCGTTTC
1351 GGCTACACCA  CAATGGGAGA  ATGGTGGAAG  GCGGGTTTTA  TCATGAGCGT
1401 AGTCAATTTT  CTGATTTTTT  TCGTTATCGG  CAGCATTTGG  TGGAAAGTTC
1451 TGGGTATTG  GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTI WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASTTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng)

from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKVMPLGALSII					
m929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
	70	80	90	100	110	120
g929.pep	AVGLVAVTGVGTADKPGAAMSDALSAFANPLIWLIAIAVMSRLLKTGLGMRIGYLFIAV					
m929	AVGLVAVTGVGTADKPGAAMSDALSAFANPLIWLIAIAVMSRLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
g929.pep	FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
m929	FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
	190	200	210	220	230	240
g929.pep	LALVNYHNSNPISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNSNPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					

1339

	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADVPAITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADVPAITGN					
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFLAAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFLAAAVSLNAPAM					
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

```

a929.seq
1   ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTCGGT TGCTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGTGCG GCGCATGAGC GATCGCTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGCTGCGG ATGCGTATCG GATATTGTGT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTCGTCGG CTATGTTTAT TACTGCAACT
601 GCCCCAACC CTTAATCGT CACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGCGC
701 TTATCGCCTT TTTGTTATG CCTTTGATT TATATTTTT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTGCCCAAAG ACCGCTCTGAG
801 GGAGATGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCC
851 GTATCTTGTT GCTGTTGTGG GCAGATGTTC CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGAATTGGGA CGATGTTTGA AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGAG TGTGGCGGA
1101 AAGTGTCGGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGGGCG ATTTTTCGCT GCTGCGGTTT CACTGAATGC
1251 CCCGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGTTTATA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```
a929.pep
1  MKLGFKPIPL AIAAVLCAIV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTSPNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*
```

m929/a929 99.6% identity in 487 aa overlap

	10	20	30	40	50	60
m929.pep	MKLGFKPIPLAIAAVLCAIVLALPVPDGVK	PQAWTLLAMFVGVIAAIIGK	AMPLGALSII			
a929	MKLGFKPIPLAIAAVLCAIVLALPVPDGVK	PQAWTLLAMFVGVIAAIIGK	AMPLGALSII			
	70	80	90	100	110	120
m929.pep	AVGLVAVTGV	TADKPGAAMSDALSAFANPLIWLIAIAVMIS	SRGLLKTGLG	MRIGYLFIAV		
a929	AVGLVAVTGV	TADKPGAAMSDALSAFANPLIWLIAIAVMIS	SRGLLKTGLG	MRIGYLFIAV		
	130	140	150	160	170	180
m929.pep	FGRKTLGIGYSLALSELLLPVTSPNTARGGGI	IHPIMQSIAGSYGSNP	AKGTEGKMGKY			
a929	FGRKTLGIGYSLALSELLLPVTSPNTARGGGI	IHPIMQSIAGSYGSNP	AKGTEGKMGKY			
	190	200	210	220	230	240
m929.pep	LALVNYHSNP	ISSAMFITATAPNPLIVNLI	AENLGSSFRLSWGAWAWAM	AVPGVIAFFVM		
a929	LALVNYHSNP	ISSAMFITATAPNPLIVNLI	AENLGSSFRLSWGAWAWAM	AVPGVIAFFVM		
	250	260	270	280	290	300
m929.pep	PLILYXLYPPEIKETPNAVQFAKDRLREMG	KMSADEIIMAVIFGILLLLW	ADVPALITGN			
a929	PLILYFLYPPPEIKETPNAVQFAKDRLREMG	KMSADEIIMAVIFGILLLLW	ADVPALITGN			
	310	320	330	340	350	360
m929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVL	KEKSAWDTIIWFGALIMMAA	FLNKLGLIKW			
a929	HAFSINATATAFIGLSLLLLSGVLTWDDVL	KEKSAWDTIIWFGALIMMAA	FLNKLGLIKW			
	370	380	390	400	410	420
m929.pep	FSGVLAESVGGLGVSGTAAGVILVLAYMYA	HYMFASSTAHITAMFGAFFAA	AVSLNAPAM			
a929	FSGVLAESVGGLGVSGTAAGVILVLAYMYA	HYMFASSTAHITAMFGAFFAA	AVSLNAPAM			
	430	440	450	460	470	480
m929.pep	PTALMMAAAS	NIMMTLTHYATGTSPVIFG	SGYTTMGEWWKAGFIMSVVNF	LIFFVIGSIW		
a929	PTALMMAAAS	NIMMTLTHYATGTSPVIFG	SGYTTMGEWWKAGFIMSVVNF	LIFFVIGSIW		
m929.pep	WKVLGYW					

a929 WKVLGYWX

g930.seq not found yet
g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

```
m930.seq
1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCCGA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTT TGCCATTAAC GAATGGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

```
m930.pep
1  MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWWLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNAL 3F GTTTTRILAA
151 PQDLNSGSFN *
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

```
g930-1.seq (partial)
1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCCGTAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCCAGG
201 ACGTATTGCA GCATTCGAAA ACAAAATTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGGC TGATTTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 AAGTGATGTC GTGGTGCAAT GCGCGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGACTGAGTG ATATGTTCTA
501 TGTAATTTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTG AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCCGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTCCGC TTCAACCGCC TGTGTATCG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACGAGGGAAA CAAAAGTTA
801 CATTCATGAT GCCGAAGTGA CTGTACAACG GCGTAAACCC ACAGGTGGT
851 TGGCAGAACT TTCCACAAA GGATATATCG GTCCGAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGGCATG AAAGATGCTC TCGCGCGGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAAACAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GCGGCAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTTATCGGG CCAAACCTCTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGGTTATTC GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

```
g930-1.pep (partial)
1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTPJ LAAPDLNSG KLQLTMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
101 TAEADLIQVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTEFG FNRLLYRDAK
251 RKTYSVVKLW TRETKSYIDD AELTVQRKKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FEGTSPMKI WTASADVNTF FOIGKOLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLW
401 QFKPGHQLYL GADVGHVSGO SAKWLSGQTL AGTAIGIRGO IKLGGNLHYL
```

m930-1.seq

m930-1.pgp

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEHHARFQFALKRALRETGFQAGKCLHAGNINQIMSLAQNALIGRGYTTTRI					
g930-1.pep				GKCLHAGDINQIMSLAQNALIGRGYTTTRI		
				10	20	30
	150	160	170	180	190	200
m930-1.pep	LAAPQDLNSGKLQLTLPSYLSIRIDRSNDDQTHAGRIAAFQNKFPTRSNDLLNLRDLE					
g930-1.pep	LAAPQDLNSGKLQLTLMPGYLSIRIDRSNDDQTHAGRIAAFQNKFPTRSNDLLNLRDLE					
	40	50	60	70	80	90
	210	220	230	240	250	260
m930-1.pep	QGLLENKRLPTAEADLQIVPVEGEPNOSDVVVQWRQLLPYRVSVGMDNSGSEATGKYQG					

1343

```

g930-1.pep  QGLENLKCLPTAEADLQIVPVEREPHOSDVVVQWEXELLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150

              270      280      290      300      310      320
m930-1.pep  NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210
g930-1.pep  NITFSADNPLGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210

              330      340      350      360      370      380
m930-1.pep  NHNGYRYHQAVSGLSEVDYNGKSYNTDFGFNRLLYRDAKRRTYLSVKLWMRETKSYIDD
              220      230      240      250      260      270
g930-1.pep  NHNGYRYHQAVSGLSEVDYNGKSYNTDFGFNRLLYRDAKRRTYLSVKLWMRETKSYIDD
              220      230      240      250      260      270

              390      400      410      420      430      440
m930-1.pep  AELTVQRKKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALRAPEEAFGEGTSRMKI
              280      290      300      310      320      330
g930-1.pep  AELTVQRKKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALRAPEEAFGEGTSRMKI
              280      290      300      310      320      330

              450      460      470      480      490      500
m930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHTVVRGFDGEMSLSAER
              340      350      360      370      380      390
g930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHTVVRGFDGEMSLPAER
              340      350      360      370      380      390

              510      520      530      540      550      560
m930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAGIRGQIRLGGNLHYE
              400      410      420      430      440      450
g930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAGIRGQIRLGGNLHYE
              400      410      420      430      440      450

              570      580      590
m930-1.pep  IFTGRALKKPEFFQSRKWASGFQVGYTF
              460      470
g930-1.pep  IFTGRALKKPEYFQTKKWTGFQVGYSEF
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorhoeae* <SEQ ID 2857>:

```

g931.seq
1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCCT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTGCGCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCCGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCCTCGACT
401 ACAAAAACCG ACAATACGGC TACACCGTTT TCGGCAGGCT AGAAAGCGGA
451 ATGGACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAC GTACCGGTAC AGCCCGTCAA AATCCGTCCG GTTGTGTGCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCG TTTCCAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1  MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKIVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA OFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

m931.seq

```

1   ATGAAACCCA AATTCAAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAGCC GATATGGGCA
101 ATATCCGTTT GGTTTGGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
151 TTCGTGCGCT ATGCCCGGAA AGGCTTTTAC GAGCAGACCG TTTTTCACCG
201 CGTTATCGAT GGTTTTGTTA TCCAGGCGGG TGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACCG CCGGCAACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACcA.kCT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCAAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAAC GTACCCGTAC AGCCCGTCAc AATCCGTCGc GTTGTTGTGG
551 GGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

m931.pap..

1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51 FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

q931/m931

		10	20	30	40	50	60
g931.pep		MKPKFKTVLTLALLAVSLPSMAATRVLMETDMGNIRLVLDESKAKTVANFVRYARKGFY					
m931		MKPKFKTVLTLALLAVSLPSMAATHVLME ⁷⁷ DMGNIRLVLDESKAPKTVANFVR ⁷⁸ ARKGFY					
		10	20	30	40	50	60
		70	80	90	100	110	120
g931.pep		DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
		: : : : : :					
m931		DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTACTIAMARTTAPDSATS					
		70	80	90	100	110	120
		130	140	150	160	170	180
g931.pep		QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKATATRGFYQNVVPQPVKIRR					
m931		QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKATATRGFYQNVVPQPVKIRR					
		130	140	150	160	170	180
g931.pep	VVVGQX						
m931	VVVGQX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

a931.seq

1	ATGAAACCCA	AATTCAAAAC	CGTTTAAACC	GCCTGCTTT	TGGCGGTTTC
51	CCTGCCGTCT	ATGGCGGCAA	CCCATGTTTT	GATGGAACC	GATATGGGCA
101	ATATCCGTTT	GGTTTGTGGAC	GACATCAAAG	CACCCAAAAC	CGTTGGCAAT
151	TTCTGTCGCT	ATGCCGGAAG	AGGCTTTTAC	GACAAATCGA	TTTTTACCG
201	CGTCATCGGC	GGCTTCGTTA	TCCAAGGCGG	CGGATTGACC	GAGGACTTTG
251	CACAAAGGCG	AAGCGATAAG	GCCGTTGCCA	ACGAATCCGG	CAACGGCTTG
301	AAAAACACTG	TCCGGCACCAT	CGCATATGGC	CGGACGGGCG	ATCCGGATTG
351	CGCCACCAGC	CAGTCTTTTA	TGCAATCTGGT	GGACAATGAT	TCTGCTCAAT
401	ACAAAAACGG	ACAATACGGC	TATACCGTTT	TCCGCGAGGT	CGAAGCGGGC

1345

```

451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGTCG
551 GGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

```

a931.pep
  1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
  51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

m931/a931 94.6% identity in 185 aa overlap

```

m931.pep      10      20      30      40      50      60
               MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY
a931           10      20      30      40      50      60
               MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY

m931.pep      70      80      90     100     110     120
               DDTV FHRVIDG FVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS
a931           70      80      90     100     110     120
               DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS

m931.pep      130     140     150     160     170     180
               QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR
a931           130     140     150     160     170     180
               QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR

m931.pep      VVVGQX
a931           VVVGQX

```

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

```

m932.seq
  1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
  51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCGT AAGGGTTTCG ACCCTTATCC CGAAAAACAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

```

m932.pep
  1 MKYIVSISLA MGLAACSPGG FKNPNWDAAS FWELKNYANP YPGSASAALD
  51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPYPENK
 101 KYEWPREEGK TK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

```

g934.seq
  1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACACACCGC

```

1346

```

51 CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
201 CGGCAACAAC GGTGAGCCCG TTACCGGCAA .AGAcggGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGG
351 GCAACCAAGA CAGCCCCGTC GCCCGTCGCG CGCGTGCTGC CTACCATCAG
401 TCCGCACGCC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCGCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAagg
551 cggtaaaCCC GGCAGCTCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTTGT TAGGGGCAAT GTTATGTTGC CGTTTGATTT TCAGACGGCA
651 TTTTGTTC AAGCGTTTGA TGTcggGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:

g934.pep

```

1 MKKIIASALI ATFALTACQD DTQARLERQO KQIEALQQQL AQQADDTVYQ
51 LTPEAVKDTI PAQAQANGMN GQPVTKRRA AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQAG KQIHTGGQPR QPRRPSRACC LPSVRTPOCA HQQGFEHAQP
151 PKCTTGAGGA ALPPDNAPAR QLPPSRYARF RQKAVNPARQ CRLKGFQTAF
201 LYLLGALLCC RLIFRRHFVS XRLMSGWQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2867>:

m934.seq (partial)

```

1 .CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51 ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
101 ACACCATTCC TGCCGAAGCA CAGGCAAACG GCAACAACG GCAACCCGTT
151 ACCGGTAA.A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
201 GGCTGCTGCA AAGCCTGGTC GGCGCGGCGG CAGGCGCGTT TATCGGCAAC
251 GCGCTGGCAA ACAAAATTCAC ACGGGCAGGC AACCAAGACA GTCCCGTCGC
301 CCGGCGCGCG CGTGACAGCT ACCATCAGTC CGCACGCCCC AATGCGCGCA
351 yCAGCAGGGA TTTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGCG
401 CAkGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACCGCCG
451 CCCCCTATG CGCGGTTTCG GCAGGAGGCG GTAAACCCCG CGCGCCAATG
501 CCGTCTGAAG AGCTTTCAGA CGGCATTThT GCATTGTGTA GGGACATTGT
551 TATGTTGCCG TTTGATTTTC AGACGGCATT TTGTTTCCAA GCGTTTGATG
601 TCGGGATGGC AATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:

m934.pep (partial)

```

1 .RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51 TGXRRAAVYL RPIDRKLAAA KPGRRGRRV YRQAGKQIH TGRQPRQSR
101 PARACSLPSV RTPQCAHQOG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151 PRYARFRQEA VNPARQCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/g934

```

                                     10      20      30
m934.pep                             RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                                     |||:|||
g934      MKKIIASALIATFALTACQDDTQARLERQOKQIEALQQQLAQQADDTVYQLTPEAVKDTI
          10      20      30      40      50      60

          40      50      60      70      80      90
m934.pep      PAEAQANGNNGQPV TGXRRAAVYLRPIDRKLAAAKPGRRGRRVYRQAGKQIHTGRQPR
          |||:|||
g934      PAQAQANGNNGQPV TGKRRAAVYLRPIDRKLAAAKPDWRGGRRVYRQAGKQIHTGGQPR
          70      80      90      100     110     120

          100     110     120     130     140     150

```

```

m934.pep      QSRRPARACSLPSVRTPQCAHQOGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPRYARF
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g934          QPRRPSRACCLPSVRTPQCAHQOGFEHAQPPCKTTGGAGAALPPDNAPARCLPPSRYARF
              130      140      150      160      170      180

              160      170      180      190      200
m934.pep      RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g934          RQKAVNPARQCRLKGFQTAFLYLLGALLCCRLIFRRHFVSKRLMSGWQFX
              190      200      210      220      230

```

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTGC CACTCGCCGC
51  CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGC GACAGCATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AACACCATT CCTGCCGAAG CACAGGCCAA
201 CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGCAGGGCA GCAGTATATT
251 TACACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCTTGG TCGGCGCGGG
301 GCGAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTG ACACGGGCGC
351 GCAACCAAGA CAGTCCCGTC GCCGGCGCGG CGCGTGCCGC CTACCATCAG
401 TCCGCACATC CCAATGCGCG CACCCAGCAG GATTTGAACA CCGCGACGCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA CGGTTACCCG CCGACAACCG
501 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TGGCGGGTTT CGCGCAAGAG
551 CGGTAAATTG GGCCTGCCAA TGCCGTGTGA AGGGCTTTCG GACGGCATTT
601 TTGATATTTG TAGGGACATT GTTATCTTGC CGTTTGATTT TTAGACGGCA
651 TTTTGTTTCC AAGAGTTTGA TGTGCGGAATG CCAATTCTGA

```

```
a934.pep
1  MKKIIIASALI ATFALAACQD DAQARLEQQQ KQIERLQQCL AQQADDTVYC
51  LTPPAVKDTI PAEAQANCNM GQVTVY*PA AVYLRPIDRK LAAAKPGRE
101 GRRVYRQRAG KQIHTGRQPR QSRRPARACR LPSVRTSQCA HQQGFEHAQP
151 PCKTTGGAGA ALPPDNAPAR QLPPRHARF RQKAVNPACQ CRLKGFQTA
201 LYLLRLTLCR LIIFRRHFVS KSLMSGWOF*
```

```

m934.pep      10      20      30      40      50      60
                RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                |||||
a934          MKKIIASALIATFALAACQDDAQAARLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                10      20      30      40      50      60

                40      50      60      70      80      90
m934.pep      PAEAQANGNNGQPVTGXRRAAVYLRPIDRKLAAAKPGRRGGRVYRQRAGKQIHTGRQPR
                |||||
a934          PAEAQANGNNGQPVTXXRRAAVYLRPIDRKLAAAKPGRRGGRVYRQRAGKQIHTGRQPR
                70      80      90      100     110     120

                100     110     120     130     140     150
m934.pep      QSRRRPARACSLPSVRTPQCAHQQGFEHAQPCKTTGGAXAALPPDNAPKRLPPPRYARF
                |||||
a934          QSRRRPARACRLPSVRTSQCAHQQGFEHAQPCKTTGGAGAAALPPDNAPARQLPPPRHARF
                130     140     150     160     170     180

                160     170     180     190     200
m934.pep      RQEAVNPARQCRLKSFQTAFXHLGLTLLCCRLIFRRHFVSKRLMSGWQFX
                ||:|||||
a934          RQKAVNPACQCRLKGFQTAFYLLGLTLLCCRLIFRRHFVSKSLMSGWQFX
                190     200     210     220     230

```

q935.sea not found yet

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGCAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GGCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTC AGTAAAAATC
801 AGCTTATGAC GACGGGTTCG GCAGAGCGTA TTTGGGTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTGTG CGGTTTGTG CGAACGCGA AACGGTGGG
1201 GCGCGGGTCA ATAATGCCG CTACCGCGC AACGTTGTT ATGCGGCTG
1251 GCGCGAGGAG TGGCGCAGT TGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCGTT CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTG CCGCGTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

```

a935.pep
1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRLKSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFGSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDAKTK RVNNRRLPPY MLAGVGVQOL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNPVYA KRRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

	10	20	30	40	50	60
m935.pep	MLYFRYGLVWVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVENDAPRVV					
a935	MLYFRYGLVWVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVENDAPRVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m935.pep	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m935.pep	AEAVARYRELHGENAADERILLDLAAAEFDDFRLKSAERHFAEAEKLDLPAPVLENVGRF					
a935	AEAVARYRELHGENAADERILLDLAAAEFDDFRLKSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m935.pep	RKKTEGLTGWRFGSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
a935	RKKAEGLTGWRFGSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m935.pep	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGAGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGCGCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAC TGACGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAATGT GGGGCGTTT CGGAAAAAAT
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTCCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAAGTCA GCCGGGCGGA GCGGGCGGCA GGGTTGAATT
701 ATGAAATCGA GGCGGAAAAG CTGACGCCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCG GTAAAAAATC
801 AGCTTATGAT GACGGGTTTC GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCA.CGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAAACAAA CGGGTAAACA ACCGCCGCTT
951 GCCGCCGTAT ATGCTGCGGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
1001 ACCGCCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CGGGTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGT TTGCGCGTTG
1251 GGCGCAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTCCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCATTG CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1  MLYFRYGLFV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVENDAPRVV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVERYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAAKLDP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YFFSKKSAYD DGFGGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDPAK RVNNRRLPPY MLAGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEVFVS
501 ADWRP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGAGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAC TGACGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGAAAAAAT
501 GGATTTGCCG GCGCCGCTTT TGGAAATGT GGGGCGTTT CGGAAAAAAG
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1350

	310	320	330	340	350	360
m935.pep	GSDGFDAKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFDAKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFVVPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFVVPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSASYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSASYARRNYKGVAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNVPIAKRRNSEVFVSADWRF					
a935	GRTESNVPIAKRRNSEVFVSADWRF					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

```

g936.seq
1  ATGAAACCCA  AACCACACAC  CGTCCGCACC  CTGATTGCCG  CCGTCCTCAG
51  CCTTGCCCTC  GGCGGCTGCT  TCAGCGCAGT  CGTCGGCGGG  GCCGCCGTCG
101 GCGCAAAATC  CGTCATCGAC  CGcgcAACCA  CCGgcgcgca  AACCGATGac
151 aACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ACCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCGGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTATACAA
351 TCACATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCGGGCGAC  ATCGCCGGCG
401 AACTTGGA  CACGTCCAAA  GTCCGCGCca  cgCTGCTGGG  CATCAGCCCC
451 GCTACACAGG  CGCGCGTCAA  AATCATTACC  TACGCAATG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCAccgT  CGCGGTACAA  AAAGTCATTA  CCCTTACCA  AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

```

g936.pep
1  MKPKPHTVRT  LIAAVLSLAL  GGCFSAVVGG  AAVGAKSVID  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GQVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIT  YGNVTYVMGI  LTPEEQAQIT  QKVSTTVGVQ  KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

```

m936.seq (partial)
1  ATGAAACCCA  AACCGCACAC  CGTCCGCACC  CTGATTGCCG  CCATTTTCAG
51  CCTTGCCCTT  AGCGGCTGCG  TCAGCGCAGT  AATCGGAAGC  GCCGCCGTCG
101 GCGCGAAATC  CGCCGTCGAC  CGCCGAACCA  CCGGCGCGCA  AACCGACGAC
151 AACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ATCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCGGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTGTACAA
351 CTATATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

```

m936.pep (partial)
1  MKPKPHTVRT  LIAAIFSLAL  SGCVSAVIGS  AAVGAKSAVD  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GQVATTEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTA...

```

1351

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from *N. gonorrhoeae*:

m936/g936

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAksAVDRRTTGAQTDDNVMALRIETT					
g936	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAksVIDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
g936	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
	130					
m936.pep	VASLPRTAXXX					
g936	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGI LTPEEQAQIT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

a936.seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTCCCG	CCGTCTTCA3
51	CCTTGCCCTC	GGCGGCTGCG	TCAGCGCAGT	CGTCGGCGGT	CCGGCGGTCT
101	GCGCGAAATC	CGCGCTCGAC	CGCCGAACCA	CCGCGCGCA	AACCGAAGAT
151	AACGTAATGG	CGCTGCGTAT	CGAAACCAACC	GCCCGCTCT	ATCTGCGGCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCCCCA	AATCTCGGT	GTGGGCTACA
251	ACCGCCACCT	GCTGCTGCTC	GGACAAGTCG	CCACTGAAGG	CGAGAAACAG
301	TTCGTCGGTC	AGATTGCACG	TTCCGAACAG	GCCGCCGA3	CCGTGTACAA
351	CTACATTACC	GTGCGCTCCC	TGCCGCGCAC	TGCCGCGGAC	ATCGCGCGCG
401	ACACTTGGAA	CACATCCAAA	GTCCGCGCCA	CGCTGTTGGG	CATCAGCCCC
451	GCCACACAGG	CGCGCGTCAA	AATCGTTACC	TACGGCAACG	TAACTACGCT
501	TATGGGCATC	CTCACCCCGG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCACCACCGT	CGCGGTACAA	AAAGTCATCA	CCCTCTACCA	AAACTACGTC
601	CAACGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2880: ORF 936.a>:

a936.pep

1	MKPKPHTVRT	LTA AVL SLAL	GGCVSAVVGG	AAVGAksAVD	RRTTGAQTDD
51	NVMALRIETT	ARSYLQNNQ	TKGYTPQISV	VGYNRHLLLL	GQVATEGEKQ
101	FVGQIARSEQ	AAEGVYNYIT	VASLPRTAGD	IAGDTWNTSK	VRATLLGISP
151	ATQARVKIVT	YGNVTYVMGI	LTPEEQAQIT	QKVSTTVGVQ	KVITLYQNYV
201	QR*				

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAksAVDRRTTGAQTDDNVMALRIETT					
a936	MKPKPHTVRTLTA AVL SLALGGCVSAVVGGAAVGAksAVDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
a936	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936.pep	VASLPRTA					

1352

```

          |||||
a936      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQQAQIT
          130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

```

g936-1.seq
1  ATGAAACCCA AACACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGcgaACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCAACC GCCCGTTCTT ACCTGCCCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAACTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCCGTC AGATTGCACG TTCCGAALAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACCTTGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGT
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

```

g936-1.pep
1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRONNQ TKGYTPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

```

m936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCAACC GCCCGTTCTT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAACTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCCGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACCTTGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACCTACGT
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

```

m936-1.pep
1  MKPKPHTVRT LIAAIFSLAL SGCVS AVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRONNQ TKGYTPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIV YGNVTYVMGI LTPEEQQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

m936-1/g936-1 95.5% identity in 202 aa overlap

```

          10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVD RRTTGAQTDDNVMALRIETT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAAGSAVDRRTTGAQTDDNVMALRIETT
          10      20      30      40      50      60

          70      80      90      100     110     120
m936-1.pep  ARSYLRONNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      ARSYLRONNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          70      80      90      100     110     120

          130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQQAQIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGCGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTT GTCGGGTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCCGCGAAG GCGGTGTACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTAAVLSLAL GGCVSAVVG AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GOVATEGEKQ
101 FVGQIARSEQ AEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

```

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAASVDRRTTGAQTEDNVMALRIETT
              |||||
a936-1      MKPKPHTVRTLTAAVLSLALSGCVSAVVGGAAGVGAASVDRRTTGAQTEDNVMALRIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLGQVATEGEKQFVGQIARSEQAEGVYNYIT
              |||||
a936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLLLGQVATEGEKQFVGQIARSEQAEGVYNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTTAgt ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAAT
101 GGAAactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCACCTGCCT CACCGGTTTA CATTcAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCC
251 GCACGCTCGG TTTGCGCTAC GGACTGAccg GCAataccgA CATTTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACTCGacg GCAACGGCAA

```

1354

```

351 AACCCGCAAC AAACGGATGT CCGACATATC CGCCGGCATC AGCCACACCT
401 TCCTtaAAGa cgGCAAAAT CCCGCACTCA TCGCTTTCCT CGAAAGCACG
451 GTTTACGAAA AATCGCGCAA CAAAGCCTCG TCGGGAAT CGTGGCTCAT
501 CGGCGCCACC ACCTACAAAG CCATAGATCC GATTGTCTT TCCCTCACCG
551 CCGCTACCG CATCAACGGC AGCAAAACCC TTTCAGACGA CGTCAAATAC
601 AAAGCAGGCA ATTACTGGAT GCTGAATCCC AACATCTCAT TTGCCGCCAA
651 CGACAGAATC AGCCTGACCG GAGGCATCCA ATGGCTGGGC AAACAGCCCG
701 ACCGATAGA CGGCAAAAA GAATCCGCAA GAAACACATC CACCTACGCC
751 CATTTCCGGC CAGGTTTCGG TTTCACCAA ACCGCGGCTT TAAACGCATC
801 CGCAGTTTC AACGTTTCAG GGCAAAGCAG TTCCGAAC TG AAATGGGCG
851 TACAGCATAC ATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2888; ORF 937.ng>:

g937.pep

```

1 MKNILLVFVS FVPLCVRTDL PLNIEDIMTD KGKWKLETS TYLNSENRA
51 ALASPVYIQT GSASFIPVPT EIQENGSTND MLAGTLGLRY GLTGNTDIYG
101 SGSYLWHEER KLDGNGKTRN KRMSDISAGI SHTFLKDGKN PALIAFLEST
151 VYEKSRNKAS SGKSWLIGAT TYKAIDPIVL SLTAAYRING SKTLDSDVKY
201 KAGNYWMLNP NISFAANDRI SLTGGIQWLG KQPDRTDGK ESARNTSTYA
251 HFGAGFGFTK TAALNASARF NVSGQSSSEL KLGVOHTF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2889>:

m937.seq

```

1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAACTT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCCG
151 GCCGAACCTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCCG ACCGAAATCC AAgAAAaCGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGGCG TACGGAAGTGA CCGGGAATAC CGACATTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG AC33CAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCTTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTTGCTGC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCTT CCAGAAACAC ATCCACCTAC
751 GCCCATTTG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2890; ORF 937>:

m937.pep..

```

1 MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTND MLVGTGLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTLDSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIOWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVOHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng) from *N. gonorrhoeae*:

g937/m937

```

          10      20      30      40      50      59
g937.pep  MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETS TYLNSENRAALASPVYIQ
          || || : : : : : : : : : : : : : : : : : : : : : : : : : :
m937      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETS TYLNSENNR AELAAPVYIQ
          10      20      30      40      50      60

          60      70      80      90     100     110     119
g937.pep  TGSASFIPVPT EIQENGSTNDMLACTLGLRYGLTGNTDIY GSGSYLWHEERKLDJNGKTR

```

[illegible]

a937.seq

```
1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGG
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCG
101 AATGGAAACT GCGAACTTCC CTTACTCTAC TGAACACGCA AAACAACCGG
151 GCCGAACCTG CGGACCGGTG TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTTCC ACCGAAATCC AAGAAAAACG CAGCAATACC GATATGCTPG
251 TTGGCAGCT CGGTTTGGCG TACGGACTGA CCGGGAATAA CGACATTTAC
301 GGCACGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCCGA AACAAACCGA TCTCGA ATCCCTCGGC ATCAGCCACA
401 CCTTCTCTAA AGACGACAAA AACCCTGCC TACTCAGCTT TCTTGAAGAG
451 ACGGTTTACG AAAATTCGCG CAACAAAGCC TCCTCGGGAA AATCCTGGCT
501 CATCGGGGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAGC CAACACCAAA
601 TACAAGCAG CCAATTACTG GATGCTGAAT CCCAATATAT CCGTCGCGCG
651 CAACGACAGA ATCAGCTTCA CGGCGGCAT CCATGGCTG GCGAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCC GCGCAGGTTC CGGTTTCACC AAAACCACGG CTTTAAACCG
801 ATCCGCACGT TTCAACGTTT CAGGGCAAG CAGTTCGGAA CTGAAATTTG
851 CGGTACAGTA TACGTTTTAA
```

```

a937.pep      1  MKRIFLPALP  AILPLSAYAD  LPLTIEDIMT  DKGKWKLETS  LTYLNSENNE
      51  AELAAPVYIQ  TGATSFPIPI  TLEQENGSTN  DMLVGLTGLR  YGLTGNTDIT
     101  GSGSYLWHEE  RKLDGNGKTR  NKRMDSVSLG  ISHTFLGDDK  NPALISFLES
     151  TVYEKSPNKA  SSGKSWLIGA  TTYKALDPVV  LSLTAAYRIN  GSKTLLSNTF
     201  YKAGNYWMLN  PNISFAANDR  ISLTGGIQWL  GKQPADRLDG  KESAPNTSTY
     251  AHFGAGGFGT  KTTALNASAR  FNVSGQSSSE  LKFGVQHTF*

```

```

      10      20      30      40      50      60
m937.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRRAELAAPVYIQ
          |||||:|||||
a937      MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRRAELAAPVYIQ
          10      20      30      40      50      60

      70      80      90      100     110     120
m937.pep  TGATSFIPIPTEIQENGSNNTDMLVGLTGLRYGLTGNTDIYSGSGYLWHEERKLDGNSKTR
          |||||:|||||
a937      TGATSFIPIPTEIQENGSNNTDMLVGLTGLRYGLTGNTDIYSGSGYLWHEERKLDGNGKTR
          70      80      90      100     110     120

```

1356

```

      130      140      150      160      170      180
m937.pep  NKRMDSVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
a937      NKRMDSVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
      130      140      150      160      170      180

      190      200      210      220      230      240
m937.pep  LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGR
a937      LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGR
      190      200      210      220      230      240

      250      260      270      280      290
m937.pep  RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX
a937      KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX
      250      260      270      280      290

```

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51 CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCGG
201 CATCCGCGAC GTAAACGCAC CC...

```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLAFV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51 PRLAAQHTAY IYHQTIGIRD VNAP...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

```

a939.seq
1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51 CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCGG
201 CATCCGCGAC GGTAACGCAC CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CGGGTATGCC GGGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTGAGCATC AGGCATATAT
501 TGTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTTGAA AGCGGTGCGC
601 AACTTTATCC AAGGTTTGCG TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLAFV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51 PRLAAQHTAY IYHQTIGIRD GKRTHGSAV MKPVVMNLSQ QDILNVSAFY
101 AKQOPKSGEA NPENPELGA KIYRGGSLDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAIVIEQ MNAYKSGQRK NTIMEDIANR MSEDLDKAVA
201 NFIQGLR*

```

m939/a939 100.0% identity in 70 aa overlap

```

      10      20      30      40      50      60
m939.pep  MKRLTLAFVLAAGAVSASPKADVEKGQVAATVCAACHAADGNSGIAMYPRLAAQHTAY
a939      MKRLTLAFVLAAGAVSASPKADVEKGQVAATVCAACHAADGNSGIAMYPRLAAQHTAY

```


1357

```

              10      20      30      40      50      60
              70
m939.pep      IYHQTIGIRDVNA P
              |||||
a939          IYHQTIGIRDGKRT HGSAAVMKPVVMNLSDDILNVS AFYAKQ QPKSGEANPKENPELGA
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1   ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51  GGCCGCCGGT GCGCTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAATC  CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1   MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51  SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1   ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1   MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAG SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

```

m950/g950      86.6% identity in 112 aa overlap
              10      20      30      40      50
m950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGSCGASKSAEGSCGA-----
              |||||
g950          MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCGASKSAEGSCGASKSAEG
              10      20      30      40      50      60

              60      70      80      90      100
m950.pep      ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |||||
g950          SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1   ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

1358

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASH ATGVHKSANG SCGASESAEG
51  SCGAAGSKAG EGKCGEGKCG ATVRKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a950.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSANGSCGASKSAEGSCGAAGSKAG					
m950	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSANGSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a950.pep	EGKCGEGKCGATVRKTHKHTKASKAKAKSAEGKCGEGKCGSKK					
m950	EGKCGEGKCGATVRKTHKHTKASKAKAKSAEGKCGEGKCGSKK					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCTACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGCACGGCGT ATGCTGCCGG CGCGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGGTGTTC ACGCTGTTGG CGGGTGAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTTGGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTTGGAATG GCCGTGTGCG TGAACGCGTT
351 TGAACAGGCG GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG CGCGGTGGCG TGCGGAACGT ATTGAGGGAA
451 GGGGGAAATC AGCATCTGGA CGGGTTGGAA GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGTCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTCG CCGTGCGGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CGGTGTTCCG
651 CGTACAGGGA CCGGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAAATA TTGCCCCCA CTTTAATGAC GTTGCGCTCG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAAATT ATGAATCTGG
851 TTTCCTGCGC TAAGCCGGAT GATGCCATG CGCGTTTGAA CGTGCTGTTG
901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTTGA CAAAGGCGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCGGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACFAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACTTTC GGCAGCGGGA
1351 AGCAGCGAAC CTTTGGCGGA AGCATGGCA CAGCGTTCCA TTATTTACGA
1401 ACAGTTCGGC AAACGGGGAA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAAATC AACCCGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAG ACGACCCGCA GCCCGAAGTT GCCGCCCAAT TGGGCGAAGT
1701 GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTTGACGTA TGGACGACGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GGCGGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MIMLPARFTI LSVLAAALLA GQMYAAGAAD VELPKVEGKV LRKHRRYSEE
```

```

51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 FEVAERALEM AVSLNAFEQA EMIIYQKWRQI EPIPGEAQKR AGWLRNVLR
151 GGNQHLDGLE EVLAQSDDDVQ KRRIFLLLVQ AAVQQGGVAQ KASKAVRRRA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL ORLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFEEQTDTON LSAVWQEMEI MNLVSLRKPD DAYARLNVLI
301 EHNPNANLYI QAAILAANRR EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLKKVS APEYLFDKGV LAAAAAAELD GGRAALRQIG
401 RVFKLPEQQG RYFTADNLSK IQMLALSCLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQTAYQI NPDDTAVNDS IGWAYYLLKG AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLRF
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1 ATGATTATGT TACCTAACCG TTTCAAAATG TTAAGTGTGT TGACGGCAAC
51 CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTTC AAGAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTGCGGCAG TGGCGGAGCG
201 GGTAAATCAG ATATTACGT TGCTGGGAGG GGAAACCGCC TTGCAAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCCG TGTCGCTGAA
351 CGCGTTTGAA CAGGCGGAAA TGATTTATCA GAAATGGCGG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAAGAG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GCGCGACCAA GGACAGAAC GCAGGGTGT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTTG GCGCAAAAAG CATCGAAAGC GGTTCGCCGC
601 GCGCGGTTGA AATATGAACA TCTGCCGCAA GCGGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGGACGCG AAAAGGAAAA GGCAATCGGA GCTTTGCAGC
701 GTTTGCGCAA SCTCGATACG GAAATATTGC CCCCCACTTT AATGACGTTG
751 CGTCTGACTG CACGCAATA TCCCGAAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTTT CGGCGTCTG GCAGGAAATG GAAATTATGA
851 ATCTGGTTTC CCTGCACAGG CTGGATGATG CCTATGCGCG TTTGAACGTC
901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTCAGG CAGCGATATT
951 GCGCGCAAA CGAAAAGAAG GTGCTCCGT TATCGACGGC TACGCCGAAA
1001 AGGCATACGG CAGGGGGACG GAGGAACAGC GGAGCAGGGC GCGGCTAACG
1051 GCGGCGATGA GTATGCCCGA CCGCAGGGAT TACGCCAAAG TCAGGCAGTG
1101 GCTGAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CGGCTGCGGC GGCTGTCGAG TTGGACGGCG GCAGGGCGGC TTTGCGGCAG
1201 ATCGGCGAGG TCGGAAACT TCCCGAACAG CAGGGGCGGT ATTTTACGGC
1251 AGACAATTTG TCCAAAATAC AGATGCTCGC CCTGTGCAAG CTGCCCCGTA
1301 AACGGGAGGC TTTGAGGGGG TTGGACAAGA TTATCGAAAA ACCGCCGTGC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTCACTTGT
1401 TTACGATCGG CTTGGCAAGC GGAAAAAAAT GATTTCAGAT CTTGAAAGGG
1451 CGTTCAGGCT TGCACCCGAT AACGCTCAGA TTATGAATAA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTTGGAC GAAGGTTTCG CCTGTCTCA
1551 GACGGCATAC CAAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGGCGTA TTACCTGAAA GCGCAGCGCG AAAGCGCGCT GCCGTATCTG
1651 CGGTATTTCG TTGAAAACGA CCCCAGCCCC GAAGTTGCCG CCCATTGGGG
1701 CGAAGTGTG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 CGCAGGCGGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCAACCT TCCGAAAAAC CTCGGAAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1 MIMLPNRRFM LTVLTATLIA GQVSAAGGGA GDMKQKEVG KVFRRQORYS
51 EEEIKNERAR LAAVGERVNO IFTLLGETA LQKQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQKWR QIEPIPGKAQ KRAGWLRNVL
151 RERGNQHLDG LEEVLAQADE GQNRVFLLL AQAAVQODGL AQKASKAVRR
201 AALKYEHLPE AAVADVFSV QGREKEAIG ALORLAKLDT EILPPTLMTL
251 RLTAARKYPEI LDGFFEQTDI QNLSAVWQEM EIMNLVSLHR LDDAYARLHV
301 LLERNPNADL YIQAAILAAN RKEGASVIDG YAEKAYGRGT EEQSRRAALT
351 AAMMYADRRD YAKVRQWLKK VSAPEYLFDK GVLA AAAAVE LDGGRAALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALS LKPKREALRG LDKIEKPPA
451 GSNTELQAEA LVQRSVVYDR LGKRKKMISD LERAFRLAPD NAQIMNNLGY
501 SLTDSKRLD EGFALLQTAY QINPDDTAVN DSIWAYYLLK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDOAV DVWTQAAHLT GDKKIWRETL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

1360

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

m951.pep	10	20	30	40	50	60
	MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVGVFRKQORYSEEEIKNERAP					
g951	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGKVLKRRYSEEEIKNERAR					
	10	20	30	40	50	
m951.pep	70	80	90	100	110	120
	LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
g951	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
	60	70	80	90	100	110
m951.pep	130	140	150	160	170	180
	QAEMIYQKWRQIEPIPGKAQKRAGWLRNVLREGRNQHLDGLEEVLAQADEGQNRVFLLL					
g951	QAEMIYQKWRQIEPIGKAQKRAGWLRNVLREGRNQHLDGLEEVLAQSDDVQKRRIFLL					
	120	130	140	150	160	170
m951.pep	190	200	210	220	230	240
	AQAAVQODGLAQKASKAVRRAALKYEHLPAAVADVVSVOGREKEKAIGALQRLAKLDT					
g951	VQAAVQQGGVAQKASKAVRRAALKYEHLPAAVADVFGVQGREKEKAIEALQRLAKLDT					
	180	190	200	210	220	230
m951.pep	250	260	270	280	290	300
	EILPPTLMTLRLTARKYPEILDGFFEQTDTONLSAVWQEMEIMNLVSLHRLDDAYARLNV					
g951	EILPPTLMTLRLTARKYPEILDGFFEQTDTONLSAVWQEMEIMNLVSLRKPDDAYARLNV					
	240	250	260	270	280	290
m951.pep	310	320	330	340	350	360
	LLEHNPANLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQSRRAALTAAMMYADRRD					
g951	LLEHNPANLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQSRRAALTAAMMYADRRD					
	300	310	320	330	340	350
m951.pep	370	380	390	400	410	420
	YAKVRQWLKKVSAPEYLFDKGVLAATAVELDGGRAALRQIGVRKLPEQQGRYFTADNL					
g951	YAKVRQWLKKVSAPEYLFDKGVLAATAVELDGGRAALRQIGVRKLPEQQGRYFTADNL					
	360	370	380	390	400	410
m951.pep	430	440	450	460	470	480
	SKIQMLALSCLPKREALRGLDKIIEKPPAGSNTLQAEALVQRSVYDRLGKRRKMISD					
g951	SKIQMLALSCLPKREALIGLNNIIAKLSAAGSTEPLAEALQRSIIYEQFGKRGKMIAD					
	420	430	440	450	460	470
m951.pep	490	500	510	520	530	540
	LERAFRLAPDNAQIMNGLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	LETALKLTPDNAQIMNGLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
	480	490	500	510	520	530
m951.pep	550	560	570	580	590	600
	GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL					
g951	GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWTQAAHLRGDKKIWRETL					
	540	550	560	570	580	590
m951.pep	610					
	KRHGIALPOPSRKPRK					
g951	KRYGIALPEPSRKPRKX					
	600	610				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCCGTTTCAC CATTATCT GTGCTCGCGG CAGCCCTGCT
51  TGCCCGGCAG GCGTATGCCG CCGGCGCGGC GGATGCCAAG CCGCCGAAGC
101 AAGTCGGAAA GGTTTTCAGA AAGCAGCAGC GTTACAGCGA GGAAGAAATC
151 AAAAAACGAA GCGCACGGCT TCGGCGAGTG GCGCAGCGGG TTAATCAGAT
201 ATTTACGTTG CTGGGAGGGG AAACCGCCTT GCAAAAGGGG CAGGCGGGAA
251 CGGCTCTGGC AACCTATATG CTGATGTTGG AACGCACAAA ATCCCCCGAA
301 GTCGCCGAAC GCGCCTTGGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GGCGGAAATG ATTTATCAGA AATGGCGGCA GATTGACCTT ATACCGGGTA
401 AGGCGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGCTGAG GGAAAGAGGA
451 AATCAGCATC TAGACGGACT GGAAGAAGTG CTGGCTCAGG CGGACGAAGG
501 ACAGAACCGC AGGGTGTTTT TATTGTTGGC ACAAGCCGCC GTGCAACAGG
551 ACGGGTTGGC GCAAAAAGCA TCGAAAGCGG TTCGCCCGCG GCGTTGAGA
601 TATGAACATC TGCCCGAAGC GCGGTTGGC GATGTGGTGT TCAGCGTACA
651 GGGACGCGAA AAGGAAAAGG CAATCGGAGC TTTGACGCGT TTGGCGAAGC
701 TCGATACGGA AATATTGCCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGCAAATATC CCGAAATACT CGACGGCTTT TTCGAGCAGA CAGACACCCA
801 AAACCTTTCC GCCGTCCTGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGACACGGCT GGATGATGCC TATGCGCGTT TGAACGTGCT GTTGAACGCG
901 AATCCGAATG CAGACCTGTA TATTCAGGCA GCGATATTGG CGGCAAAACG
951 AAAAGAAGGT GCTTCCGTTA TCGACGGCTA CGCCGAAAAG GCATACGGCA
1001 GGGGGACGGG GGAACAGCGG GGCAGGCGCG CAATGACGCG GCGCATGATA
1051 TATGCCGACC GAAGGGATTA CACCAAAGTC AGGCAGTGGT TGA AAAAAGT
1101 GTCGCGCCCG GAATACCTGT TCGACAAAAG TGTGCTGGCG GCTGCGGCGG
1151 CTGTCGAGTT GGACGCGCGC AGGCGCGCTT TCGCGCAGAT CGGCAGGGTG
1201 CGGAAACTTC CCGAACAGCA GGGGCGGTAT TTTACGGCAG ACAATTTGTC
1251 CAAAATACAG ATGTTGCGCC TGTGCAAGCT GCCCGACAAA CGGGAGGCTT
1301 TGAGGGGGTT GGACAAGATT ATCGAAAAC CGCCTGCCCG CAGTAATACA
1351 GAGTTACAGG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGGCAAGCGG AAAAAATGA TTTAGATCTT TGAAGGGCGG TTCAGGCTTG
1451 CACCCGATAA CGCTCAGATT ATGAATAATC TGGGCTACAG CTGCTTTTCC
1501 GATTCCAAAC GTTGGACGA AGGCTTCGCC CTGCTTCAGA CGGCATACCA
1551 AATCAACCCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACCTGAAAGG CGACGCGGAA AGCGCGCTGC CGTATCTGCG GTATTGCTTT
1651 GAAACGACCC CCGAGCCCGA AGTTGCCGCC CATTGGGCGG AAGTGTGTGT
1701 GGCATTGGGC GAACGCGATC AGGCGGTTGA CGTATGGACG CAGGCGGCAC
1751 ACCTTACGGG AGACAAGAAA ATATGGCGGG AAACGCTCAA ACGTCACGGC
1801 ATCGCATTGC CCCAACCTTC CCGAAAACCT CGGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAAALLAGQ AYAAGAADAK PPEVKGKVF R KQORYSEEEI
51  KNERARLAAY GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEM IYQKWRIEP IPGKAQKRAG WLRNVLRERG
151 NQHLDGLEEV LAQADEGQNR RVFLLLAQAA VQODGLAQKA SKAVRRAALR
201 YEHLPEAAVA DVVFSVQGRE KEKAIGALQR LAKLDTIELP PTLMTLRLTA
251 RKYPEILDGF FEQTDTONLS AVWOEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNADLYIQA AILAANRKEG ASVIDGYAEK AYGRGTGEOR GRAAMTAAMI
351 YADRRDYTKV RQWLKKVSAP EYLFDKGVLA AAAAVELDGG RAALRQIGRV
401 RKLPEQGRY FTADNLSKIQ MFALSCLPKD REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLLS
501 DSKRLDEGFA LLOTAYQINP DDTAVNDSIG WAYYLGKDAE SALPYLRYSF
551 ENDPEPEVAA HLGEVLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRHG
600 IALPQPSRKP RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```

          10      20      30      40      50
a951.pep  MLPARFTILSVLAAALLAGQAYAAAG--AADAKPPKEVGKVFRRKQORYSEEEIKNERAR
          ||| || :||:|:|:|:|:|: ||| | :| | | | | | | | | | | | | | |
m951      MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKKEVGKVFRRKQORYSEEEIKNEPAR
          10      20      30      40      50      60
a951.pep  LAAVGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE

```

1362

```

m951      |||
          LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
          70      80      90      100      110      120

a951.pep  120      130      140      150      160      170
          QAEMIIYQKWRQIEPIPGKAQKRAGWLRNVLRRGNQHLDGLEEVLAQADEGGQNRVFLLL
          |||

m951      130      140      150      160      170      180
          QAEMIIYQKWRQIEPIPGKAQKRAGWLRNVLRRGNQHLDGLEEVLAQADEGGQNRVFLLL
          |||

a951.pep  180      190      200      210      220      230
          AQAAVQQDGLAQKASKAVRRAALRYEHLPEAAVADVVSVOGREFEKAIGALQRLAKLDT
          |||

m951      190      200      210      220      230      240
          AQAAVQQDGLAQKASKAVRRAALKYEHLPEAAVADVVSVOGREFEKAIGALQRLAKLDT
          |||

a951.pep  240      250      260      270      280      290
          EILPPTLMTLRLTARKYPEI LDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
          |||

m951      250      260      270      280      290      300
          EILPPTLMTLRLTARKYPEI LDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
          |||

a951.pep  300      310      320      330      340      350
          LLERNPNADLYIQAAI LAANRKEGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
          |||

m951      310      320      330      340      350      360
          LLERNPNADLYIQAAI LAANRKEGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
          |||

a951.pep  360      370      380      390      400      410
          YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRLPEQCGRYFTADHL
          |||

m951      370      380      390      400      410      420
          YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRLPEQCGRYFTADHL
          |||

a951.pep  420      430      440      450      460      470
          SKIQMFALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQSVVYDRLGFRKHMISD
          |||

m951      430      440      450      460      470      480
          SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQSVVYDRLGFRKHMISD
          |||

a951.pep  480      490      500      510      520      530
          LERAFRLAPDNAQIMNNLGYSLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYYLK
          |||

m951      490      500      510      520      530      540
          LERAFRLAPDNAQIMNNLGYSLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYYLK
          |||

a951.pep  540      550      560      570      580      590
          GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQA AHLTGDKKIWRETI
          |||

m951      550      560      570      580      590      600
          GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQA AHLTGDKKIWRETI
          |||

a951.pep  600      610
          KRHGIALPQPSRKPRK
          |||

m951      610
          KRHGIALPQPSRKPRK
          |||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

```

g952.seq (partial)
1      ..TTGCTTATC GTTTGAATGC TGCACCGATG TTTAACGATA ATCCTGTTST
51     TTACGGAAAA ATCAAAATGC AGAGTTGGAA AGCGCGGCGG GATTTCATA
101    TTGTAAAGCA GGATTGGAT TTTTCCTGCG GGGCGGCTTC GGTGGCGACG
151    CTTTTGAACA ATTTTACGG GCAAAAGCTG ACGGAAGAAG AAGTGTGGA
201    AAAACTGGGT AAGGAACAGA TGC CGCGCTC GTTTGAGGAT ATGCGGCGCA
251    TTATGCCCGA TTTGGGTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301    CAGCTCGCGC AGTTGAAAAT CCCCCTCATC GTGTATCTGA AATACCGCAA
351    AGACGACCAT TTTTCGGTAT TGC CGCGAGT GGATGGCAAT ACGGTTTTGC
401    TTGCCGACCC GTCGCGGGGT CATGTTTCGA TGAGCAGGGC GCAGTTTTT
451    GAGGCTTGGC AAACCCGTGA GGGAAATTG GCAGGCAAAA TTTTGGCGGT
501    CGTGCCGAAA AAAGCGGAGG CGATTTCAAA TAAATTGTTT TTCACACATC
551    ATCCCAAGCG GCAGACGGAG TTTGCAGTCG GACAGGTAAA ATGGTGGCGT

```

1363

601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

```

g952.pep (partial)
1  ..LSYRLNAAPM FNDNPVYVGK IKLQSWKARR DFNIVKQDLD FSCGAASVAT
51  LLNNFYGQHL TEEEVLEKLG KEQMRASFED MRRIMPD LGF EAKGYALSFE
101 QLAQLKIPVI VYLKYRKDDH FSVLRGVDGN TVLLADPSFG HVSMSRAQFL
151 EAWQTRGNL AGKILAVVPK KAEAISNKL FTHHPKRQTE FAVGQVKWWF
201 AY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

```

m952.seq
1  ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
51  ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG CGCGCGGGA TTCAATAT
151 GTAAGCAGG ATTTGGATTT TTCCTGTGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTACGGGC AACCGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCTGATT TGGGTTTGA GCGGAAGGGC TATTCCTGT CTTTCGAGCA
351 GCTCGCGCAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGGCA TGTTCATG AGCAGGGCGC AGTTTTTGGA
501 TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCTGTCA
551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
601 CCAAACGGC AGACGGAGTT TACAGTCGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

```

m952.pep
1  MMKFYVFL ACVVVLSYR LNAAPMENDN PVVYGKIKVQ SWKARRDFNI
51  VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKLDKEQM RASFEDMRRI
101 MPDLGF EANG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFTQH
201 PKRQTEFTVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952: 92.5% identity in 201 aa overlap

```

g952.pep          10      20      30      40
                  LSYRLNAAPMENDNPVYVGKIKLQSWKARRDFNIVKQDLD FSCG
m952              10      20      30      40      50      60
MMKFYVFLACVVVLSYRLNAAPMENDNPVYVGKIKVQSWKARRDFNIVKQDLD FSCG

g952.pep          50      60      70      80      90     100
                  AASVATLLNNFYGQKLT EEEVLEKLGKEQMRASFEDMRRIMPD LGF EAKGYALSFEQLAQ
m952              50      60      70      80      90     100
AASVATLLNNFYGQTLTEEVLKLDKEQMRASFEDMRRIMPD LGF EAKGYALSFEQLAQ

g952.pep          110     120     130     140     150     160
                  LKIPVIVYLKYRKDDHFSVLRGVDGNTVLLADPSFGHVMSRAQFLEAWQTRGNLAGKI
m952              110     120     130     140     150     160
LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVMSRAQFLDAWQTRGNLAGKI

g952.pep          170     180     190     200
                  LAVVPKKA E AISNKLFFTHHPKRQTEFAVGQVKWWRAYX
m952              170     180     190     200
LAVIPKKAETISNKLFFTOHPKRQTEFTVGQIRQARAE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

```

a952.seq
1  ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT

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1364

```

51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGGCGGGA TTTCATATTT
151 GTAAAGCAGG ATTTGGATTT TTCCTGCGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATTT CTCGGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTTCAATG AGCAGGGCGC AGTTTNGGA
501 TGCTTGGCAA ACCCGTGAGG GAAATTGGC AGGTAAGATT TTGGCGGTCG
551 TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1 MMKFYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDFSCG AASVATLLNN FYGQTLTEE VLKKLDKEQM RASFEDMRRJ
101 MPDLGFEEKG YALSFELAQ LKIPVIVYL YKDDHFSVL RIGDGNVTLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

a952/m952 97.7% identity in 218 aa overlap

```

a952.pep      10      20      30      40      50      60
MMKFYVFLACVVVLSYRLNAAPMFNDNPVVYGKIKVQSWKERRDFNIVKQDLDFSCG
|||||
m952          10      20      30      40      50      60
MMKFYVFLACVVVLSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLDFSCG
|||||

a952.pep      70      80      90     100     110     120
AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPDLGFEEKGYALSFEQLAQ
|||||
m952          70      80      90     100     110     120
AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPDLGFEEKGYALSFEQLAQ
|||||

a952.pep     130     140     150     160     170     180
LKIPVIVYLKYRKDDHFSVLRIGDNTVLLADPSLGHVSM SRAQFXDAWQ TREGNLAGKI
|||||
m952         130     140     150     160     170     180
LKIPVIVYLKYRKDDHFSVLRIGDNTVLLADPSLGHVSM SRAQFLDAWQ TREGNLAGKI
|||||

a952.pep     190     200     210     219
LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAE
|||:|||||
m952         190     200     210
LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1 ATGAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51 CTCCGCCACC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCGCTCG AGTTGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCCGTC GCCAACCTGC AAAGCGGTTC GCAACCCTTC ACCGGCCACC
251 TGAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTTCACCA AATTCAACTT CAACGGCAAA AAAGTTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACCGCCCC CGTCAAACTC AAAGCCGAAA
401 AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGCGCGGCG
451 GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGCGGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAACAATA A

```


This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

g953.pep
 1 MKKIIFAALA AAAVGTASAT YKVDEYHANV RFAIDHFNTS TNVGGFYGLT
 51 GSVVEFDQAK DKGIDITIPV ANLQSGSQPF TGHLSADIF DAAQYDPIR
 101 VSTKFNFNKG KLVSV DGNLT MRGKTAPVKL KAEKFNCYQS PMAETEVC GG
 151 DFSTTIDRTK WGV DYL V NAG MTKNVRIDIQ IEAAKQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

m953.seq
 1 ATGAAAAA AA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC
 51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCG
 101 CCATCGACCA TTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
 151 ACCGGTTCCG TCGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
 201 CACCATCCCC ATTGCCAAC TGCAAAGCGG TTCGCAACAC TTACCGACC
 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
 301 TTTGTTTCCA CCAAATTCAA CTTCAACGGC AAAAACTGG TTTCCGTTGA
 351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAA CTCAAAGCCG
 401 AAAAATTCAA CTGCTACCAA AGCCCGATGG AGAAAACCGA AGTTTGTGGC
 451 GGC GACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
 501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
 551 CAGCCAAACA ATAA

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

m953.pep
 1 MKKIIFAALA AAAISTASAA TYKVDEYHAN RFAIDHFNT STNVGGFYGL
 51 TGSVEFDQAK RDGKIDITIP IANLQSGSQH FTDHLKSADI FDAAQYPIR
 101 FVSTKFNFNKG KLVSV DGNLT TMHGKTAPVK LKAEKFNCYQ SPMEKTEVC GG
 151 GDFSTTIDRT KWM DYL V NVV GMTKSVRIDI QIEAAKQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

m953/g953 93.0% identity in 187 aa overlap

	10	20	30	40	50	60
m953.pep	MKKIIFAALAAAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
g953	MKKIIFAALAAAAVGTASA-TYKVDEYHANVRFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	
m953.pep	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPIRFDVSTKFNFNKKLVSV DGNL					
g953	RDGKIDITIPVANLQSGSQPFTHGLKSADIFDAAQYPIRFDVSTKFNFNKKLVSV DGNL					
	60	70	80	90	100	110
m953.pep	TMHGKTAPVKLKAEFNCYQSPMEKTEVC GGDFSTTIDRTKWM DYL V NVV GMTKSVRIDI					
g953	TMRGKTAPVKLKAEFNCYQSPMAETEVC GGDFSTTIDRTKWM DYL V NAGMTKNVRIDI					
	120	130	140	150	160	170
m953.pep	QIEAAKQX					
g953	QIEAAKQX					
	180					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

a953.seq
 1 ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC
 51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCT
 101 CTATCGACCA TTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
 151 ACCGGTTCCG TTGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
 201 CACCATCCCC GTTGCCAACC TGCAAAGCGG TTCGCAACAC TTACCGACC
 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
 301 TTTGTTTCCA CCAAATTCAA CTTCAACGGC AAAAACTGG TTTCCGTTGA

1366

```

351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGGCGC
451 GCGGACTTCA GCACCAACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
1  MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHENT STNVGGFYGI
51  TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNPNK KKLVSVDGNL TMHGKTAPVK LKAKEFNICY SPMLKTEVCG
151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

a953/m953 97.3% identity in 187 aa overlap

```

a953.pep      10      20      30      40      50      60
MKKIIIAALAAAIGTASAATYKVDEYHANARFSIDHENTSTNVGGFYGI TGSVEFDQAK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953          10      20      30      40      50      60
MKKIIFAALAAAIASTASAATYKVDEYHANARFAIDHENTSTNVGGFYGLTGSVEFDQAK

a953.pep      70      80      90      100     110     120
RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNKHLVSDGNL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953          70      80      90      100     110     120
RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNKHLVSDGNL

a953.pep      130     140     150     160     170     180
TMHGKTAPVKLKAKEFNICYSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953          130     140     150     160     170     180
TMHGKTAPVKLKAKEFNICYSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI

a953.pep      QIEAAKQX
|||||
m953          QIEAAKQX

```

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
1  ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
51  GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
101 AATATCAATT TGCAGATGAG AAACAGGCTT TTTATTTTGA ACGCGCCGCC
151 CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251 TTAICTAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301 TACCGCGTCT GCAACACAGC TCGCGCAAGT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTTAGAT AAGGAAAGTT
401 ATCAAAATTA CCGAAAATCA ATGCAAGAAT GCCGTAAAC AATAACGGAA
451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
1  MKKFYFVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KQAFYFERAA
51  RFRVLQQGLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTHGDDDP
101 YRVCKQAAQD AEILMKSMVT SGGGGTTDLQ KESYQNYRKS MQECLKTITE
151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

```
g957.seq (partial)
  1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
 51 TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CCGGGAAAAA TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGG ATTTGATGCG GCGGGGCGCG GGAATAATCG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGGCG ATTATGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCCG GGGGatgaaG gcgaacaqtc ttgtggtcgg
801 ctatgatgcg gacggtCtgc CqcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaaacc ccaaagtgtc gaatatattt tgaaaaacgg aaatcttttt
901 attgcccaat cttcgacggt aaccttgaag acggatggcg taacggcggg
951 tatgcaaaacc tatcatgcgc aacaaacgtt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

```
g957.pep (partial)
  1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNFV
 51 AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFVSU VYGGTAHGEN YETTGEYRVV WQPDGVSFDA AGRGKIGEDV
201 YEHLGICYOM AQVYLAKYRD VANDEQKQVD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVGIDA DGLPQKVYWS VDNKKPKQSV EYILKNGNLF
301 IAQSSTVTLK TDGVTADMQT YHAQQTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

```
m957.seq
  1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
 51 TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAACG GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CCGGGAAAAA TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGG ATTTGATGCG GCGGGGCGCG GGAATAATCG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAG
701 AGAGCAACCG AATTGCGTCT GACTCSCGCA ATTCTGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCCG AGGGATGAAG CGCAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTGACCGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GGCGGGCGGA
1001 TTGTCGCGCA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGAAAATT TGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

```
m957.pep
  1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVKPNPNFV
 51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFVSU VYGGTVHGEN YETTGEYRVV WQPDGVSFDA AGRGKIGEDV
201 YEHLGICYOM AQVYLAKYRD VANDEQKQVD FRKESNRIAS DSRNSVFYQN
```

1368

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251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS FDNGKKRSF EYYLKNLNF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFAFV	KLARLFRNA				
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKPNFAFVAKLARLFRNA					
	70	80	90	100	110	120
g957.pep	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLAIRLSRLKEKAKWFHVTEQEHGEEV					
m957	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLAIRLSRLKEKAKWFHVTEQEHGKEV					
	130	140	150	160	170	180
g957.pep	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTAHGENYETTGEYRVV					
m957	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV					
	190	200	210	220	230	240
g957.pep	WQPDGSVFDAAGRGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m957	WQPDGSVFDAAGRGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	250	260	270	280	290	300
g957.pep	DSRDYVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSVDNGKKPQSV EY LKNGNLF					
m957	DSRNSVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRSF EY LKNGNLF					
	310	320	330			
g957.pep	IAQSSVTTLKTDGVTADMOTYHAQQTLYLDG					
m957	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	340	350	360			
m957	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

```

a957.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCCTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAATCCGA ATGCTTTTGT GCGGAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCACTG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT CCACTCGCTG TCCGGCTCAG TCGTTTGAAA
301 GAAAAGGCCA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAATCG GGAAGATGT TTATGAGCAT
601 TGCCCTCGGT GTTATCAGAT GGCCACGGTA TATTGGCGA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCG . GAGAGTAACC
701 GGATTGCGTC GGAATCGGCG GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTCGACAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC

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951 CTATCATGCG CAACAGACGT GSTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGAT. TCCTTTTGA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCGCG
1101 CGGCAGGCGC GACCTTTC TC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

```

a957.pep
1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51 ARIFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL POKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

	10	20	30	40	50
a957.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE--NPNAFVAKLARLFRNA				
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA				
	10	20	30	40	50
	60	70	80	90	100
a957.pep	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLAALAVRLSRLKEKAKWFHVTEQEHGEEV				
m957	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLAALAVRLSRLKEKAKWFHVTEQEHGKEV				
	70	80	90	100	110
	120	130	140	150	160
a957.pep	WLDYYIGEGGLVAVLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV				
m957	WLDYHIGEGGLVAVLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV				
	130	140	150	160	170
	180	190	200	210	220
a957.pep	WQPDGSVFDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS				
m957	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS				
	190	200	210	220	230
	240	250	260	270	280
a957.pep	DSRDSVFYQNMRELMPRGMKANSLVVGYDADGLPOKVYWSFDNGKKRQSFEYYLKNGNLF				
m957	DSRNSVFYQNMRELMPRGMKANSLVVGYDADGLPOKVYWSFDNGKKRQSFEYYLKNGNLF				
	250	260	270	280	290
	300	310	320	330	340
a957.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDLEKEVSR				
m957	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRP				
	310	320	330	340	350
	360	370			
a957.pep	YAEAAARRSGGRRDLSHX				
m957	YAEAAARRSGGRRDLSHX				
	370				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

```

g958.seq
1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51 TTTCCGCACG CATTGCGCCG CCGATACCGT TCGCGCGGAA GAGCGGACG

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101 GCGGTGTGCG AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAAGCT
151 TCCGATTGTA CCTTCGGTTC GACCTGCCTG TTTTGCACTA ACGAAAGCGG
201 CAGCCCCGAG AGAACCAGAG CCGCCGTCCA AGGCACGGC GAAGCATCCG
251 TCCCCGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TCGCGCGCGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTCCGC CTCCAACAGG ACCGTACGCT GATTCTGGGC
451 GAAACCCCTGA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAAAGT
501 CCGTATGGA ACCGAACAAG GCGGACGGCG GCTGCAAGC GTCAGCCGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCAATTC
601 AACACCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAAG CCGCCTCTGT
651 CGAAGCCGAT CGGGGAAAG GCATAGGCGT TGCCAAACAC GCCCCTCTCG
701 TGTTCGGCGG CGTTCCTCTT TTCTATACGC CTGGGGCGGA CTTCCCGCTT
751 GACGGCAACC GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCGGGTTC
801 GGACGGCGTT TCCCTTTCCG TCCCTTATTA TTTCAACCTT GCCCCCAACT
851 TCGATGCCAC TTTCGCCCCC GGCATTATCG GCGAACGCGG CGGACGTTT
901 GACGGACAAA TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GGCGGGTGTC
1051 GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGGACT TTTACGGCGG
1101 CGAAGAAATC GCCGCAACG TCAACCTCAA CCGCCCGGTA TGGCTGGATT
1151 ATGGCGGCAG GCGCGCGGGA GGCAGCCTGA ATGCGCGCCT TTCGGTTAG
1201 AAATACCAGA CGCTGGCAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAACGCA GGCAGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGCGCGCAA
1351 GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAAATGGG ATTTACGCAA
1401 CAGCTGGGGC TACGTCGGCC CCAAACCTCG GCTGCACGCC ACTTATTACA
1451 GCCTCGACAG TTTCGGCGGC AAAGCATCCC GCAGCGTCGG GCGGCTTTG
1501 CCGTTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCGCGCGCTG TTCTACAAC
1601 ATATTCTTGC CAAATCTCAA AACGACCTGC CCAATTTCGA TTCTCGGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACCGCGCCA ACAGCCTTTC CACCGCGGTG CAGAGCGGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCGGG TATCGGTCAG
1801 AAATTCTATT TCAAGGATGA TGCGGTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCCT ACTGGGTGGC ATTCGCTCCG GGCGGCATAG
1901 CGGGCGGTTT CACCCTCGAC AGCAGCATCC ACTACAACCA AACGACAAA
1951 CGCGCCGAAC ATTACGCCGT CGGCGCAGGC TACCGCCCGC CCCCCGAAA
2001 AGTGTGTAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGGCGGACGG TTCCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTCTGCC GCTACAAC
2151 CGGTTTTGAA GCCAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGGCG TGTACGCCCA ACGCTACGTT
2251 ACCGGCGAAA ACACCTACAA AAACGCCGTC TTTTTCCTAC TTCAGTTGAA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCCGC AGGCAGGATG GATGTCGCCG
2351 TTCCCGGCTA CATCCCGGCC CACTCTCTTT CCGCCGGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

g958.pep

```

1 LARLFLSKPL VLALGFCFGT HCAADTVAAE EADGRVAEGG AQGASEAQQA
51 SDLTLGSTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRMEGQS
101 KVKVRAEGSV IIERDGAVALN TDWADYDQSG DTVTVGDRFA LQQDGTILRG
151 ETLTYNLDDQ TGEAHNVME TEQGGRRLLQ VSRTAEMLGE GRYKLTETQF
201 NTCAGDAGW YVKAASVEAD RKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLRPD YSGQDILTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DENQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSLNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSHDGRQ
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TYSLDSFGG KASRSVGRVL
501 PVVNIDGGTT FERNTLFGG GVVQTIEPRL FYNYPKASQ NDLPNFDSSSE
551 SSFGYQGLFR ENLYYGNDRI NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSGVKNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLDAGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRVY
751 TGENTYKNAV FFSLLQLKDL SVGRNPAGRM DVAVPGYIPA HSLSAGRNRK
801 P*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

m958.seq

```

1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTCTTG
51 CTTTCGGCAGC CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGTCCGA ACCCATACAG

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAACCG
351 GACGACCCTC AATACCGATT GGGCGGATTA CGACCACTCG GCGGACACCG
401 TTACCGCAGG CGACCCGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCGG
451 GGCAGAAACC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGCATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGTGCAAGCC GATCGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
701 TCGTGTTCGG CGGCGTTCCT ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTCGGACGGC GTTCCCTTTT CCGTTCCTTA TTATTTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTCCGG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCGG GATTATGCGC GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTC A CCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCGT GTATGGCTGG
1151 ATTATGGCGG CAGGGCGGCG GCGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAAACCGTA
1251 TGCCCTCATG CCGCGCCTTT CCGTCGAGTG GCGTAAAAAC ACCGGCAGGG
1301 CGCAAAATCG CGTGTCCGCA CAATTTACCC GATTACGCCA CGACAGCCCG
1351 CAAGACGGCA GCCGCCGTGT CGTCTATCCG GACATCAAAAT GGGATTTACG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAACT CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCGCAGT
1501 CTGCCCATTG TCAACATCGA CAGCGGCGCA ACTTTTGAGC GGAATACGCG
1551 GATGTTCCGG GGAGAAGTCC TGCAAAACCT CGAGCCGCGC CTGTCTTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTTCGTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAGGCC
1751 GTATTTTGGG CCGCGCGACG GGGGAAGAGC GTTTCGCGCG CGGCATCGGT
1801 CAGAAATTCT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTTGCC TCCGGCAGCA
1901 TCGGCAGCCG CTTCACTCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAACTACGC CGTCGGTGC ACGTACCGT CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTG GCAGAAACCC CGCAGACAGG ATGGATGTG
2351 CCGTTCGCGG CTATATCACC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CGACCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```

m958.pep
1 LARLFSKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51 PLSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQCDGTLIR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRRLLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFVFGGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VLSVPYYFN LAPNLDAFPA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QFTRFSHDSR
451 QDGSRLLVYP DIKWDFNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSR
501 LPIVNIIDSGA TFERNTRMFG GEVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSPGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGSVGKKP RNRSDWVAFS SGISGRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVRYNYGF EAKKPIEVLA GAELYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

1372

m958/g958 89.3% identity in 802 aa overlap

```
m958.pep      10      20      30      40      50      60
LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC
|||||
g958          10      20      30      40      50
LARLFSLKPLVLALGFCFGTHCAA-DTVAAEEADGRVAEGGAQGASEAQASDLTLGSTC

m958.pep      70      80      90     100     110     120
LFCSNESGSPERTEAAVQSGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL
|||||
g958          60      70      80      90     100     110
LFCSNESGSPERTEAAVQSGSGEASVPEDYTRIVADRMEGQSKVKVRAEGSVIIERDGAVL

m958.pep     130     140     150     160     170     180
NTDWADYDQSGDVTAGDRFALQQDGTLLIRGETLTYNLEQOTGEAHNVNRMIEQGGRRLO
|||||
g958          120    130    140    150    160    170
NTDWADYDQSGDVTVGDRFALQQDGTLLAGELTYNLEQOTGEAHNVNRMETEQGGRRLO

m958.pep     190     200     210     220     230     240
SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKIGIVAKHAAFFVGGVP
|||||
g958          180    190    200    210    220    230
SVSRTAEMLGEGRYKLTETQFNTCSAGDAGWYVKAASVEADRGKIGIVAKHAAFFVGGVP

m958.pep     250     260     270     280     290     300
IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLAFLNLDATFAPSVIGERGAV
|||||
g958          240    250    260    270    280    290
IFYTPWADFPLDGNRKSGLLVPSVSAGSDGVSLSVPYYFNLAFLNLDATFAPGIIGERGAT

m958.pep     310     320     330     340     350     360
FDGQVRYLRPDYAGQSDLTWLPDHHKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG
|||||
g958          300    310    320    330    340    350
FDGQVRYLRPDYAGQSDLTWLPDHHKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG

m958.pep     370     380     390     400     410     420
YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM
|||||
g958          360    370    380    390    400    410
YYRDFYGGEEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVQKYQTLANQSGYKDEPYAIM

m958.pep     430     440     450     460     470     480
PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVPYDIKWDFSNWGYVRPKLGLH
|||||
g958          420    430    440    450    460    470
PRLSADWHKNAGRAQIGVSAQFTRFSHDSRQDGSRLVVPYDIKWDFSNWGYVRPKLGLH

m958.pep     490     500     510     520     530     540
ATYYSLNRFSGQEARRVSRILPIVNIDSGATFERNTRMFGGEVLQTLERLFFNYIPAKS
|||||
g958          480    490    500    510    520    530
ATYYSLDSFGGKASRSVGRVLPVVNIDGGTTFERNTRMFGGGEVLQTLERLFFNYIPAKS

m958.pep     550     560     570     580     590     600
QNDLPNFDSSSESSFGYGQLFRENLYYGNDRIANTANSLAAVQSRILDGATGEERFRAGIG
|||||
g958          540    550    560    570    580    590
QNDLPNFDSSSESSFGYGQLFRENLYYGNDRIANANSLSTAVQSRILDGATGEERFRAGIG

m958.pep     610     620     630     640     650     660
QKIFYKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA
|||||
g958          600    610    620    630    640    650
QKIFYKDDAVMLDGSVGKPRNRSDWVAFASGGIGGRFTLDSSIHYNQNDKRAEHYAVGA

m958.pep     670     680     690     700     710     720
SYRPAQKVLNARYKYGRNEKIYKSDGSYFYDKLSQLDLAQWPLTRNL SAVVRYNYGF
|||||
g958          660    670    680    690     700     710
GYRPAQKVLNARYKYGRNEKIYKSDGSYFYDKLSQLDLAQWPLTRNL SAVVRYNYGF
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1373

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              730      740      750      760      770      780
m958.pep      EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQKDLSSVGRNPADR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g958           EAKKPIEMLAGA EYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQKDLSSVGRNPAGR
              720      730      740      750      760      770

              790      800
m958.pep      MDVAVPGYITAHSLSAGRNRKP
              |||||:|||||:|||||:|||||:
g958           MDVAVPGYIPAHSLSAGRNRKPX
              780      790      800

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

```

a958.seq
1   TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTGCGCACG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACATATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCGCA ACCCATACAG
151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GCGGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCTGTC AACGCAATCG
351 GACGACCTTC AATGCCGATT GGGCGGATTA CGACCAGTCG GGCACACCCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTTCGG
451 GCGCAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGATATG GAAACCGAAC ACGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAA AAGCATAGG CGTTGCCAAA CACGCCGCTC
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCTGCTC GTTCCCTCAC TGTCCGCGCG
801 TTGCGGACGGC GTTCCCTTTT CCGTTCCTTA TTATTTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTCCGG CCCGGCGTGA TCGGCGAACG CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCGG GATTATGCCG CCGAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CCGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCACCCG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTC AACCAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGGCGGCG GCGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAAACGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAAC ACCGGCAGGG
1301 CGCAAAATCG CGTGTCCGCC CAATTTACCC GCTTCAGCCA CGACAGCCGC
1351 CAAGACGGCA GCCGCCTCGT CGTCTATCCC GACATCAAAT GGGATTTCAG
1401 CAACAGCTGG GGTACGTCC GTCCCAAAC TCGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGCG
1551 GATGTTTCGG GCGGAGTCC TGCAAACCC TCGAGCCGCG CTGTCTTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCTGCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTTT CGTGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCGCCGCC GTGCAAGGCC
1751 GTATTTTGA CGGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGG
1801 CAGAAATTCT ACTTCAAAA CGACGCAGTC ATGCTTGACG GCAGTGTCCG
1851 CAAAAAACCG CGCAGCCGTT CCGACTGGGT GGCATTGCGC TCCAGCGGCA
1901 TCGGCAGCCG CTTCATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAATACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTCTG
2351 CCGTCCCGCG CTATATCCCC GCCACTCTC TTTCCGCGCG ACGCAACAAA
2401 CGGCCCTGA

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This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

```

a958.pep
1   LARLFSLKPL VLALGFCFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PTLSLGSLG LFCNSGSGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQODGTLIR
151 GETLTYNLEQ QTGEAHNVPM ETEHGGRRLO SVSRTAEMLG EGHYKLTETO
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFVFGGVP IFYTPWADFP

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1374

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251 LDGNRKSGLL VPSLSAGSDG VLSVPPYYFN LAPNLDTFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLOAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAOIGVSA QTFRSHDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFFAGIG
601 QKFYFKNDV MLDGSVGKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KPAENYAVGA SYRPAQGVKL NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GAEEKSSCGC WGAQVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 96.1% identity in 377 aa overlap

a958.pep	10	20	30	40	50	60
	LARLFSLKPLVLALGFCGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC					
m958	10	20	30	40	50	60
	LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSE					
a958.pep	70	80	90	100	110	120
	LFCNSGSGSPERTEAAVQSGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTL					
m958	70	80	90	100	110	120
	LFCNSGSGSPERTEAAVQSGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTL					
a958.pep	130	140	150	160	170	180
	NADWADYDQSGDVTAGDRFALQDGTLRGETLTYNLEQQTGEAHNVRMETEHGGRRLQ					
m958	130	140	150	160	170	180
	NTDWADYDQSGDVTAGDRFALQDGTLRGETLTYNLEQQTGEAHNVMEIEQGGRRRLQ					
a958.pep	190	200	210	220	230	240
	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKIGIVAKHAAFFVGGVP					
m958	190	200	210	220	230	240
	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKIGIVAKHAAFFVGGVP					
a958.pep	250	260	270	280	290	300
	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVLSVPPYYFNLAPNLDTFA PGVIGERGAV					
m958	250	260	270	280	290	300
	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVLSVPPYYFNLAPNLDTFA PPSVIGERGAV					
a958.pep	310	320	330	340	350	360
	FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLOAGVDFNQVSDSG					
m958	310	320	330	340	350	360
	FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLOAGVDFNQVSDSG					
a958.pep	370	380	390	400	410	420
	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
m958	370	380	390	400	410	420
	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
a958.pep	430	440	450	460	470	480
	PRLSADWRKNTGRAOIGVSAQFTFRSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
m958	430	440	450	460	470	480
	PRLSEWRKNTGRAOIGVSAQFTFRSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
a958.pep	490	500	510	520	530	540
	ATYYSLNRFSGQEARRVSRTLPIVNIDSGMTFERNTRMFGGVLQTLLEPRLFYNYIPAKS					
m958						
	ATYYSLNRFSGQEARRVSRTLPIVNIDSGATFERNTRMFGGVLQTLLEPRLFYNYIPAKS					

1375

	490	500	510	520	530	540
a958.pep	550	560	570	580	590	600
	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRI	TANSL	SAVQSRILDGATGEERF	FRAGIG		
m958	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRI	TANSL	SAVQSRILDGATGEERF	FRAGIG		
a958.pep	610	620	630	640	650	660
	QKIFYKNDVAVMLDGSVGGKPRSRSDWVAFAS	SGISRFILDSSIHYNQNDKRAENYAVGA				
m958	QKIFYKNDVAVMLDGSVGGKPRSRSDWVAFAS	SGISRFILDSSIHYNQNDKRAENYAVGA				
a958.pep	670	680	690	700	710	720
	SYRPAQGGKVLNARYKYGRNEKIYLS	DGSGYFYDKLSQDL	LSAQWPLTENLSAVVRYNYGF			
m958	SYRPAQGGKVLNARYKYGRNEKIYLS	DGSGYFYDKLSQDL	LSAQWPLTENLSAVVRYNYGF			
a958.pep	730	740	750	760	770	780
	EAKKPIEVLAGAEYKSSCGCWGAGVYAQR	YVTGENTYKNAVFFSLQKDLSSVGRNPALF				
m958	EAKKPIEVLAGAEYKSSCGCWGAGVYAQR	YVTGENTYKNAVFFSLQKDLSSVGRNPALF				
a958.pep	790	800				
	MDVAVPGYIPAHSLSAGRNRKRF					
m958	MDVAVPGYIPAHSLSAGRNRKRF					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq
 1 ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
 51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
 101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
 151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCAG
 201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2936: ORF 959.ng>:

g959.pep
 1 MNIKHLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDHIISF
 51 AQAEKAARAR VGGKITDIDL EHDGRPHYD VEIVKNGQEV KVVVDARTGR
 101 VISSRRDD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq
 1 ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
 51 CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
 101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
 151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2938: ORF 959>:

m959.pep
 1 MNIKHLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
 51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEV KVVVDARTGR
 101 VISSRRDD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

1376

m959/g959 95.4% identity in 108 aa overlap

```

      10      20      30      40      50      60
m959.pep MNIKHLLTSAATALISAPALAHHDGHDGDDHGHAHHQHNKQDKIISRAQAEEKAALAF
g959      MNIKHLLTAAATALLGISAPALAHHDGHDGDDHGHAHHQHNKQDKIISRAQAEEKAALAF
      10      20      30      40      50      60

      70      80      90     100     109
m959.pep VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX
g959      VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX
      70      80      90     100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

```

a959.seq
1  ATGAAGTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51 CATTTCGGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT STCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCG GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCCTTG TCGATGCCCG TACCGCCGCG
301 GTGATTCCTC CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

```

a959.pep
1  MNFKRLLLTA AATALMGISA PALAHHDGHS DDDHGHAHQ HSKQDKIISF
51  AQAEEKAALR VGGKITDIDL EHDNGRPHYD VEIVKNGQY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

```

      10      20      30      40      50      60
a959.pep MNFKRLLLTAATALMGISAPALAHHDGHDGDDHGHAHHQHNKQDKIISRAQAEEKAALAF
m959      MNIKHLLTSAATALISAPALAHHDGHDGDDHGHAHHQHNKQDKIISRAQAEEKAALAF
      10      20      30      40      50      60

      70      80      90     100     109
a959.pep VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX
m959      VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX
      70      80      90     100

```

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

```

m960.seq
1  ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51  TAAGCCCCCC TTGTTTGAAG CTCGCGGGCT CCTGCCGAGC TTCACCGACC
101 CCGTTGTGCC CAAGCTCTCT GCTCCGGGCG GCTACATTGT CGACATCCCG
151 AAAGGCAATC TGAACACCGA AATCGAAAAG CTGGCCAAAC AGCCCGAGTA
201 TGCCATATCTG AAACAGCTCC AAGTAGCGAA AAACGTCCT TGGAAACGAG
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGC CTTAACCCAG
301 GCCCGTGCGC CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGT
351 GGGAGTCGGA GCCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG
401 ATGCCGCGCTT TGCTCACTC GCTTCTCAGG CTTCCGTATC GCTCATCAAT
451 AATAAAGGCG ATGTCGGCAA AACCTGAAG GAAGTGGGCA GAAGCCGCAT
501 GGTAAAAAAT CTGTTGTAG CCGCGGCAAC GGCAGGCGTA TCCAACAAAT

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1377

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551 TCGGTGCCTC TTCCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAAACAAC
601 CTCAACGTTA ACCTGGCCAA TCGGGGCAJ. GCCGCGCTGA TCAACACCCG
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAT ATCCTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCA CAAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG GCGAATAAGG GCAAATGTCA GGACGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTGGG GAGGCTTTGG TTAATAATAC CGATTTTAGC
901 GATATGACCC CGGAACAAAT AGATCTGGAA GTTAAGAAA TTACCGCCTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGTGTC ACAACCCGCA CAAAACGCGG TAGAAAATAA TGCGGTTAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTCTGA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTAT
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGAAAAA CAGCTGGCTC AAATTTTACA
1401 AAAGACAAAC CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAAAA ACCGGTGATA GGTTTTATTT AGATGGCCAA
1501 CATAAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAC TTAAGTTTGT
1551 TCTAAATATG GATGGTTCGC TTAACCAAAT GAAACTGGG GCAGCAAAAG
1601 GTCGTAAATT AAACTTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

m960.pep

```

1 MQVNIQIPCM LYRRGSVKPP LFEAPRLPS FTDVVPKLS APGGYIVDIP
51 KGNLKTIEIK LAKOPEYAYL KQLQVAKNVN WNQVQLAYDK WDKQOGLTR
101 AGAAIIALAV TVVTAGAGVG AALGLNGAAA AAADAFAFSL ASQASVSLIN
151 NKGDVGTLLK ELGRSRTVKV LVVAAATAGV SNKLGAASSL TWSETPWVNN
201 LNVHLNAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEAAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKQDGA IGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTTLFDETL
401 DWNDAKAVID IVVGTELNRA NKGEAAQKVK EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPFGK QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGDRLFYLDGQ
501 HKNHLEVFDEK NGNFKFVLNM DGSLNQMKTG AAKGRKLNK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

m961.seq

```

1 ATGAGCATGA AACACTTTCC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51 CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCCTCAAT
301 GAAAAACAA ACACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTGCTGTA AGAGACTAAG ACAATATCG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAAAACA
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAAGCCG
701 AAGCTGCCGC TGGCACAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGTACGA ACAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCCTGTTCC AACCTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
951 CGGCGGCTAC AAATCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GTTCTTCCG CAGCCTACCA TGTCGCGCTC AATTACGAGT GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

m961.pep

```

1 MSMKHFPKLV LTTAILATFC SGALAAATSDQ DVKKAATVAI VAAVYNNQGEI

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1378

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51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKH VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNNLGE
151 NITTFAEETK THIVKIDEKL EAVADTVDKH AEAFNDIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV D AKVKAETAA GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATHKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPYNVGR FNVTAAVGGY KESAVAIGT GFRFTENFAA KAGVAVGTSS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet
a961.pep not found yet

g972.seq not found yet
g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCArTTCCA AGACTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATC GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GArGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTCAGC GTTGCAAGTC CGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAAT CTCGTTTTGT TCGTGTATAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAA AGCAAATGGG TAAGGTTCTG GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCCGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTATC CATGAACAGC CGGATATTGA
1101 TTTGAAATG GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGAALK TXSKSSERMS EVEYFSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWISFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFQXQNTV LVLEKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KKNRFRVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAPPICRKFK NMPVPERFDQ RKKKLNLTFE
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVYHQNVDDY YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
151 GTTGATTGGA TTTCATTAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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1379

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251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTCG GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC CTTGCAAGTC CGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTGGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAAATATG TCTGGAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATG GAACCTGATG AATTCGCGGT TATTGCTTTT AAAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948: ORF 972.a>:

a972.pep

```

1  LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWISFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDVDVYGE VHFGGQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE DSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFPICRKF NMPVPERFDQ RKKTLNLTFE
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPPDYDVE
401 KERKYQEYLS KVVYQNVVDY.

```

m972/a972 99.3% identity in 422 aa overlap

m972.pep	10	20	30	40	50	60
a972	10	20	30	40	50	60
m972.pep	70	80	90	100	110	120
a972	70	80	90	100	110	120
m972.pep	130	140	150	160	170	180
a972	130	140	150	160	170	180
m972.pep	190	200	210	220	230	240
a972	190	200	210	220	230	240
m972.pep	250	260	270	280	290	300
a972	250	260	270	280	290	300

1380

```

          310      320      330      340      350      360
m972.pep  HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPGKLEPEKYALEMLRDGLKHGFI
          |||||
a972      HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPGKLEPEKYALEMLRDGLKHGFI
          310      320      330      340      350      360

          370      380      390      400      410      420
m972.pep  HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVVDYD
          |||||
a972      HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVVDYD
          370      380      390      400      410      420

m972.pep  YFX
          |||
a972      YFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

```

g973.seq
1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTGACAGGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CCTGCCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCCGG
501 TTTGGTCACC TTTCAAGACA TCATCGAGCa aatcgtcggt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
601 GAACGCTTGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTGGTACG GAatacggca gcgaagaagc cgacaccatc ggcggctTGG
701 TCATTcAGGA ATTGGGACAC CTGCCCCGTG CCGGCGAAAA AGTCCTTAtc
751 ggcgGTTTGC agttcaccgt CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcccgttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

```

g973.pep
1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQPHLKSVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFFGT EYGSEEDTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

```

m973.seq
1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCG
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTCCGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTGACAGGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TCGTGCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTCATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCcgaca ATATCCATGC CGTTTCTTcm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

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1381

651 CTTCCGGCAGC GAATACAGCA kCGAAGAAGC CGACACCATT GGCGGCCTGG
 701 TCATTCAAGA GTTGGGACAT CTGCCCCTGC GCGGCGAAAA AGTCCTTATC
 751 GGCGGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973.pep
 1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLLE
 51 KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGLV FEDIIEQIVG EIEDEFDEDD SADNIHAVSS
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVL
 251 GGLQFTVARA DNRRLHTLMA TRVK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

m973.pep	10	20	30	40	50	60
	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFAELEV					
	10	20	30	40	50	60
m973.pep	70	80	90	100	110	120
	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
g973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973.pep	130	140	150	160	170	180
	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
m973.pep	190	200	210	220	230	240
	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFPGTEYGSEADTIGGLVIQELGH					
	190	200	210	220	230	240
m973.pep	250	260	270			
	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973.seq
 1 ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
 51 ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGCGACGCGA TGATTACGGC
 201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG
 251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCGTCAT CGGTGAAGAC
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAAAATATAT
 351 GTTCAACCCC GAGCAGTTCC ACCTCAAATC GATATTGCGC CCTGCCGTCT
 401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAGA GTTCCGCGAA
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG
 551 ATGAGTTTGA CGAATACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCC

1382

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601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCACG GAATACAGCA GCGAAGAAGC CGACACCATC GGCGGCCTGG
701 TCATTTCAGGA ATTTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
751 GGCGGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLLRLRLE
51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFGT EYSSEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRHLTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLLRLRLEKVLDFSDLEV					
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLLRLRLEKVLDFSDLEV					
	10	20	30	40	50	60
m973.pep	RDAMITSRMNVLKENDSIE RITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
a973	RDAMITSRMNVLKENDSIE RITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973.pep	RDAMITSRMNVLKENDSIE RITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
a973	RDAMITSRMNVLKENDSIE RITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVID EYGGTSGLVT FEDIIEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVID EYGGTSGLVT FEDIIEQIVG					
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVID EYGGTSGLVT FEDIIEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVID EYGGTSGLVT FEDIIEQIVG					
	130	140	150	160	170	180
m973.pep	EIEDEFDEDD SADNIHAVSSERWRIHAATEIEDINTFFGTEYSKEEADTIGGLVIQELGH					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFGT EYSSEADTIGGLVIQELGH					
	190	200	210	220	230	240
m973.pep	EIEDEFDEDD SADNIHAVSSERWRIHAATEIEDINTFFGTEYSKEEADTIGGLVIQELGH					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFGT EYSSEADTIGGLVIQELGH					
	190	200	210	220	230	240
m973.pep	LPVRGEKVLIGGLQFTVARADNRRHLTLMATRVKX					
a973	LPVRGEKVLIGGLQFTVARADNRRHLTLMATRVKX					
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRHLTLMATRVKX					
a973	LPVRGEKVLIGGLQFTVARADNRRHLTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
51 TGCCTGCCGC GGTACGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAACTC
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAATAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCGCGCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGTAACCA TTACCGACA CGCAACACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCACCAGG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTCTTCCGA AGATTTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
451 CACACGGCGC ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCCCTGAT TATCAAGAA CTGGAACG
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
601 AAAACAACC CGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAATATTT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

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1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

```

g981.pep
1   MKKWIAAALA CSALALSACG GQGKDAAPAA ANPGKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK KMNKVGVTG
151 HTGDFSUSKL LGNDNPFIAR FENVPLIIKE LENGGLDSVV SDSAVIANVY
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GGQAAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

```

m981.seq
1   ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAAGGCA AAGATACCGC CGCGCCTGCC GCCAACCCCG
101 ACAAGTGTGA CCGCGTGGCT TCCAACGCGC AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAATAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCGCTTAA AACAAACGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAAACGGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATATCG CAATTATGTG
601 AAAAAACAATC CGGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATTACG CCAATATTTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A

```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

```

m981.pep
1   MKKWIAAALA CSALALSACG GQGKDTAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK NMNKGVTG
151 YTGDFSUSKL LGNDNPFIAR FENVPLIIKE LENGGLDSVV SDSAVIANVY
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGQAAK*

```

m981/g981 98.1% identity in 266 aa overlap

	10	20	30	40	50	60
981.pep	MKKWIAAALACSALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
g981	MKKWIAAALACSALALSACGGQGKDAAPAAANPGKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMSGVTITDDRKQSMDFSDPYFE					
g981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
981.pep	ITQVVLVPKGKKVSSSEDLKMNKVGVTGYTGDFSUSKLLGNDNPFIARFENVPLIIKE					
g981	ITQVVLVPKGKKVSSSEDLKMNKVGVTGHTGDFSUSKLLGNDNPFIARFENVPLIIKE					
	130	140	150	160	170	180
981.pep	LENGGLDSVSDSAVIANVVKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
g981	LENGGLDSVSDSAVIANVVKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTACGGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCC
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATTCAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTTTG AACACGGCG ATGCGGACGT TGTGATGTCG
301 GGCCTAACCA TTACCGACGA CCGCAAACAG TCTATGGAAT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAATAT
401 CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAAACGGC
451 TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAAACAATC CGACCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAAATATTT TGCAAAGAA GACGGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1  MKKWIAAALA CSALALSACG GQGKDAAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPGK KISSSEDLK MNKVGCVVTG
151 YTGDFSVSKL LGNDNPKIAR FENVPLIIE LENGGLDSV SDSAVIANV
201 KNNPTKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALACSALALSACGGQGKDAAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALACSALALSACGGQGKDAAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m981.pep	ITQVVLVPGKGVSSSEDLKNMNKVGCVVTGYTGDFSVSKLLGNDNPKIARFENVPLIIE					
a981	ITQVVLVPGKGVSSSEDLKNMNKVGCVVTGYTGDFSVSKLLGNDNPKIARFENVPLIIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m981.pep	LENGGLDSVVSASAVIANVKNKPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVVSASAVIANVKNKPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
	250	260				
m981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
a981	KKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1   atcgcatcgc aaaaccttcg attcgacaat cgattccctcc aaaaaatggt
51  caacggcgTg aatattttgc cggccgcCga ttgggtagcC ttgGGcgCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAAG CGCGTCCAAA ACCAAcgaCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAaggcA TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCGGCTtt ggttgAAGAg cTGAAAAACA
401 TCGCCAAACC TTGCGATACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTG TTGCTGTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCCGTGTG GGAACAAGTG GCGAAAGCCA GCCGCCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCGGTCAA AGCccccggc tTCGGcGACC
851 GCCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTtccGAAG Aagtccggcct GTCTTTGGAA AAAGcgactT TGgaagcATT
951 Gggtcaaacc aaACGcatCG AAATCGGtga agaaaacact ACCGTCATcG
1001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTTCG CGAAATCCCG
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGGCAG GAGCGGTGGC AGTGATCAAA GTCGCGCGCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCCGGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGCGCT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TCGCGGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAactacgG TTACAACGCa ggcctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCTGCG CAAAGTAACC
1501 CGTTCGCGCG TGCAACACGC CGCGTCTAtC GCCGGTCTGA TGCTGACGAC
1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1601 TGGGGGGAAT GGGCGGTATG GCGGCATGA TGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1   IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSI
101 AEGMKYVTAG MNPTDLKRG DKAAVALVEE LKNIAKPCDT SKEIAQVGS
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLLPVLEQV AKASRPLLI
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGVV
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENLH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKNGYGYNA GSGEYGMIG MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGM GMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1   ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGCGCGGCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAAG TCGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGGACAA

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1386

651	TCCGTTTGTA	TTGTTGTTTCG	ACAAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCGTGTTTT	GGAAACAAGTG	GCAAAAGCCA	GCCGTCGCGT	GTGTGATTATC
751	GCTGAAGACG	TAGAAGGCCA	AGCCTTGGCG	ACTTTGGTGC	TGAACAACATC
801	CCGAGGCATC	CTGAAAAACCG	TTCGGCTCAA	AGCCCTGCGC	TTCCGGCGAC
851	GCCGCAAGC	GATGTTGCAA	GACATCGCCA	TCCTGACCGG	CGGCGTGGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCTTTGGAA	AAAGCGACTT	TGGACGACCTT
951	GGGTCAAGCC	AAACGCATCT	AAATCGGTAA	AGAAAACACC	ACCATCATCTG
1001	ACGGCTTTTG	CAGCGCAGCC	CAAAATCGAG	CGCGTGTTGC	CGAAATCCGC
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GACAAAGAAA	AACTGCAAGA
1101	GCGCGTGGCT	AAATTGGCAG	GCGGGCTGGC	AGTCAATCAA	GTTCGGTCCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAG	ACCGCGTGG	AGACGCGCTG
1201	CACGCTACCC	CGCGACCCGT	TGAAGAAGGC	GTGGTTGCAG	CGCGCGCGCT
1251	AGCCCTGTTG	CGTGCCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGCAGGCGTA	CAAATCGTCT	TGGCGCGCCT	TGAGTCTCCG
1351	CTGCGCCAAA	TCGTTGCCAA	CGCAGGCGGC	GACCCGACGC	TGGTTGTGAA
1401	CAAAGTATTG	GAAAGCAAAG	GCAACTACGG	TTACAACGCT	GGCAGCGCGC
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAAGTAACC
1501	CGTTCTCGCG	TGCAACACGC	CGCATCTATC	GCCGCGCTTG	TGCTGACCAC
1551	TGATTGTCATG	ATCGCTGAAA	TCCCCGAAGA	CAATCCCGCT	GTGCCTGATA
1601	TGGTCGGCAT	GGGTGGTATG	GCGCGCATGA	TGTAA	

m982.seq

1	ATGGCAGCAA	AAGACGTACA	GTTCCGGCAAT	GAAGTCCGTC	AAAAATGGT
51	AAACGGCGTG	AACATTCTGG	CAAACGCCGT	CCGCGTAACG	TTGGGCCCCA
101	AAGGTCGCAA	CGTAGTCGTT	GACCCGCGAT	TCGGCGCGCC	GCACATCACC
151	AAAGACGGCG	TACACGCTCG	CAAGAAGATC	GAAGTGAAS	ACAAGTTTGA
201	AAATATGGGC	GCGCAAATGG	TGAAAGAAGT	TGCGTCCAAA	ACCAACGACG
251	TGCGACGGCA	CGGTACGACT	ACCCGCCAGT	TACTGGGCGA	ATCCATCGTT
301	GCGGAAGGTA	TGAAATATGT	TACCGCAGG	ATGAATCGGA	CCGACCTGAA
351	ACGCGGTATC	TGAAAGCCG	TCGCCGCTTT	GGTTGACGAA	CTGAAAAACA
401	TCGCAAAACC	TTGCGACACT	TCTAAAGAAA	TCGCCCAAGT	CGGCTCTATT
451	TCGCGCAACT	CCGACGAACA	AGTCGGCGCG	ATTATCGCG	AAGCGATGGA
501	AAAAGTCGCG	AAAGAAGGCG	TGATTACCGT	TGAAGACGGC	AAAGCTTTTG
551	AAAACGAGCT	GGACGTAGTT	GAAGGTATGC	AGTTCGACCG	CGGCTACCTG
601	TCTCTTACT	TCATCAACGA	TGCGGAAAAA	CAATTCGCTG	CTTTGGACCA
651	TCGCTTTGTA	TTGTTTGTCG	ACAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCGTTGTTT	GGACAAGATG	GCAAAAGCCA	GCGCTCCGTT	GTTGATTATC
751	GCTGAAGACG	TAGAAGGCCA	AGCCTTGCGG	ACTTTGGTCG	TGAACAACAT
801	CCGAGGCATC	CTGAAAACTG	TGCGCTGACA	AGGCCCTGGC	TTCCGGCGAC
851	CGCGAAAGC	GATGTTGCAG	GATCTGCCA	TCCTGACGGT	CGGCGTGGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCCTTGGA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAACACC	ACCATCATCG
1001	ACGGCTTTGG	CGACGCAGCC	CAAACTGAAG	CGCGTGTTCG	CGAATATCCG
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GCAAAAGAAA	AACATGCAAGA
1101	GCGCGTGGCT	AAATTGGCAG	GCGGCGTGGC	AGTCATCAAA	GTCGGTGCCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	ACCGGCTGGA	AGACGCGCTG
1201	CACGCTATCC	CGCGAGCCGT	TGAAGAAGGC	GTGGTTGCAG	GCGGCGCGCT
1251	AGCCCTGTTG	GTCGCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGCGAATG
1301	CCGACCAAGA	GCGAGGCGTA	CAAATCGTCT	TGCGCGCCGT	TGAGTCTCCG
1351	CTCGGCCAAA	TCGTTGCCAA	GCGAGCGCGG	GAACCCAGCG	TGCTGTGTGA
1401	CAAGATATTG	GAGGCAAGAG	GCAACTACGG	TTACACGCGT	GCGACGCGCG
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCGC	TGCAACACGC	CGCATCTATC	GCGGCGCTGA	TGCTGACCAC
1551	TGATTTCGATG	ATCGCTGAAA	TCCCAGAA	CAAAACCGCT	GTGCGTGATA
1601	TGGCGCGCAT	GGTGGTATG	GCGGCGATGA	TGTAA	

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m982/g982 95.8% identity in 544 aa overlap

m982.pep MAAKDVFQGNFVRQKMGVNGVILANAVRVTLGPKGRNVVDRAFGGPHITKDGVTVAKEI
::: ::| | ||||| | :|| |||||

1387

g982	IASQNLRFDNRFLOKMNNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
m982.pep	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
g982	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
g982	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
m982.pep	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
g982	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLDIAILTG
	250 260 270 280 290 300
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLDIAILTG
	250 260 270 280 290 300
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
g982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVAVAGGGVALL
	370 380 390 400 410 420
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVAVAGGGVALL
	370 380 390 400 410 420
m982.pep	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKGNYG
	430 440 450 460 470 480
g982	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKGNYG
	430 440 450 460 470 480
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGM
	490 500 510 520 530 540
g982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

```

a982.seq
1  ATGGCAGCAA AAGACGTACA ATTCGGCAAT GAAGTCCGCC AAAAAATGGT
51  AAACGGCGTG AACATTTTGG CAAACGCCGT GCGCGTAACC TTGGGTCCCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCG GCACATCAC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT CGCGTCCAAA ACCAACGACG
251 TGGCGGGCGA CGGTACGACT ACCGCCACCG TATTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATACGT TACCGCCGCT ATGAACCCGA CCGACCTGAA
351 ACGCGGTATC GACAAAGCCG TCGCCGCTTT GGTGAAGAG CTGAAAAACA

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1388

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401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGGA AAAA CAAATCGCCG GCTTGGACAA
651 TCCGTTTGTG TTGCTGTTTC AAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCGGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTAA AGCTCCGGGC TTCGGCGACC
851 CCGCAAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAACCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTGC CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AACTGGCAG GCGGCGTGGC AGTAATCAAA GTCGGTGCCG
1151 CGACCGAAGT GGAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCG TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TC GTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTGTTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCGCGC TGCAACACGC CGCGTCTATC GCCGGCCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCGATGA GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

```

a982.pep
1 MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51 KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSVI
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV L LFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVVNNIRGI L KTVAVKAPG FGDRRKAMLQ DIAILTGGTV
301 ISEEVGLSLE KATLDDLQGA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYDMIE MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGM GMM*

m982/a982 99.3% identity in 544 aa overlap

          10      20      30      40      50      60
m982.pep MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          |||
a982      MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          10      20      30      40      50      60

          70      80      90      100     110     120
m982.pep ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          |||
a982      ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          70      80      90      100     110     120

          130     140     150     160     170     180
m982.pep DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          |||
a982      DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          130     140     150     160     170     180

          190     200     210     220     230     240
m982.pep KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
          |||
a982      KLENELDVVEGMQFLRGYLSFYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
          190     200     210     220     230     240

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1389

	250	260	270	280	290	300
m982.pep	AKASRPLLI IAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLLI IAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
a982	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982.pep	RARAALLENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKGNYGNA					
a982	RARAALLENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKGNYGNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM					
a982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCCTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTCA	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTT
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCGT	CAAAATCGGC	AATCCCAAAA	ATTTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCCG
651	CATCGTGTC	GCCAAAGGCA	GAAGCTTGCC	CAACGAAAgc	tACACACCTT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgtCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCATT	GACGTTGCCA
851	TGAATGTCGC	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTCAGGA	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCCT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TGGCGGACAT
1101	TACGCCGGGA	AAAGAAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	ccgagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAGcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtccacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

1390

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1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGGTCAtgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CTTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

```

g986.pep
  1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVAGMGS I
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVVQRGQ
301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

```

m986.seq
  1 GTGTTCAAAA AATACCAATA CCTCGCTT.G GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGCACAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCA...TGA GGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCGGGC
201 AGTCGTCAAT ATTCAGGCAG CCCC CGCCCC GCGCACCCAA AACGGCAGCG
251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
301 GAATTTTTC AACGCCTCGT CCCGAATATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GCGGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTACAT CTGACCAAT ACCCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCTG CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCGGCCA TCGGCGCGCC CTTGCGCTTC GACAAACAGCG TGACCGCGCG
651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCTT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGCGGGA TTCTGCGGCA TTTCTTTCG CATCCCGATT GACGTTGCCA
851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTCGGCAC AATCGTTTCG
951 TTTGGACAAA GCGGCGGCG CACTGATTGC CAAAATCTG CCCGGCAGCC
1001 CCGCAGAACG TGCGGCGCTG CAGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GCGGAGAGAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GCGGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCC CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTGGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGTTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGAAC ACGCTGTTTA TCGCATTAAA CTTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

```

m986.pep..
  1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVTGMGS I
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVVQRGQ
301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

```

Computer analysis of this amino acid sequence gave the following results:

1391

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
g986	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPAVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
g986	VQSEGPAVVNIQAAPAPRTQNGSGNAETSDPLADSDPFYEFFKRLVPNMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGI ⁹ FAIPIDVAMNVAEQLKNTGKVQRGQ					
g986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

1392

	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQHTDSSGGHVLVVRVSDAAERAGLRRGDEILAVGQVPVNDAGFRKAMDKAGKN					
g986	AGITLQHTDSSGKHLVVRVSDAAERAGLRRGDEILAVGQVPVNDAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1  GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCCGCTC
51  GCTGGCAGGC TGCGACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACGT GTTCAAAGCG AAGGCCGGGC
201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCG GCGCACCCAA AACGGCAGCA
251 GCAATGCCGA AACCGATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTTC AAGCCCTCGT CCCGAACATG CCCGAAATCC CCAAGAAGA
351 AGCAGATGAC GNGGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCACGTCG TTACCGGCAT GGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGGCGCGCC CTTTCGGCTT GACAAACAGC TGACCGCGCG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCTT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGCGCGA TTCATGGGCA TTTCTTCGCG CATCCCGATT GACGTTGCCA
851 TGAATGTCGC CGAACAGCTG AAAAAACACG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCCGGCTG CGGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GGCGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCTGAATC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1  VFKKYQYLAL AALCAASLAG CDKAG--FGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKDGYILTN THVVTGMGSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIFI DVAMNVAEQL KNTGKVRQGO

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1393

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301 LGVIIQEVSY GLAQSFGLK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGHLLVVVR VSDAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

```

m986/a986 98.2% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
a986	VFKKYQYLALAALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
a986	VQSEGPVVNIQAAPAPRTQNGSSNAETDSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGXVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLLVVVRVSDAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
a986	AGITLQTHTDSSGGHLLVVVRVSDAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

```

g987.seq
1 ATGAAACAC GCAGCCTCAT TTCCTTTTA TGCCTCCTC TCTGTTTCATG

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1394

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51  TTCTTCATGG  TTGCCCCCAC  TGAAGAAGC  GACGGAAAGC  CGTCATTTTA
101 ATACTTCCAA  ACCTGTCCTC  CTGGACAACA  TCCTGCAAAT  CCGGCACACC
151 CCTCATAACA  ACGGGCTATC  CGACATCTAC  CTGCTCGACG  ACCCCCACGA
201 AGCCTTTGCC  GCCCGCGCCG  CCCTTATCGA  ATCTGCCGAA  CACAGCCTCG
251 ATTTGCAATA  CTACATTTGG  CGCAACGACA  TTTCCGGCAG  GCTGCTGTTC
301 AACCTCATGT  ACCTTGCCGC  agaacgcggc  GTGCGCGTAC  GCCTGCTGTT
351 ggacgacaAC  AACAcgcgcg  gcttggacga  tctcctGCTC  GCCCTCGACA
401 GCCATCCCAA  TAtctaagtG  CGCCTGTTCA  ACCCCTTcgt  CTTACGCAAA
451 TGGCGCGCAC  TCGGCTACCT  GACCGACTTC  CCCCgcCTCA  ACCGCGCAT
501 GCACAACAAA  TCCTTTACCG  CCGACAACCG  CGCCACCATA  CTCGGCGGAC
551 GCAATATCGG  CGACGAATAC  TTCAAAGTCG  GTGAGGACAC  CGTTTTCGCC
601 GACCTGGACA  TCCTCGCCAC  CGGCAGCGTC  GTCgCGCAAG  TATCGCACGA
651 CTTGACCGC  TACTGGGCAA  GCCATTCCGC  CCACAACGCC  ACGCGCATCA
701 TCCGCAGCGG  CAACATCGGC  AAGGGTCTTC  AAGCACTCGG  ATACAACGAC
751 GAAACATCCA  GACACGCGCT  CCTGCGCTAC  CGCGAAACCG  TCGAACAGTC
801 GCCCCTCTAC  CAAAAAATAC  AGACGGGACG  CATCGACTGG  CAGAGCGTCC
851 AAACCCGCCT  GATCAGCGAC  AGCCCTGCAA  AAGGACTCGA  CCGCGACCGC
901 CGCAAACCGC  CGATTGCCGG  GAGGCTGCAA  GACGCGCTCA  AACAGCCCGA
951 AAAAAAGCGT  TATCTGGTTT  CACCCTATTT  CGTCCCTACA  AAATCCGGCA
1001 CAGACGCACT  GGCAAAACTG  GTGCAGGACG  GCATAGACGT  TACCGTCCTG
1051 ACCAACTCGC  TACAGGCGAC  CGACGTTGCC  GCCGTCCATT  CCGGCTACGT
1101 CAAATACCGA  AAACCGCTGC  TCAAAGCCGG  CATCAAACTC  TACGAGCTGC
1151 AACCCAACCA  TGCCGTCCCC  GCCACAAAAG  ACAAAGGCCT  GACCGGCAGC
1201 TCGTAACCA  GCCTGCATGC  CAAAACCTTC  ATTGTGgacg  gCAAAACGAT
1251 CTTTCATCGC  TCATTCAACC  TCGACCCCG  TTCGCGACGG  CTCATACCG
1301 AAATGGGCGT  CGTCATCGAA  AGCCCCAAA  TCGCAGAACA  GATGGAGCGC
1351 AccctCGCCG  AtacCACACC  CGAATACGCC  TACCGCGTTA  CCTCGACAA
1401 ACACAACCGC  CTGCAATGGC  ACGATCCCGC  CACCCGAAAA  ACCTACCCGA
1451 ACGAACC CGA  AGCCAAACTT  TGA AACGCA  TCGCCGCAA  AATCCTATCC
1501 CTGCTGCCCA  TCGAAGGTTT  ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

```

g987.pep
1  MKTRSLISLL  CLLLCSSSW  LPPLEERTES  RHFNTSKPVL  LDNILQIRHT
51  PHNGLSDIY  LDDDPHEAFA  ARAALIESAE  HSLDLQYYIW  RNDISGRLLF
101 NLMYLAERG  VRVRLLLDDN  NTRGLDLLLL  ALDSHPNI*V  RLFPFVLRK
151 WRALGYLDF  PRLNRRMHNK  SFTADNRATI  LGGRNIGDEY  FKVGEDTVFA
201 DLDILATGSV  VGEVSHDFDR  YWASHAHNA  TRIIRSGNIG  KGLQALGYND
251 ETSRHALLRY  RETVEQSPLY  QKIQTGRIDW  QSVQTRLISD  SPAKGLDRDR
301 RKPPIAGRLQ  DALKQPEKSV  YLVSPYFVPT  KSGTDALAKL  VQDGIDVTVL
351 TNSLQATDVA  AVHSGYVKYR  KPLLKAGIKL  YELQPNHAVP  ATKDKGLTGS
401 SVTSLHAKTF  IVDGKRIFIG  SFNLDPRSAR  LNTEMGVVIE  SPKIAEQMER
451 TLADTTPEYA  YRVTLDKHNR  LQWHPATRK  TYPNEPEAKL  WKRIA AKILS
501 LLPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

```

m987.seq
1  ATGAAAACAC  GCAGCCTAAT  TTCCCTTTTA  TGCCTCCTTC  TCTGTTTCATG
51  TTCTTCATGG  TTGCCCCCAC  TGAAGAAGC  GACGGAAAGC  CGTCATTTTCA
101 ATACTTCCAA  ACCCGTCCGC  CTGGACAACA  TCCTGCAAAT  CCGGCACACC
151 CCTCATAACA  ACGGGCTATC  CGATATCTAT  CTGTTGAACG  ACCCCCACGA
201 AGCCTTTGCC  GCCCGCGCCG  CCCTTATCGA  ATCTGCCGAA  CACAGCCTCG
251 ATTTGCAATA  CTACATCTGG  CGCAACGACA  TTTCCGGCAG  GCTGCTGTTC
301 AACCTCGTGT  ACCTTGCCGC  AGAACGCGGT  GTGCGCGTAC  GCCTGCTGTT
351 GGACGACAAC  AACACGCGCG  GATTGGACGA  CCTCCTGCTT  GCCCTCGACA
401 GCCATCCCAA  TATCGAAGTG  CGCCTGTTCA  ACCCCTTCGT  CTTACGAAAA
451 TGGCGCGCAC  TCGGCTACCT  GACCGACTTC  CCCCgcCTCA  ACCGCGCAT
501 GCACAACAAA  TCCTTTACCG  CCGACAACCG  CGCCACCATA  CTCGGCGGAC
551 GCAATATCGG  CGACGAATAC  TTCAAAGTCG  GTGAGGACAC  CGTTTTCGCC
601 GATTGGACA  TCCTCGCCAC  CGGCAGCGTC  GTCGGCGAAG  TATCGCACGA
651 CTTGACCGC  TACTGGGCAA  GCCATTCCGC  CCACAACGCC  ACGCGCATCA
701 TCCGCAGCGG  CGACATCGGC  AAGGGTCTTC  AAGCACTCGG  ATACAACGAC
751 GAAACGTCCA  GACACGCGCT  CCTGCGCTAC  CGCGAAACCG  TCGAACAGTC
801 GCCCCTCTAC  CAAAAAATAC  AGACAGGATG  CATCGACTGG  CAGAGCGTCC
851 GAACCCGCCT  CATCAGCGAC  GACCCTGCAA  AAGGACTCGA  CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTTCCACCA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCGT
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGT TCGTTCAACC TCGACCCCGG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTTCATCGA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1  MKTRSLISLL CLLLCSSSW LPPIERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAAERG VRVRLLLDDN NTRGLDDLLL ALDHPNIEV RLFNPFVLRK
151 WRALGYLTFD PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPPIAGRLO DALKQPEKSV YLVSPYFVPT KSGTDLAKL VQGDIVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPARSR LNTEMGVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIAAKILS
501 LLPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPIERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
g987	MKTRSLISLLCLLLCSCSSWLPPIERTESRHFNTSKPVLLDNILQIRHTPHNGLSDIY					
	10	20	30	40	50	60
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLLLDDN					
g987	LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLLLDDN					
	70	80	90	100	110	120
m987.pep	NTRGLDDLLLALDHPNIEVRLFNPFVLRKWRALGYLTFDPRNRRMHNKSFTADNRATI					
g987	NTRGLDDLLLALDHPNIXVRLFNPFVLRKWRALGYLTFDPRNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVEVSHDFDRYWASHAHNATRIIRSGDIG					
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVEVSHDFDRYWASHAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR					
g987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	RKPPIAGRLODALKQPEKSVYLVSPYFVPTKSGTDLAKLVQGDIVTVLTNSLQATL					
g987	RKPPIAGRLODALKQPEKSVYLVSPYFVPTKSGTDLAKLVQGDIVTVLTNSLQATL					
	310	320	330	340	350	360
m987.pep	RKPPIAGRLODALKQPEKSVYLVSPYFVPTKSGTDLAKLVQGDIVTVLTNSLQATL					
g987	RKPPIAGRLODALKQPEKSVYLVSPYFVPTKSGTDLAKLVQGDIVTVLTNSLQATL					

1396

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|||||
g987      RKPP|IAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNLSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          |||||
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNTEMGVVIESPKIAEQMERTLA|TTPAYAYRVTLDRHNRLQWHDPATRK
          |||||
g987      SFNLDPRSARLNTEMGVVIESPKIAEQMERTLA|TTPEYAYRVTLDKHNRLQWHDPATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIA|AAKILSLPIEGLLX
          |||||
g987      TYPNEPEAKLWKRIA|AAKILSLPIEGLLX
          490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTTCATGG TTGCCCCCAC TGGAGAAGAC GACGGAAAGC CGTCATTTCAC
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCCG ACTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTC AACCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGTACCT GACCGACTTC CCCCCTCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCCGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGCGCAAG TATCGCACGA
651 CTTGACCCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGCTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT CATCAGCGAC GACCTGCAA AAGGACTCGA CCGCGACCCG
901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGTCA AACAGCCGCA
951 AAAAAGCGTC TATCTGTTT CACCCTATTT CGTCCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGCGCAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACTC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCT GCCACAAAAG ACAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTCATCGGC TCATTCAACC TCGACCCCGG TTCCGCACGG CTAATACTG
1301 AAATGGGCGT TGTTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1  MKTRSLISLL CLLLSCSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERGV VRVRLLLDDN NTRGLDLLLL ALDSHPNIEV RLENPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPP|IAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL

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